GenCore version 5.1.6 Copyright (c) 1993 - .2003 Compugen Ltd.

OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	August 30, 2003, 18:46:00; Search time 1971.58 Seconds (without alignments) 9026.108 Million cell updates/sec
Title: Perfect score: Sequence:	US-08-836-455-1 435 1 ATGGGGGCCCTGCTCAGATCACCATCCAGTAAGCTTGGG 435
Scoring table:	OLIGO_NUC Gapop 60.0 , Gapext 60.0
Searched:	2888711 segs, 20454813386 residues
Word size :	. 0
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Listing first 45 summaries
Database :	Gen Emb1:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	- 488118878888888888888888888888888888888	AC122260 Mus muscul L41880 Mus muscul AJ242670 Mus muscul AJ242670 Mus muscul AB050017 Mus muscul AB050077 Mus muscul AB050084 Mus muscul AB050084 Mus muscul AB050085 CDNA encodi I3291 Sequence 45 M5920 Mouse IG ge L48667 Mus muscul AF14902 Mus muscul AF14902 Mus muscul AF14902 Mus muscul AF139248 Mus muscul AF139248 Mus muscul AF139248 us muscul AF139248 Mus musc
SUMMARIES	05 37 37 449 6AFA 6AFA 88 88 88 84 84 84 96 90 90 90 617 811 811 811 811 811 811 811 811 811 8	0 AC12280 AC1 0 MUSIKCC 0 MW0124267 AJ2 0 MW0124267 AJ2 0 AB05007 AB0 0 AB05007 AB0 0 AB050084 AB0 13291 IJ329 0 MUSIGKAN3 BVS 0 AF045510 AF0 0 AF139248 AF0 0 AF13
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a Query e Match	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0	000 23.0 20 999 22.8 97 22.3 97 22.1 98 22.1 991 20.9 991 20.9 90 20.7 90 20.7 90 20.7 90 20.5 89 20.5 89 20.5 89 20.5 89 20.5 89 20.5 89 20.5 89 19.8 10.0000000000000000000000000000000000
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Result No.		C 31 33 34 35 36 36 37 38 39 40 40 41 42 44 44 45 44 45 60 60 60 60 60 60 60 60 60 60 60 60 60

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AF124721 381 bp mRNA linear ROD 22-MAY-2001
Mus musculus immnogloblín light chain mRNA, partial cds.
AF124721
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Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
Location/Qualifiers
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Coonstruction and characterization of a chimeric fusion protein consisting of an anti-lidiotype antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF 99306687
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Pred. No. 2.6e-258;
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                        Location/Qualifiers
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/mol_type="genomic DNA"
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a 111 c 102 g 122
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Chatterjee, S.K. and Tripathi, P.K.
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Chatterjee, M. and Foon, K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11D10
Patent: JP 2001523269-A 1 20-NOV-2001;
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                                                                                       GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
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7A CHATTERJEE, KENNETH A FOON

A61K39/395,A61K39/39//C07K16/42

Strandedness: Single;
                                                                                        Score 435; DB 6; I
Pred. No. 2.6e-258;
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13-JUN-1997 US 60/0495
              1. .435 /organism="unknown"
Location/Qualifiers
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JP 2001523269-A/1.
unidentified
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ACCESSION VERSION KEYWORDS

ORGANISM REFERENCE AUTHORS

SOURCE

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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  мизысыдка 303 bp mRNA linear ROD 27-APR-1993
Mouse Ig kappa-chain mRNA V region, partial cds, from hybridoma
H220-23.
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Avaler, J., Caton, Staudt, L.M., Schwartz, D. and Gerhard, W. A set of closely related antibodies dominates the primary antibody response to the antigenic site CB of the A/PR/8/34 influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 ATCAGCAGCCTTGAGTCTGAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Original source text: Mouse (strain BALB/c), cDNA to mRNA, from hybridoma H220-23.
Draft entry and computer-readable sequence for [J. Immunol. (1990) In press] kindly submitted by J.Kavaler, 06-JUL-1990.
Location/Qualifiers
1. 303
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Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma University Health Sciences Center, 940 St. Young Blvd, Oklahoma City, OK 73190, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 GATTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCT
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Pred. No. 1.5e-60;
0; Mismatches 2;
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Local Similarity 99.1%;
nes 217; Conservative
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/protein_id="AAK55120.1"
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FVAXYCLQYASSPYTFGGGTKLEIK"
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AF163749.1 GI:5690304
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Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.
Molecular analysis of cross-reactive anti-myosin/anti-streptococcal
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

    >>381
/note="anti-idiotype antibody 11D10; mimics a breast
cancer-associated antigen, human fat globule (HMFG)"

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                                                                                                                                                                                                                                                                                                                     86.7%; Score 377; DB 10; Length 3: 100.0%; Pred. No. 3e-222; 1ve 0; Mismatches 0; Indels
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Mol. Immunol. 37 (15), 901-913 (2000)
21179651
               /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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Mertens, N.M. and Cunningham, M.W.
Direct Submission
                                                                     /db_xref="taxon:10090"
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Mus musculus
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Gaps

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282

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302 bp mRNA linear ROD 14-SEP-2001
Mus musculus anti-DNA immunoglobulin light chain IgG, antibody
363s, partial cds.
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Marion.T.N.
Direct Submission
Submitted (18-APR-1996) Tony N. Marion, Dept. of
Microbiology/Immunology, University of Tennessee, 858 Madison Ave.,
Memphis, TN 38163, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="anti-DNA immunoglobulin light chain IgG"
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/protein_id="1870292"
/db_xref="id:1870292"
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IYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGGGTKL"
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                                                                                                                                                                                                                                                                                                         ENKATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 302).
Krishnan,M.R., Jou,N.T. and Marion,T.N.
Correlation between the amino acid position of arginine in VH-CDR3 and specificity for native DNA among autoimmune antibodies 96399071
                 285 CAGCAGCCTTGAGTCTGAAGATTTTGTAGCCCTATTACTGTCTACAATATGCTAGTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
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Pred. No. 2.4e-54;
0; Mismatches 2; Indels
                                                               345 GTACACGTTCGGAGGGGGGGCCCAAGCTGGAAATAAAACG 383
                                                                              285 GTACACGTICGGAGGGGGACCAAGCTGGAAATAAACG 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="taxon:10090"
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Mus musculus
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llarity 99.0%;
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                                                                                                                                                                                                                            /translation="SPSSLSASLGERVSLTCRASQDIGSSLNWLQQEPDGTIKRLIYA
TSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGGGTKLXIK"
71 c 70 g 83 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204
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                                                                                                                                                                            /product-"immunoglobulin kappa-chain VK-1"
/protein_id-"AAA39105.1"
/db_xref-"GI:197632"
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Pred. No. 5.8e-55;
0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xxef="taxon:32630"
/note="light chain AB 6H4"
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                                                                           /tissue_type="hybridoma"
1.303
/gene="IgM"
<1.>303
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Sequence 2 from Patent WO03025181.
AX722008
AX722008.1 GI:30422583
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/map="chromosome 6"
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/strain="BALB/c"
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synthetic construct
artificial sequences.
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Matches 208; Conservative
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Best Local Similarity 99.4
Matches 158; Conservative
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PAT 10-0CT-2001
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                 Length 771;
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24.6%; Score 107; DB 6; L
99.0%; Pred. No. 2.5e-54;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
1 358 c 407 g 368 t
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Sequence 1 from patent US 6291208.
AR169918.1 GI:17907877
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synthetic construct
artificial sequences.
                                   Best_Local Similarity 99.0
Matches 207; Conservative
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Matches 207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuschel, R. Riethmueller, G., Lutterbuese, R., Borschert, K., Kischel, R., Mayer, M. and Hofmelster, R. Multifunctional polypeptides comprising a binding site to epitope of the nkg2d receptor complex Patent: WO 0171005-A 66 27-SEP-2001;
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                                                                                     linear
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/db_xref-"taxon:32630"
190 c 206 g 194 t
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Sequence 66 from Patent WO0171005.
AX256296
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Sequence 54 from Patent W00171005.
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Location/Qualifiers
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Query Match

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 AX256284

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REFERENCE AUTHORS 1302

222

RESULT 9
AX256296
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VERSION
KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

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/codon_start=2
/codon_start=2
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GSRSGSDYSLTISSLESEDFVDYXCLQYASSPVDVRWRHQAGNQT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (O2-OCT-1990) Yamagishi H., Dept of Biophysics Faculty of
Science Kyoto University, Sakyo-ku Kyoto 606, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAVJIG7 25-JUL-2002 ONA linear ROD 25-JUL-2002 Mouse rearranged kappa immunoglobulin light chain (V,J).
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                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 269)
                                                           1 (bases 1 to 387)
Anand,N.N., Barber,B.H., Cates,G.C., Caterini,J.E. and Klein,M.H.
Cates,G.C., Caterini,J.E. and Klein,M.H.
Thimeric antibodies for delivery of antigens to selected cells of
the immune system
Patent: US 6291208-A 1 18-SEP-2001;
Location/Qualifiers
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Lack of feedback inhibition of V kappa gene rearrangement productively rearranged alleles
J. Exp. Med. 173 (2), 409-415 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                 108 TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 149
                                                                                                                                                                                                                                   23.4%; Score 102; DB 6; I
100.0%; Pred. No. 3.2e-51;
ive 0; Mismatches 0;
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1. .199
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X54760.1 GI:21998644
Ig light chain; immunoglobulin.
Mus musculus (house mouse)
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95 c 90 g
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Best Local Similarity 100.
Matches 102; Conservative
                                            Unclassified.
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273 bp mRNA linear ROD 14-FEB-1996 Mus musculus immunoglobulin kappa chain V-J regions mRNA, clone . U21066
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/translation="LSGRKSQSHCRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDSG
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                                                                                                                                                                                                                           B cell selection and allelic exclusion of an anti-DNA Ig transgene in MRL-lpr/lpr mice J. Immunol. 154 (9), 4444-4455 (1995)
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/product="immunoglobulin kappa chain variable and joining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 273) Roark,J.H., Kuntz,C.L., Nguyen,K.A., Mandik,L., Cattermole,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-FEB-1995) Jessica H. Roark, Wistar Institute, 3601
Spruce St., Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                     163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
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/cell_type="splenic B cell hybridoma"
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Pred. No. 5.5e-50;
); Mismatches 1;
                                                                                                                    Ouery Match 23.0%; Score 100; DB 10; Best Local Similarity 99.3%; Pred. No. 5.5e-50; Matches 150; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                     /note="V kappa gene segment"
200. .267
/note="J kappa gene segment"
a 61 c 65 g 74 t
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99.3%;
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Best Local Similarity 99.3
Matches 150; Conservative
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PAT 29-SEP-1999
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Smith, R., McCafferty, J., Chiswell, D., Darsley, M.J., Fitzgerald, K.,
Kenten, J.H., Martin, M.T., Titmas, R.C. and Williams, R.O.
Isolation and production of catalytic antibodies using phage
technology
Patent: US 5855885-A 44 05-JAN-1999;
Location/Qualiflers
1. 276
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                                                                   163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 276)
Smith, R., McCafferty, J., Chiswell, D., Darsley, M.J., Fitzgerald, K., Kenten, J.H., Martin, M.T., Titmas, R.C. and Williams, R.O.
Isolation and production of catalytic antibodies using phage
            163 IGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
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                                                                                                        199 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 229
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Patent: US 5855885-A 52 05-JAN-1999;
                                                                                                                                                                                                      AR026090 276 bp 1
Sequence 44 from patent US 5855885;
AR026090.1 GI:5936930
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Sequence 52 from patent US 5855885.
AR026094
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65 c 64 g
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                                                             163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
                        0;
Length 276;
                        Indels
Score 100; DB 6;
Pred. No. 5.5e-50;
0; Mismatches 1
                                                                                                                                                             199 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 229
                                                                                                                                                283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313
                                                                                                                                                                                                             Search completed: August 30, 2003, 21:04:54 Job time : 1972.58 secs
 23.0%;
Query Match 23.0
Best Local Similarity 99.3
Matches 150; Conservative
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August 30, 2003, 17:38:10 ; Search time 190.312 Seconds (without alignments) 6170.144 Million cell updates/sec
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1 ATGGGGGCCCCTGCTCAGAT......CACCATCCAGTAAGCTTGGG 435
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              2552756 seqs, 1349719017 residues
                                                                           OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Post-processing: Listing first 45 summaries

N_Geneseq_19Jun03:*

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| SIDS1/gcgdata/geneseq-geneseqn-embl/NA2001.B.DAT:*
| SI

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Murine monoclonal	Antibody 11D10 lig	Mouse 11D10 antibo	P4-3 single chain	P5-10 single chain	3B10xP4-3 bispecif	Murine anti-human	Murine 44H104 mab
SUMMARIES	ID	AAT85149	AAV83772	AAL51273	AAS97136	AAS97142	AAS97145	AAT77851	AAD32138
	DB	18	20	25	24	24	24	18	24
	Length	435	435	435	756	771	1497	387	387
æ	Query Match Length DB ID	100.0	100.0	100.0	24.6	24.6	24.6	23.4	23.4
	Score	435	435	435	107	107	107	102	102
	Result No.	-	7	9	4	S	9	7	8

Mouse derived RT3	Mouse derived RT3	Sequence encoding	Consensus DNA segu	DNA encoding anti-	Murine m166 antibo	Mouse monoclonal a	Human secreted exp	Antibody 3G2 light	TSH receptor antib	TSH receptor antib	WOW-1 Fab light ch	Mouse DNA encoding	Mouse antibody F4-	Nucleotide sequenc	Chimeric antibody	MAD 4197X light ch	Mouse anti-IL-18 a	Mouse light chain	pEscFv#125-2H reco	pEscFv#125-2H.HT r	Monoclonal antibod	TSH receptor antib	TSH receptor antib	Mouse DNA encoding	Murine antibody 1D	Mouse anti-idiotyp		R6-5-D6 anti-ICAM-	ICAM-1 inhibiting	Mouse secreted exp	Mouse DNA encoding	650E2 hybridoma VL	Filamentous phage	Fialmentous phage	cDNA for Ig light	_
AAX00879	AAX00875	AAN30165	AAV20086	AAQ90431	ABS52791	AAT85091	AAA44346	AAT87818	ACC44908	ACC44909	AAA27849	ABX16574	AAQ92503	AAZ61037	AAN91657	AAQ85387	AAZ49534	AAZ49548	AAZ49542	AAZ49543	AAQ48038	ACC44928	ACC44929	ABX16570	AAD13177	AAT70809	AAQ14801	AAQ14651	AAQ27140	AAA43470	ABX16572	AAA38909	AAC66996	AAC67002	AAT96344	AAT96346
20	20	4	19	16	24	18	21	17	25	25	21	25	16	21	10	16	21	21	21	21	14	22	22	25	22	18	12	12	13	21	25	21	22	22	18	18
276	276	450	535	438	979	642	651	652	654	654	678	869	723	738	639	465	324	407	711	729	882	654	654	729	426	438	537	537	366	451	504	321	456	867	360	1848
23.0	23.0	23.0	21.4	20.7	19.8	19.5	19.5	19.5	19.5	19.5		19.5	٠		19.3	19.1		18.9	18.9	18.9				٠	٠	18.2			•		٠		•	16.8	16.1	16.1
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σ.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
                                                          Murine monoclonal anti-idiotype antibody 11D10 VL cDNA.
                                                                                                                   Location/Qualifiers
AAT85149 standard; cDNA; 435 BP.
                                                                                                                                                                                                                    95US-0575762.
96US-0591965.
96US-0766350.
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                                 (updated)
(first entry)
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/*tag=
61..435
/*tag=
                                                                                                                                                                                                                    20-DEC-1995;
26-JAN-1996;
13-DEC-1996;
                               25-MAR-2003
04-JAN-1998
                                                                                                                                                                     WO9722699-A2.
                                                                                                    Mus musculus
                                                                                                                                                                                                     19-DEC-1996;
                                                                                                                                                                                    26-JUN-1997
                                                                                                                            sig_peptide
                                                                                                                                            mat_peptide
                AAT85149;
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61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAGAGTCAGT 120
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                                                                                            Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the coding sequence for the murine antibody 11D10 light chain variable region. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma,
                                                                                                                                                                                                                                    /*tag= a
/product= "antibody 11D10 light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AFGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT
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/note= "no stop codon is given at the 3' end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delaying development of, or treating, HMFG-associated tumours - using anti-idiotype antibody 11D10 raised against antibodies to human milk fat globule protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 435; DB 20; Length 435; 100.0%; Pred. No. 6.5e-210;
                                                       Antibody 11D10 light chain variable region coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
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                                                                                                                                                                                           Location/Qualifiers
1..435
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97US-0049540.
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                                                                                                                                                                                                                                                                                                                                                         /*tag=
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P-PSDB; AAW87593.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   W09856419-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-1997;
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                  16-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CTCACTTGTCGGCCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                   This cDNA sequence encodes the light chain variable region VL (AAM85149) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line Arcc 12020. 11D10 was obtained by immunising naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tunnours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are aliagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMFG-
                                                                                                                                                    Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours, especially breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 435;
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                                                     Chatterjee M, Chatterjee SK, Foon KA;
                                                                                                                                                                                                                                Claim 11; Page 94; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV83772 standard; cDNA; 435
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Matches 435; Conservative
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              (KENT ) UNIV KENTUCKY
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Query Match

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AAV83772;

RESULT 2 AAV83772

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delaying the development, of or treating HMFG/CEA-associated tumours. present cDNA sequence encodes the light chain variable region of the mouse 11D10 anti-idiotype antibody.
                                              Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
                                                                 ; Score 435; DB 25;
; Pred. No. 6.5e-210;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 435; Conservative 0
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/product- "Mouse 11D10 anti-idiotype antibody light chain
variable region"
/note= "No stop codon is given"
                                                                                                   GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 420
                                                                              360
                                                                                                                        GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for RMFG (e.g. 3H1). The method is useful for
                                                                                                                                                                                                                                                                                                                      HMFG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
                                                                   GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG
              AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                                                                                                                                                                                                                                             Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA; 11D10; 3H1; HWFG-associated tumour; anti-idlotype antibody.
                                                                                                                                                                                                                                                                                            Mouse 11D10 antibody light chain variable region coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                           AAL51273 standard; cDNA; 435 BP
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61..435
/*tag= 0
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/*tag=
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                                                                                                                                                                                                            GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCTCTCTGGGACAAAGAGTCAGT
                                                                                                                                                                                                                                                                           CTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA
                                                                                                                                                                                                                                                                                                 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                               GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG
                                                                                                                                                                                 61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT
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                                                                                       1 ATGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT
                                           Gaps
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435;
Length
                                           Indels
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Borschert K, Kischel R;

Lutterbuese R,

o,

(KUFE/) KUFER P.

26-MAR-2001; 2001WO-EP03414. 24-MAR-2000; 2000EP-0106467

WO200171005-A2. Homo sapiens.

27-SEP-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC 282
                                                                                                                                                                                                                                                                                      The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NGGD receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, meloma, leukeses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 GATTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                    recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating
                     Borschert K, Kischel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune hepatitis. The sequences represent DNA encoding the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 107; DB 24; Length 756; 99.0%; Pred. No. 5.5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 756 BP; 184 A; 180 C; 204 G; 188 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                     Lutterbuese R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 CCGTACACGTTCGGAGGGGGGACCAAGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Fig 16; 114pp; English.
                                                                                                                                                                                                             cancers and infectious diseases
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                     Riethmueller G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P5-10 single chain Fv DNA.
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Matches 207; Conservative
                                       Hofmeister R;
                                                                                 WPI; 2002-055119/07
                                                                                                      P-PSDB; AAU72862
                   Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKGDr receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, cosphagus, colon, liver, intrahepatic bile ducts, pancreas, lung, ladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protocoa or helminiths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent autoimmune hepatitis. The sequences represent DNA encoding the autoimmune hepatitis. The sequences represent DNA encoding the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 GGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.6%; Score 107; DB 24; 99.0%; Pred. No. 5.5e-44; ive 0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                     cancers and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.07
Matches 207; Conservative
                                                                                                                                                                                                                    Riethmueller
Hofmeister R;
                                                                                                                                                                                                                                                                   WPI; 2002-055119/07
P-PSDB; AAU72868.
                                                                                                                                                                                                                     Kufer P,
Mayer M,
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AAS97145 standard; DNA; 1497

RESULT 6 AAS97145 AAS97145;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancras, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 GGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1497 BP; 364 A; 358 C; 407 G; 368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 107; DB 24;
Pred. No. 5.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                3B10xP4-3 bispecific single chain Fv DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.6%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2001; 2001WO-EP03414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-2000; 2000EP-0106467
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ິບ
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Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riethmueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-055119/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAU72871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200171005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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antibody specific for a surface structure of antigen presenting antibody specific for a surface structure of antigen presenting cells (APC), genetically modified to contain at least one antigen exclusively at one or more preselected sites. The conjugate is capable of delivering the antigen to APC and eliciting an immune response to the antigen. The new conjugates are useful as vaccines and are able to elicit an enhanced immune response without the use of an adjuvant. In a specific example, a conjugate was constructed using the murine anti-human class II monocional antibody secreted by hybridoma anti-human persent sequence concodes the light chain variable region which was PCR amplified from 44H104 and used in the preparation of a conjugate with antigen CLTB36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                          Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.
                                                                                                                                                                                                                                     Antibody; light chain; variable region; hybridoma cell line 44H104; immune response; enhance; stimulate; vaccine; immunodiagnosis; antigen delivery; ss.
                                                                                                                                                                                                                                                                                                                                                                        a
"Encodes 44H104 light chain variable region,
including secretion signal; termination
codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant conjugate antibody mol., modified for delivering an antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 23.4%; Score 102; DB 18; Length 387; Best Local Similarity 100.0%; Pred. No. 1.9e-41; Matches 102; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cates GC,
                  343 CCGTACACGTTCGGAGGGGGGACCAAGCT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caterini JE,
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..387
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1A; 64pp; English.
                                                                                                            AAT77851 standard; cDNA; 387 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-CA00400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0483576.
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anand NN, Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-077271/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immuno:diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW22537
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9640941-A1.
                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1996;
                                                                                                                                                                           03-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-DEC-1996
                                                                             RESULT 7
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42 GTTTCCAGGTACCAGATGTGACATCCAGATGACCCCAGTCTCCATCCTCCTTATCTGCCTC 101

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283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCT 342-

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48 GITICCAGGIACCAGAIGIGACACCACAGAIGACCACCAGTCTCCATCCTCCTTATCIGCCTC 107
               42 GTTTCCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-1993;
14-JUL-1994;
                                                                                                                                                                                                                                             29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin MT,
                                                                                                                                                                                                                                                                                                        Catalytic;
                                                                          102
                                                                                                                                                                                                              AAX00879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIS/)
(DARS/)
                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                    AAX00879
                                                                                                                                                     RESULT
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The invention relates to a recombinant conjugate antibody, comprising a monoclonal antibody specific for a surface structure of antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presenting cells genetically modified to contain an antigen molety for the purpose of delivery of the antigen moiety to antigen-presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable
                                                                                                                                                                                                                                                                        Murine; mab; light chain; VL; conjugate antibody; antigen delivery; immune system; vaccine; detecting agent; antibacterial; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                      /product "Murine 44H104 mab VL"
/troduct (pos:277...279, aa:Thr)
/note This translation exception occurs while decoding for murine mab VL alternative version (AAE20204); CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.4%; Score 102; DB 24; Length 387; Ilarity 100.0%; Pred. No. 1.9e-41; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cates GA, Caterini JE, Klein MH;
                                              TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 143
                                                            TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
                                                                                                                                                                                                                                            Murine 44H104 mab variable light chain (VL) DNA.
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1A; 28pp; English.
                                                                                                                                                   AAD32138 standard; DNA; 387 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0007093.
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                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BARBER B H.
CATES G A.
CATERINI J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anand NN, Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             light chain (VL) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BARB/) BARBER B H.
(CATE/) CATES G A.
(CATE/) CATERINI J E
(KLEI/) KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-267519/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002025315-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JAN-1998;
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                                                                                                                                                                                                               18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2002.
               48
                                            102
                                                                                                                                                                                 AAD32138;
                                                                                                                                                                                                                                                                                                                      Mus sp.
                                                                                                                        RESULT
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The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a mary peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for
                                                                                                                                                                                                        Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
                                                                                                                                                                                                                                          antibody; phage display; immunising; phage expression vector;
                                                                                                                                                                                                                                                                                                                                       1..276
/*tag- a
/note= "the start and stop codons are not indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams RO;
                TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 149
TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kenten JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fitzgerald K, Kenten
Smith R, Titmas RC,
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 11; 117pp; English.
                                                                                                             AAX00879 standard; DNA; 276 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0273146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0007684
94US-0273146
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Darsley MJ,
McCafferty J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FITZ/) FITZGERALD K. (KENT/) KENTEN J H. (MART/) MARTIN M T. (MCCA/) MCCAFFERTY J. (SMITA/) SMITH R. (TITM/) TITMAS R C. (WILL/) WILLIAMS R O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DARSLEY M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-105036/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                           prodrug; scFV; ss.
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10-MAR-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAN30165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                 163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 222
                                                                                                                                                                                                                                                                       223 GGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFV; ss.
catalytic activity to substrate, and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of light chain PCR pattern C from mouse derived RT3 phage antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
                                                                                                                                                                                                                  Gaps
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/note= "the start and stop codons are not indicated"
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                                                                                                                                                                          DB 20; Length 276;
                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fitzgerald K, Kenten JH;
Smith R, Titmas RC, Wi
                                                                                                                                 Sequence 276 BP; 67 A; 65 C; 64 G; 80 T; 0 other;
                                                                                                                                                                      Score 100; DB 20
Pred. No. 2e-40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX00875 standard; DNA; 276 BP.
                                                                                                                                                                      23.0%;
ilarity 99.3%;
Conservative
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94US-0273146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chiswell D, Darsley MJ,
Martin MT, McCafferty J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITM/) TITMAS R C. WILL/) WILLIAMS R O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DARSLEY M J.
FITZGERALD K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCCAFFERTY J. SMITH R.
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 150; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-105036/09.
P-PSDB; AAW95476.
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MARTIN M T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHISWELL D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-1993;
14-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX00875;
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(MCCA/)
(SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PITZ/)
(KENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX00875
   8888888
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displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains from the immunised animal; cloning the VH and VL domains from the selected phage display antibodies for catalytic antigodies for catalytic activity to substrate; and isolating the catalytic antibodies.

Where the phage expression vector incorporates a histidine peptide in catalytic antibodies, which can be used for in vivo activation of a produce catalytic antibodies, which can be used for in vivo activation of a produce. The present sequence represents a generic sequence of light chain pattern A from mouse derived RT3 phage antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1) TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                           The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene 1
inserting coding into a phage expression vector and isolating the catalytic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoding the leader, variable region and first 16 AAs of
the constant region of the kappa-chain (light chain) of MOPC41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 100; DB 20; Length 276;
Pred. No. 2e-40;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 276 BP; 68 A; 65 C; 63 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= variable region 403..450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= c
/product= constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis; therapy; immunoglobulin; ss
                                                                                                            Example 4; Fig 9A-F; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
13..78
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79..402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.0%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAN30165 standard; DNA; 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83EP-0001655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= b
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Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-1983
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343 CCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                active against human alpha4-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha4-beta7 integrin binding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Variable regions were amplified from DNA encoding to primers Av2003-84. The degeneracy of the PCR primers Av2003-84. The degeneracy of the PCR primers produced several different sequence, of which the present sequence is a consensus sequence. The present sequence was used to construct chimeritc, humanised Act-1 antibodies, which contain mutine antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infilitation of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising the variable region of murine Act-1 antibody determined from several independent mouse light chain variable region clones. Act-1 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the consensus nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region, ds.
                                                                                                                                                                                                                                                                                                                            Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 535;
                                                                                                                                                                                             Ringler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding anti-idiotype antibody Idio17 clone 17KB1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 535 BP; 126 A; 128 C; 132 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 93; DB 19; I
Pred. No. 6.7e-37;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 GTATCCATCTTCCCACCATCCAGTAAGCTTGGG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 GTATCCATCTTCCCACCATCCAGTAAGCTTGGG 465
                                                                                                                                                                                             Ponath PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection, isolation and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 3; 145pp; English.
                                                                                                                                                                                             Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 21.4%; Soc
Local Similarity 100.0%; Pi
es 93; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ90431 standard; DNA; 438 BP.
                                                                                                        96US-0700737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1996 (first entry)
                                                                                                                                                                                               Jones ST,
                                                                                                                                                    (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                                                              WPI; 1998-159172/14.
                                                                                                                                                                                                                                                                                     P-PSDB; AAW53817
                                                              06-AUG-1997;
                                                                                                                                                                                               Bendig MM,
Saldanha J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ90431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ9043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GATICIGGIGICCCCAAAAGGIICAGIGGCAGIAGGICIGGGICAGAIIATICICICACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGGTTATTCTCTCACC
                                                                                                                                                                                                                                                                                                                                                                                           The pref. vector or plasmid of the invention has a double-stranded DNA seq. coding for a variable region of a light or heavy chain of IgG, or for a variable region of a light or heavy chain of an immunoglobulin specific for an enzyme or surface protein. The sequence esp. codes for a variable region of a light chain having 95-115 AAS or for a variable region of a heavy chain having 110-125 AAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
inflammatory bowel disease; ss.
                                                                                                                                                                                                                                              Transformed expression vectors or plasmid(s) - with double stranded DNA sequence coding only for desired part of polypeptide chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus DNA sequence of the murine variable light chain region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.0%; Score 100; DB 4; Length 450; llarity 99.3%; Pred. No. 1.9e-40; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 450 BP; 108 A; 114 C; 104 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             __dg_ a /note= "no stop codon given" 16.75 /*tag= b 76.435 /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AAs or for a variable region of a heavy chaesp. including the D region of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ATCAGCAGCCTTGAGTCTGAAGATTTTGTAG 331
                                                                                                                                                                                                                                                                                                                                                      Example; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV20086 standard; DNA; 535 BP
                  82US-0358414
83US-0558551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                    Moore KW, Zaffaroni A;
                                                                              (SCHE ) SCHERING CORP. (DNAX-) DNAX RES INST.
                                                                                                                                                                                             WPI; 1983-772290/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 150; Conserv
                                                                                                                                                                                                                    P-PSDB; AAP30251
                  15-MAR-1982;
05-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9806248-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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us-08-836-455-1.oli.rng

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AAT85091;
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                                                                                                                                                                                                                                                                                                                               a
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                                                                                                                                                                                                                                                                               346 TACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTA 405
                                                                                                                                                                                                                                                                                         AAQ90425-Q90434 are DNA molecules encoding anti-idiotype antibodies Idio3, Idio17, Idio20, Idio27 and Idio33 against a human anticancer monoconal antibody. These antibodies and DNA encoding them are useful in pharmacological, medical and blochemical fields of research.
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                      Novel anti-idlotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; m166 light chain; gene; ss; antibacterial; PcrV antigen; Pseudomonas aeruginosa infection.
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                Length 438;
                                                                                                                                                                                                                                                                0; Indels
/product= anti-idiotype_antibody_Idio17
1..39
                                                                                                                                                                                                                               Sequence 438 BP; 104 A; 120 C; 112 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Murine m166 light chain"
                                                                                                                                                                                                                                               Query Match 20.7%; Score 90; DB 16; L
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                               406 TCCATCTTCCCACCATCCAGTAAGCTTGGG 435
                                                                                                                                                                                                                                                                                                                        Murine m166 antibody light chain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                      Example 5; Page 19; 28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                       ABS52791 standard; cDNA; 979 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2001; 2001US-0770916.
29-JAN-2001; 2001US-264795P.
                                                               93JP-0272950.
                                                                               93JP-0272950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2002; 2002WO-US02382
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MCWR-) MCW RES FOUND INC.
               /*tag=
                                                                                                               WPI; 1995-182987/24.
                                                                                               (HAGI/) HAGIWARA Y.
                                                                                                                      P-PSDB; AAR74966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200264161-A2.
                               JP07101999-A
                                                                               36-OCT-1993;
                                                              36-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2002
        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-2002
                                               18-APR-1995
                                                                                                                                                                                                                                                                                                                              394
                                                                                                                                                                                                                                                                                                                                                                                       ABS52791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds sn.
                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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The invention relates to a method of inhibiting Pseudomonas aeruginosa infection by inoculating a patient with PcrV antigen. Or inoculating a patient with a gene vaccine encoding the PcrV antigen. The method is useful for inhibiting P.aeruginosa infection in a patient, preferably a human patient, for treating P.aeruginosa infection, where the infected patient is incculated with PcrV antigen, and for diagnosing P.aeruginosa infection. An antibody to the antigen, or its fragments, (preferably monoclonal antibodies) is useful for modulating cytotoxicity of Pseudomonas to a human cell which involves contacting the Pseudomonas with the antibody in the presence of the human cell. A pharmaceutical composition comprising the monoclonal antibodies can be used for treating or preventing Pseudomonas infection, or for reducing pathogenicity of Pseudomonas in a patient. This sequence represents cDNA encoding a murine mi66 antibody light chain polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 CTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                               Inhibiting Pseudomonas aeruginosa infection by inoculating a patient with PcrV antigen, or inoculating a patient with a gene vaccine encoding the PcrV antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 979;
                                                                RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse monoclonal antibody B9 light chain encoding cDNA.
                                                                Frank DW, Wiener-Kronish J, Yahr TL, Sawa T, Fritz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 979 BP; 285 A; 259 C; 204 G; 231 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.8%; Score 86; DB 24; I
llarity 100.0%; Pred. No. 2.3e-33;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not shown"
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1..642
//tag= a /
/produc= B9L
/note= "stop codon no
                                                                                                                                                                                                                                                                                                                                             Example 6; Fig 7; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT85091 standard; cDNA; 642 BP
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/label= Ckappa
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(REGC ) UNIV CALIFORNIA.
                                                                                                                           WPI; 2002-636608/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 86; Conserv
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DNA encoding mouse antibody binding human plasma apo-lipoprotein B-100 - useful for removing arteriosclerotic lipoprotein(s)
                (KOAD ) KOREAN SCI & TECHNOLOGY RES CENT.
                                                                                  Claim 4; Fig 6; 17pp; Japanese.
95KR-0039459
                                 WPI; 1997-367067/34.
P-PSDB; AAW27089.
02-NOV-1995;
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The present sequence encodes the mouse monoclonal antibody B9 light chain (B9L), which binds specifically to human blood apolipoprotein B-100. The nucleic acid can be used in a method for the preparation of a reconstituted antibody which specifically binds human plasma apolipoprotein B-100. The antibody can be used as a reagent for determining the concentration of human plasma apolipoprotein B-100 in a sample. The antibody is also useful in a drug composition for selectively removing arteriosclerotic lipoproteins containing human plasma apolipoprotein B-100.

Sequence 642 BP; 188 A; 152 C; 152 G; 150 T; 0 other;

342 TCCGTACACGTTCGGAGGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAAC 401 0; Gaps Score 85; DB 18; Length 642; Pred. No. 7.4e-33; 0; Mismatches 0; Indels 402 TGTATCCATCTTCCCACCATCCAGT 426 Query Match 19.5%; Scc Best Local Similarity 100.0%; P: Matches 85; Conservative 0; g ò ò

Search completed: August 30, 2003, 19:57:02 Job time : 191.312 secs

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Sequence 1, Appli
Sequence 5, Appli
Sequence 17, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 27, Appl
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Sequence 20, Appl
Sequence 10, Appl
Sequence 16, Appl
Sequence 95, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 10, Appl
                                                                            August 30, 2003, 19:44:55; Search time 158.756 Seconds (without alignments) 6286.388 Million cell updates/sec
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                                                                                                                                                                   1 ATGGGGGCCCCTGCTCAGAT......CACCATCCAGTAAGCTTGGG 435
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                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/pubpna/US10n_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-840-459-101
US-10-006-773-14
US-10-268-883-10
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US-09-224-099-11

US-09-924-099-11

US-09-924-099-20

US-09-924-099-20

US-09-924-099-20

US-09-779-784-16
                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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US-09-007-093-1
US-08-779-784-17
                                                                                                                                                                                                                                          1533700 seqs, 1147125425 residues
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                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                      - nucleic search, using sw model
                                                                                                                                                                                                OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                        US-08-836-455-1
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Match Length
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223.4.8
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9,	Sequence 9, Appli Sequence 10, Appl	, v, -	Sequence 1, Appii Sequence 1, Appli	ω, α,	Sequence 18, Appl Sequence 34, Appl	Sequence 22, Appl	, 10°	Sequence 3, Appli Sequence 17, Appl	11,	11,	8,	_	Sequence 13, Appl	13,	20,	Sequence 7, Appli	Sequence 3, Appli	Sequence 27, Appl	Sequence 5, Appli	-	Sequence 3, Appli	GENERAL INFORMA	
929-665-	US-09-929-546-9 US-09-929-546-10 US-09-887-853-5	US-10-146-305-5	US-US-390-205-1 US-10-153-401-1	96-60-8	US-08-779-784-18 US-09-726-258-34	US-10-281-479A-22	US-10-216-484-10	US-US-303-32/A-3 US-10-176-380-17	US-09-897-006-11	US-09-897-511A-11	US-00-897-006-8	US-09-897-511A-8	US-09-897-006-13	US-09-897-511A-13	US-09-905-243-20	US-09-919-344-7	US-09-797-941A-3	US-09-905-243-27	US-09-797-481-5	US-09-800-908-10	US-09-469-485-3	US-10-195-752-2	•
111	111	13	14	1	11 8	12	14	1 4	10	1	10	11	10	11	σ	10	10	σ	σ	10	11	14	
363	363 739	390	447	443	391	705	714	3344	5691	5691	5711	5711	6255	6255	384	7.37	364	. 387	472	358	351	393	
14.7	14.7	13.1	13.1	12.4	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	11.0	•	10.3	10.3	10.1	10.1	10.1	•	9.7	9.7	
64	4 4 4	57	57	54	4.4 8.80	48	4 4	4 4 0 8	48	48	48	48	48	48	45	45	44	44	44	43	42	42	
17 c 18		22					29		32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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US-09-861-294-1

| Sequence I. Application US/09861294 |
| Sequence I. Application US/09861294 |
| Sequence I. Application US/09861294 |
| Sequence I. Application I. US/002009190A1 |
| GEMERAL INFORMATION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: TOWNORS BEARING HMFG AND CEA ANTIGENS FILE OF INVENTION: UNMBER: US/09/861,294 |
| CURRENT APPLICATION NUMBER: US/09/861,294 |
| PRIOR FILING DATE: 1997-06-13 |
| PRIOR FILING DATE: 1997-06-13 |
| PRIOR FILING DATE: 1999-06-11 |
| NUMBER OF SEQ ID NOS: 38 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 1 |
| LENGTH: 435 |
| SEQ ID NO 1 |
| LENGTH: 435 |
| NAME/KEY: CDS |
| COCATION: (1)...(40) |
| NAME/KEY: Sig_peptide |
| COCATION: (1)...(435) |
| US-09-861-294-1 |
| OUETY MATCh |
| US-09-861-294-1 |
| OUETY MATCh |
| Matches 435; Conservative 0; Mismatches 0; Indels 0;
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0; 60 60

	RESULT 3 GS-08-79-78-5 Sequence 5, Application US/08779784 Sequence 5, Application WOS02001643251 EDENERAL INFORMATION: SEQUENCES TO WOSS APPLICANT: MAILET David J. CORRESPONDINGE ADDRESS: 37 CORRESPONDINGE ADDRESS: 37 CORRESPONDINGE ADDRESS: 37 CORRESPONDINGE ADDRESS: 37 CORPUTER READABLE FORM: APPLICATION USA CURRENT: USA CURRENT: INM FO Compatible COMPUTER READABLE FORM: APPLICATION NUMBER: US 08 06/92, 084 FILING DATE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION ATA PRICATION NUMBER: US 08 06/92, 084 FILING DATE: DAVID ATA APPLICATION NUMBER: US 08/235, 520 ATTORNEY/AGENT INPORMATION: APPLICATION NUMBER: US 08/235, 520 ATTORNEY/AGENT INPORMATION: APPLICATION NUMBER: US 08/28, 520 ATTORNEY/AGENT INPORMATION: TELEDOMMOUNT PRESS: 201-49-580 TELEDOMMOUNT PRESS: 201-49-580 TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDOMMOUNT PRESS: 201-49-580 TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDOMMOUNT PRESS: 201-49-580 TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDRAMI AND SECONDESS: 1199-1-001 CIPA TELEDOMMOUNT PRESS: 201-49-580 TELEDRAM: ATORNEY/AGENT INPORMATION: TELEDRAMI AND SECONDESS: 1199-1-001 CIPA TELEDOMMOUNT PRESS: 201-49-580 SECONDENCE CHARACTERISTICS: LENDTH ATORNEY/AGENT INPORMATION: TELEDRAMI AND SECONDESS: LENDTH ATORNEY/AGENT INPORMATION: TELEDRAMI AND SECONDESS: SECONDESS: SECONDESS: ATORNEY/AGENT ATORNEY/AG
03 03 04 05 05 05 05 05 05 05	RESULT 2 US-10-367-506-1 US-10-367-506-1 Sequence 1, Application US/10367506 Sequence 1, Application US/10367506 Sequence 1, Application Wo. US203031527541 APPLICANT: MAIASA CHATTEREE APPLICANT: MAIASA CHATTEREE APPLICANT: MAIASA CHATTEREE APPLICANT: WENNER, A. FOON TITLE OF INVENTION: CURPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: UNDERS: US/10/367,506 CURRENT APPLICATION NUMBER: US/20/961,294 PRIOR FILITOR DATE: 2001-05-17 PRIOR FILITOR DATE: 2001-05-17 PRIOR FILITOR DATE: 2004-05-13 PRIOR FILITOR DATE: 1090-06-13 PRIOR FILITOR DATE: 100-06-13 PRIOR PARTOR FILITOR DATE: 100-06-13 PRIOR FILITOR DATE: 100-06-13 PRIOR PARTOR DATE: 100-0

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Gaps

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Indels

Pred. No. 2e-46;

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42 GTTTCCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTC 101
100.08; to
                                Conservative
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STATE: New Jersey
                 Best Local Similarity
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Best Local Similarity
Matches 150; Conserv
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APPLICANT: Rodrigu
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HYPOTHETICAL:
US-08-779-784-17
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                                  Matches 102;
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-08-779-784-17
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                                                                                                                                                                                                                                    235 CCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09007093

Sequence 1, Application US/09007093

Patent No. US20020025315A1

GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Caterini, Judith E
APPLICANT: Caterini, Judith E
APPLICANT: CATERINI MACHAIN E
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
TITLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: 310 & MCBUINEY
                                                                                                                                                                                                   ö
                                                                                                                                                               Length 402;
                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  355 GGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT 393
                                                                                                                                                                                                                                                                                                                                                                                                         361 GGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
                                                                                                                                                             Score 108; DB 8;
Pred. No. 9.2e-50;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038-765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                               24.8%;
99.4%;
                                                                                                     ORGANISM: Mus musculus
                                                                                                                                                                                               Matches 158; Conservative
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M5G 1R7
                                linear
                                                                                                                                                           Query Match
Best Local Similarity
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COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toronto
               STRANDEDNESS:
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                                                                                                                      US-08-779-784-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-007-093-1
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DB 9; Length 387;

23.4%; Score 102;

Query Match

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48 GITICCAGGIACCAGAIGIGACATCCAGAIGACCCAGTCTCCATCTTAICTGTCCTC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 TGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 GGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                      APPLICANT: Rodriguez, Moses
APPLICANT: Miler, David J.
APPLICANT: Miler, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Trait
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.0%; Score 100; DB 8; Length 351; 99.3%; Pred. No. 2.6e-45;
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                                                          102 TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 143
                                                                                  108 TCTGGGACAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGA 149
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      Sequence 17, Application US/08779784 Publication No. US20020164325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                  GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACATGCTTCGGAGGG 360
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                          241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
                                                                                                                    APPLICANT: NUSHIDA, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: OKURA, Takanori
APPLICANT: Tadao
APPLICANT: Tadao
APPLICANT: TAUMOYO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
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Pred. No. 2.9e-35;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/09924099; Patent No. US20020128450al; GENERAL INFORMATION:
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EDEREAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.2%;
Matches 132; Conservative
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301 GGGACCAAGCTGG 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/RET.
LOCATION: (1)...(4v.,
NAME/KEY: sig peptide
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US-09-924-099-27
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Fublication No. US20020132983A1
GENERAL INFORMATION:
APPLICANT: JUNGHANS, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antipersense: 003
CURRENT PELING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 66/250,089
PRIOR APPLICATION NUMBER: 66/250,089
PRIOR APPLICATION NUMBER: 66/250,089
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
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229 GATTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACC 288
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APPLICANT: NISHIDA, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: OKURA, Takanori
APPLICANT: OKURA, Takanori
APPLICANT: GENERA, Takanori
APPLICANT: KURIMOTO, Tadao
TITLE OF INVENTON: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: J999-06-23
PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-22
NUMBER OF SEQ ID NOS: 33
LENGTH: 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 19.5%; Score 85; DB 13; Length 698; Best Local Similarity 100.0%; Pred. No. 6.2e-37; Matches 85; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (6)...(401)
COTHER INFORMATION: 3E11 Light chain V region, plus leader US-10-006-773-18
                                         402 TGTATCCATCTTCCCACCATCCAGT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419 TGTATCCATCTTCCCACCATCCAGT 443
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Patent No. US20020128450A1
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; ORGANISM: Mus musculus
US-09-924-099-11
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18.4%; Score 80; DB 100.0%; Pred. No. 3.8
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Publication No. US2002016432541
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
TITLE OF INVENTION: PROMOTION OF CTITLE OF INVENTION: REWTELINATION UNMER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 CCATCTTCCCACCATCCAGT 426
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Best Local Similarity 100.0
Matches 80; Conservative
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                                                                                                                361 GGGACCAAGCTGG
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SEQ ID NO 10
LENGTH: 729
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Factor No. US20020128450al
GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: NURHIDA, Yashihiro
APPLICANT: NURHOTO, Tadao
APPLICANT: WIRIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT APPLICATION NUMBER: BALLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR PLILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR PLILING DATE: EARLIER FILING DATE: 1999-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
NUMBER OF SEQ ID NOS: 33
NUMBER OF SEQ ID NOS: 33
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SECTION 199
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Pred. No. 2.9e-35;
0; Mismatches 1; Indels
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Pred. No. 2.9e-35;
0; Mismatches 1
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99.2%;
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Best Local Similarity 99.2%;
Matches 132; Conservative
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CHER INFORMATION: ID NO:10
US-09-924-099-20
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Best Local Similarity 99.2
Matches 132; Conservative
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US-09-924-099-20
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LENGTH: 729
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% Sequence 10, Application US/10006773

Sequence 10, Application US/10006773

Publication No. US20020132983A1

SERENTAL INFORMATION:

APPLICANT: Junghans, Richard P.

TITLE OF INVERTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A.

CURRENT APPLICATION NUMBER: US/10/006,773

CURRENT FILMS DATE: 2001-12-10

PRIOR APPLICATION NUMBER: 60/250,089

PRIOR APPLICATION NUMBER: 00/250,089

PRIOR FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 19
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GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
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; LCCATION: (15)..(410)
; OTHER INFORMATION: 3D8 Light chain V region, plus leader
US-10-006-773-10
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STATE: New Tore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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342 TCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAAACGGGCTGATGCTGCACCAAC 401
                                                                                                                                                                                                                                              US-09-840-459-101/c; Sequence 101, Application US/09840459; Patent No. US20020150576A1; GENERAL INFORMATION:
                                                                                                                                          IGTATCCATCTTCCCACCA 426
                                                                                                                402 TGTATCCATCTTCCCACCA 420
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Matches 79; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.2%; Score 79; DB 8; Length 351
Best Local Similarity 100.0%; Pred. No. 1.3e-33;
Matches 79; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LAROSA, Gregory J.
APPLICANT: LAROSA, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: O'Reien, Slobhan H.
APPLICANT: O'Reien, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/09/840, 459
FILE REFERENCE: 1855.105-012
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SUFFRARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.2%; Score 79; DB 10; L
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 79; Conservative 0; Mismatches 0;
                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-A0G-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 95, Application US/09840459 Patent No. US20020150576A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GAGTCTGAAGATTTTGTAG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 GAGTCTGAAGATTTTGTAG 313
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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; ORGANISM: Mus musculus
US-09-840-459-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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HYPOTHETICAL: NO
US-08-779-784-16
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SEQ ID NO 95
LENGTH: 426
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DESCRIPTION OF SEQUENCE 14, Application US/10006773
Sequence 14, Application US/10006773
Sequence 14, Application US/10006773
Sequence 14, Application US/10006773
Sequence 14, Application No. US20020132983A1
SERENAL INFORMATION:
APPLICANT: Junghans, Richard P.
TITLE OF INFORMATION: Antibodies as Chimeric Effector Cell Receptors Against Tumor A TILE REFERENCE: 003
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR PLING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 TCCGTACACGTTCGGAGGGGGACCAAGCTGGAAAAAAAGGGGGTGATGATGCTGCACCAAC 407
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APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOSTWARR: FRAISEQ for Windows Version 3.0
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FEATURE:
NAME/KEY: CDS
LOCATION: (7). (402)
OTHER INFORMATION: 4D4 Light chain V region, plus leader
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		0; Gaps	TATCCA	TATCCA
		ó	ACTG	ACTG
	Query Match 17.7%; Score 77; DB 13; Length 504; Best Local Similarity 100.0%; Pred. No. 1.8e-32;	Matches 77; Conservative 0; Mismatches 0; Indels	350 CGTTCGGAGGGGGCACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCA 409	368 CGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCA 427
	Score 77; Pred. No	0; Mismat	AGCTGGAAATA	GCTGGAAATA
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14	imilarity	; Conserv	CGTTCGGAGG	CGTTCGGAGG
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US-10-006-773-14	Query Match Best Local 9	Matche	Οy	qq

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Search completed: August 30, 2003, 22:02:42 Job time: 160.756 secs

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Mus muscu AGENCOURT

Mus

601780387 602993614

602829112

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602826515

AGENCOURT

602835104 AGENCOURT

602102583 602891329

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Word size

Searched:

Minimum DB seq Maximum DB seq

Database :

Title: . Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

602830592 601104076

602828830

602112548 AGENCOURT

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BE309592 594 bp mRNA linear EST 26-OCT-2000 601094848F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3489635 5',
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NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outract: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Hitp://image.llnl.gov
Plate: LLAM86330 row: o column: 12
High quality sequence stop: 591.
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BG964076
BG968518
BQ939046
BF687485
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BI659552
BG518527
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BF164906
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BG961850
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BG964076
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Mus musculus
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BE309592
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BE309592
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BI454240 603170666
BM194777 L0700H12-
BG963055 602828068
                                                                                                    August 30, 2003, 18:52:40; Search time 1513.76 Seconds (without alignments) 6984.224 Million cell updates/sec
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1 ATGGGGCCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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    nucleic search, using sw model

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19.8
19.5
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Score

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Result

87 85 85 85

602916512 603303102 602578261

602894523

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/tissue_type="Germinal Center B Cell"
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/lab_host="DalloB"
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NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA
).FACS-sorted Germinal Center B cells were provided by
Drs. Richard Hodes, Emily Klotz (National Institute on
Aging and National Cancer Institute, USA) and Garnett
Kelsoe (Duke University, USA). Double-stranded cDNAs were
synthesized from 0.46 ug of total RNA with an Oligo(dT)
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L0700H12-3 NIA Mouse Germinal Center B Cell cDNA Library Mus musculus cDNA clone L0700H12 3', mRNA sequence.
                                                                                                                                                                                                                                      341 CTCCGTACACGTTCGGAGGGGGGCCCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAA 400
                                                                                                                                                                                                                                                             356 CTCCGTACACGTTCGGAGGGGGACCAAGCTGGAATAAAAACGGGCTGATGCTGCACCAAA 415
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Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Klotz, E., Kelsoe, G., Hodes, R. and Ko, M.S. H.
providing samples: Lothar Hennighausen/Robin Humphreys.
NIH"
                                                                                                                                                                                           Gaps
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
and Casell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plater: L0700 row: H column: 12
Seg primer: -21M13 Forward
High quality sequence stop: 585
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                                                                                                                                        Length 805;
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19.8%; Score 86; DB 12; 1
Best Local Similarity 100.0%; Pred. No. 2.5e-34;
Matches 86; Conservative 0; Mismatches 0;
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                      401 CTGTATCCATCTTCCCACCATCCAGT 426
                                                                                                                                                                                                                                                                                                                                                               416 CTGTATCCATCTTCCACCATCCAGT 441
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Mus musculus
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                                                                                                                                                                                                                                                                                      /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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/note="Grgan: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 805)
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov d column: 18
High quality sequence stop: 790.
Location/Qualifiers
1. 805
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.0%; Score 87; DB 10; Length 594; Best Local Similarity 100.0%; Pred. No. 6.6e-35; Matches 87; Conservative 0; Mismatches 0; Indels
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/fissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                      /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Mam5"
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                                                                    /organism="Mus musculus"/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3489635"
                                                                                                                                                                                                                                                                                                                                                                                                          143 g
                      Location/Qualifiers
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/strain="C57BL/6J"
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followed by Centricon 100 purification. The CDNAs were digested with SalI and Not! enzymes and cloned into SalI/NotI site of pSPORTI plasmid vector. The DH10B E. coll host was transformed with the ligation mixture by the standard chemical method. The average insert size is 1.2 standard chemical method of the average insert size is 1.2 is 1.1 c 167 g 160 t
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602888068F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982825 5',
mRNA sequence.
BG963055
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/lab_host="DHIOB (T1 phage-resistant)"
/clone_lib="NGLCGAP_CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                        19.5%; Score 85; DB 12; Length 58
100.0%; Pred. No. 7.6e-34;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.1e-34;
Live 0; Mismatches 0; Indels
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Mus musculus
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/strain="FVB/N"
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nes 85; Conserve
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602093833F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4208144 5', BF579422
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602112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
5', mRNA sequence.
BF785914
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 891)
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                          Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9772 row: a column: 09 High quality sequence stop: 711.
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                                                                                                                                   Mus musculus (house mouse)
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                                                                                                      BF579422.1 GI:11653134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://image.lin.gov
Plate: LiAM9855 row: p column: 11
High quality sequence stop: 718.
Location/Cualifiers

1. 906
| coganism="Mus musculus" |
| coganism="Mus musculus" |
| companism="Musmusculus" |
| clone="Iaxon:10090" |
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMM4024 row: h column: 02
High quality sequence stop: 692.
Location/Qualifiers
rce 1. 926
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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                                                                                                                  Unpublished
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAL at: http://image.llnl.gov Series: IRAK Plate: 67 Row: j Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTC 03-JUN-2002
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                                                                                                 /dlohes-mAdde: MAGE(479377"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 251 c 202 g 235 t l others
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 935)
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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This clone has the following problem: no cloning site,
                                                                                                                                                                                                                                                                                                                                                                                                     19.5%; Score 85; DB 13; Length 926; 100.0%; Pred. No. 8.7e-34; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nc1.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC031349 935 bp mRNA
Mus musculus, clone IMAGE:1514385, mRNA.
BC031349
/organism="Mus musculus"
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                     /mol_type="mRNA"
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/db_xref="taxon:10090"
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1. .935
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Mus musculus
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Direct Submission
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BC031349
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/organism="Mus musculus"
/mol_type="mrRA"
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/clone="lost="phi0B"
/clone="tumory"
                                                                                                                                                                                                                                                                               854 bp mRNA linear EST 21-AUG-2002 AGENCOURT_8909039 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:641024 5', mRNA sequence.
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Mus. 2 (bases 1 to 854)
Mus. 2 (bases 1 to 854)
Mus. 3 (bases 1 to 854)
Mus. 4 (bases 1 to 854)
Mus. 5 (bases 1 
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
15 CCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAAACGGGCTGATGCTGCACCAACT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contract: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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100.0%; Pred. No. 2...
... 0; Mismatches
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Location/Qualifiers
1. 854
                                                            403 GTATCCATCTCCCACCATCCAGT 426
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BQ947692.1 GI:22363170
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LOCUS
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="KPUSN"
/db_xref="taxon:10090"
/clone="InAGE:6395978"
/Jab_host="BH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_CO4"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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AGENCOURT_8921909 NCI_CGAP_CO24 Mus musculus cDNA clone
IMAGE:5395978 5', mRNA sequence.
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                                                                                                                      /tissue_type="Mammary gland, lactating mouse"
/clone_lib="Soares_mammary_gland_NMLMG"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                            Length 935;
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                                                                                                                                                                                                                                                                                                                                                  19.5%; Score 85; DB 11; Length 93
100.0%; Pred. No. 8.7e-34;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 2.6e-33;
tive 0; Mismatches 0;
                                                                                                                                                                                                                        /note="Vector: pT7T3D-Pac"
247 c 208 g 229
/organism="Mus musculus"
                              /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1514385"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 100.
85; Conservative
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KEYWORDS

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EST 21-AUG-2002

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="kPubN"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
/Average insert size I of kb. Constructed by Life
/rechnologies. Note: this is a NCI_CGAP Library."
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BU524124
BU524124.1 GI:22834563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oilgo dr. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
Tobna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMHAI33 row: f column: 02
High quality sequence stop: 604.
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                                                                                                                                                    /db_xref-"taxon:10090"
/clone="liMAGE:6476176"
/lab.host-"DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 84; DB 13; 100.0%; Pred. No. 2.9e-33; tive 0; Mismatches 0;
  Plate: LLAM14016 row: b column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                         /organism="Mus musculus"
                       High quality sequence stop: 626.
Location/Qualifiers
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Mus musculus
                                                                                                            /mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: McC clone distribution information con be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM3892 row: n column: 02
High quality sequence stop: 630.
Location/Qualifiers
rce 1...871
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 871)
NIH-WGC http://mgc.nci.nih.gov/.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 886)
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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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ilarity 100.0%; Pred. No. 2.9
Conservative 0; Mismatches
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Mus musculus
  Mus musculus (house mouse)
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84; Conserv
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Query Match 19.3:
Best Local Similarity 100.
Matches 84; Conservative
                 mRNA sequence.
BG961850
                                                                                                                                                                                                                     Unpublished
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DEFINITION
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                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                  ACCESSION
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                                                                                        402
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/clone="IndioB (Tl phage-resistant)"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://mage.llnl.gov
Plate: LLAM14131 row: f column: 12
High quality sequence stop: 646.
Location/Qualifiers
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941 bp mRNA linear EST :
AGENCOURT_10169180 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:5530124 5', mRNA sequence.
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             Query Match 19.3%; Score 84; DB 13; I
Best Local Similarity 100.0%; Pred. No. 2.9e-33;
Matches 84; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
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100.0%; Pred. No. 3e-33;
Live 0; Mismatches 0
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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BU523453.1 GI:22833892
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Matches 84; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10982 row: n column: 04
High quality sequence stop: 743.
Location/Qualifiers
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/clone="IMAGE:4981443"
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/clone=lib="will CGAP_CGAP"
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602826515F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4981443 5'
                                                                                                                                                                                Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Muses 1 to 975)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/strain="FVB/N"
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Page 1

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5.1.6	Compugen Ltd.
version	- 2003
	c) 1993
	Copyright (

OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	August 30, 2003, 13:43:39; Search time 1971.09 Seconds (without alignments) 9028.331 Million cell updates/sec	
Title: Perfect score: Sequence:	US-08-836-455-1 435 1 ATGGGGGCCCCTGCTCAGATCACCATCCAGTAAGCTTGGG 435	
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	
Searched:	2888711 segs, 20454813386 residues	
Total number of	Total number of hits satisfying chosen parameters: 5777422	
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : GenEmbl:*

20: em_on: *
21: em_or: *
23: em_or: *
24: em_ov: *
25: em_ph: *
26: em_ro: *
27: em_sts: *
27: em_ur: *
28: em_ur: *
30: em_htg_hum: *
31: em_htg_hum: *
32: em_htg_or, hum: *
33: em_htg_pro: *
34: em_htg_pro: *
35: em_htg_or, vt: *
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37: em_htg_or, vt: *
38: em_htg_or, vt: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C12N15/00
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mismatches 0;
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Patent: JP 2000236884-A 15 05-SEP-2000;
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Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11010
Patent: JP 2001523269-A 1 20-NOV-2001;
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A61K39/395, A61K39/39//C07K16/42
Strandedness: Single;
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PAT 31-JAN-2002

MASASHI

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300

source

FEATURES

BASE COUNT ORIGIN

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/codon_start=1
/product="immunoglobulin light chain"
/product="immunoglobulin light chain"
/db_xref="G1:14164547"
/db_xref="G1:14164547"
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ASQDIGINLHWLQQPEDGTIRRLIYATSSLGSGVPRRFSGSRSGSDYSLTISSLESED
FVAYYCLQYASSPYTFGGGTKLEIK"
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clone 125-2H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-1998) Yoshihiro Nishida, Hayashibara Biochemical Laboratories, Inc., Fujisaki Institute; 675-1, Fujisaki, Okayama, Okayama 702-8006, Japan (E-mail:fujih@po.harenet.or.jp, Tel:+81-86-276-3141, Fax:+81-86-276-6885)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
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Was musculus (house mouse)

Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mushida,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCACTIGICGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA
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                                                                                                                                                                                                                                                                                                                                                                       ATGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT

    >>381
    /note="anti-idiotype antibody 11D10; mimics a breast
    /note="anti-idiotype antibody 11D10; mimics a breast
    /note="antiden, human fat globule (HMFG)"

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Light chain,
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Pred. No. 1.2e-103;
0; Mismatches 1;
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                                         /db_xref="taxon:10090"
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                        /strain="BALB/c'
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                                                                                                                                                                                                                                                                                             Query Match 87.2%;
Best Local Similarity 99.7%;
Matches 380; Conservative
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                                                       .>381
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AB017434
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Chatterjee, S.K. and Tripathi, P.K.
Direct Submission
Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                      CTCACTIGICGGCAAGTCAGGACATIGGTATIAACTIACATIGGCTICAGCAGGAACCA 180
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AGGITCAGIGGCAGIAGGICIGGGICAGAITAITCICICACCAICAGCAGCCIIGAGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tripathi, P.K., Oln, H., Bhattacharya-Chatterjee, M., Ceriani, R.L. Foon, K.A. and Chatterjee, S.K. Construction and characterization of a chimeric fusion protein consisting of an anti-idiotype antibody mimicking a breast encer-associated antigen and the cytokine GM-CSF Hybridoma 18 (2), 193-202 (1999)
                                                                                                                                                                                                                                                                                               ATGGGGCCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT
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                                                                                                                                                                                                                          Length 407;
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Location/Qualifiers (1). (407)
Location/Qualifiers (1). (60).
Location/Qualifiers (1). 407
                                                                                                                                                                                                                      Score 384.6; DB 6;
Pred. No. 3.1e-105;
0; Mismatches 14;
                                                                                                                                                                     ų
                                                                                                                                                                   116
                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/organism="Mus musculus"
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                                                                                                                                                                                                                        88.4%;
96.6%;
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Best Local Similarity 96.6
Matches 393; Conservative
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                                                          sig_peptide
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE PUBMED

AUTHORS REFERENCE

JOURNAL

TITLE

FEATURES

LOCUS

RESULT 4 AF124721

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Page

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Asakura,K.
Direct Submission
Submitted (24-JUL-1997) Immunology, Mayo Clinic, 200 First Street
SW, Rochester, MN 55905, USA
Original source text: Mus musculus (strain BALB/c, sub_species
                                                                                                                                                                                                                                                                                                                                                                                  Score 361.6; DB 10;
Pred. No. 2.9e-98;
0; Mismatches 14;
                                                                                                                                             /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="hybridoma HNK-1"
                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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                                                                               Location/Qualifiers
                                                                domesticus) cDNA to mRNA
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96.4%;
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Best Local Similarity
Matches 370; Conserv
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mat_peptide
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ORIGIN
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  AUTHORS
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ASQDIGSKLYWLQQEPDGTFKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESED
FVDYYCLQYASSPYTFGGGTKLAIKR"
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Asakura, K., Millar, D.J., Pogulis, R.J., Pease, L.R. and Rodriguez, M. Oligodendrocyte-reactive Ol. 04, and HNK-1 monoclonal antibodies are encoded by germline immunoglobulin genes
Brain Res. Mol. Brain Res. 34 (2), 283-293 (1995)
                                                                                                                                                                                                                                                                                                                                           1 ATGGGGCCCCTGCTCAGATTCTTGGGTTĆTTGTTGCTCTTGTTTCCAGGTACCAGATGT
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                 /product="variable region precursor of anti-IL-18
Light chain"
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                                                                                                                                                                                                                                                                              Length 384;
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Mus musculus immunoglobulin kappa chain mRNA, 5' e
L41880
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/product="anti-IL-18 IgG Light chain"
91 q 110 t
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                                                                                                                                                                                                                                                                            Score 361.6; DB 1
Pred. No. 2.9e-98;
0; Mismatches 14
                                                                                                                               /protein_id="BAA89228.1"
/db_xref="GI:6683474"
             musculus
                                     /db_xref="taxon:10090"
/clone="125-2H"
                                                             /cell_type="Hybridoma"
1. .>384
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACCAAGCTGGCAATAAAACGG 384
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Mus musculus
                          /mol_type="mRNA"
             /organism="Mus
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ilarity 96.4%;
Conservative
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370; Conser
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 source
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PUBMED
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/codon_start=1
/product="immunoglobulin kappa chain"
/product="immunoglobulin kappa chain"
/db_xref="ig:-79811"
/translef="ig:-79811"
/translef="immunoglepGTIKRLIYATSSLDSGVPKRFSGSRSGSDXSLTISSLES
EDFYDYXCLQYASSPYTFGGGTKLEIRR"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                             Length 390;
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                                                                                                                                                                                                       /product="immunoglobulin kappa chain"
90 c 95 g 109 t
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/protein_id="AAC04536.1"
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/tb_xref="G1:2906100"
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ASQUIGSSLWWLQOBPGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESED
FVDYYCLQYASSPWTFGGGTKLEIK"
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          (bases 1 to 381)

O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies

O'Dubblished

(bases 1 to 381)

O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.

Direct Submission

Submitted (02-FBB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
                                                                                                                                                                                                                                                                                                                                               /product="anti-poly(dC) monoclonal antibody kappa light
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 352.2; DB 10;
95.3%; Pred. No. 2e-95;
iive 0; Mismatches 18;
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/gene="IgK"
61. .345
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346. .>381
/gene="lgK"
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/procein_id="AAC04523.1"
/db_xref="G1:2906074"
/db_xref="G1:290607
                                          Mus musculus dC4 anti-poly(dC) monoclonal antibody kappa light chain variable region, (IgK) mRNA, partial cds.
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O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D. Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA Location/Qualifiers

1. 381
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product" anti-poly(dC) monoclonal antibody kappa light
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O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Direct Submission
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/cell_line="spleen cell hybridoma"
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Pred. No. 1.9e-94;
0; Mismatches 20;
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/strain="C57BL/6"
/db_xref="taxon:10090"
/chromosome="6"
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94.8%;
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/gene="IgK"
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/gene="IgK"
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	Oy 361 GGGACCAAGCTGGAATAAAA 381	SOURCE Mus musculus (house mouse) ORGANISM Mus musculus CREANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. REFERENCE 1 (bases 1 to 380) AUTHORS Darsley,M.J. and Rees,A.R. TITLE Nucleocitde sequences of five anti-lysozyme monoclonal antibodies JOURNAL EMBO J. 4 (2), 393-398 (1985) MEDLINE 85257466 FEATURES Location/Qualifiers Source //organism=Mus musculus"	// Ab_xref="taxon:10090" // Ab_xref="taxon:10090" // Ab_xref="taxon:10090" // Codon_start=3 // Product="Immunoglobulin G kappa light chain" // Ab_xref="G1:663215" // Ab_xref="G1:663215" // Ab_xref="G1:663215" // Ab_xref="G1:663215" // Ab_xref="GFLLIMFPGTRCDIOMTOSPSSLSASLGERVSLTCRASQEISG // Ab_xref="GFLLIMFPGTRCDIOMTOSPSSLSASLGERVSLTCRASGEISG // Ab_xref="Taxolact="Taxola	misc_feature 30633 // mote="hypervariable region CDR3" J_segment 326364 // mote="hypervariable region of IgG kappa light chain" C_region 365>380 // product="constant region of IgG kappa light chain" BASE COUNT 88 a 93 c 89 g 110 t GR (Rappa light chain") ORIGIN 76.38; Score 332; DB 10; Length 380; Best Local Similarity 92.18; Pred. No. 2.7e-89; Matches 350; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCATTGAGTCT 300 Db 241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGCATTCTCTCACCATCAGCAGCTTGAGTCT 300 QY 301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTACCATCAGCAGCG 360 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	VERSION AF045510.1 GI:2906103 KEYWORDS WAS MUSCULUS (house mouse) ORGANISM MAS musculus CRGANISM MAS musculus Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; MAMMANIA; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musculus AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D. TITLE ATTI-DA antibodies of normal mice immunized with poly(dC) are JOURNAL Unpublished STREERENCE 2 (bases 1 to 381) AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D. AUTHORS O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.	JUINE DIFFER 1998 Blochemistry, Tufts University School of JOURNAL Submitteed (02-FEB-1998) Blochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA FEATURES Location/Qualifiers FEATURES Location/Qualifiers Organism="Mus musculus" Anol_Lype="mRNA" Astrain="C57BL/6" Ab_xref="taxon:10090" Actrain="C57BL/6" Ab_xref="taxon:10090" Actrain="C57BL/6" Actra	CDS //gene="1gk" /codon_start=1 /fordon_start=1 /fordon=1 /f	BASE COUNT 93 a 90 c 87 g 112 t ORIGIN Query Match 79.5%; Score 345.8; DB 10; Length 381; Best Local Similarity 94.2%; Pred. No. 1.8e-93; Antches 359; Conservative 0; Mismatches 22; Indels 0; Gaps 0; Oy 1 ATGGGGGCCCTGCTCAGATTCTTGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT 60 I 111 11

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M.musculus mRNA for IgG kappa light chain (partial) Gloop 2.
X02178
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GYLSWLQQKPDGTIKRLIXAASTLDSGVPKRFSGRRSGSDYSLTISSLESEDFADYYC
                                                    AGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCC 199
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Sciurognathi; Muridae; Murinae; Mus
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Darsley, M.J. and Rees, R. R.
Nucleotide sequences of five anti-lysozyme monoclonal antibodies 85257466
2410256
        TGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAAAGGTTCAGTGGCAGTAGGT
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region; variable region.

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    'variable region of IgG kappa light chain"

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/note="hypervariable region CDR1"
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327, 365
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/note="hypervariable region 307. .333
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Corganism="Mus musculus"
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Mammalia; Eutheria; Rodentia;
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/translation="AQVFGFLLLWFPGARCDIQMTQSPSSLSASLGERVSLTCRASQD
IHGYLNLFQQKPGETIKHLIYETSNLDSGVPKRFSGSRSGSDYSLIIGSLESEDFADY
YCLQYASSPPTFGGGTKLEIKRADA"
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Bernard, O., Gough, N.M. and Adams, J.M. Plasmacytomas with more than one immunoglobulin kappa mRNA: implications for allelic exclusion Proc. Natl. Acad. Sci. U.S.A. 78 (9), 5812-5816 (1981)
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                                          Length 381;
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Mouse Ig active kappa-chain VJ2C mRNA from
Partial cds.
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                                            Score 327.2; DB 1
Pred. No. 7.6e-88;
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<1. .>383
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/db_xref="imgr/light.ab016620"
//db_xref="imgr/light.ab016620"
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FADYYCLQYASDPWTFGGGTKLEIR"
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Anand, N.N., Barber, B.H., Cates, G.C., Caterini, J.E. and Klein, M.H. Chimeric antibodies for delivery of antigens to selected cells of
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            /codon_start=1
/rodon_start=1
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/protein_id="BAA32080.1"
/db_xref="G1:3395671"
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Pred. No. 1.1e-86;
0; Mismatches 36;
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Pred. No. 8.1e-87;
0; Mismatches 37
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100 c 97 g 110
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Patent: US 6291208-A 1 18-SEP-2001;
Location/Qualifiers
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Sequence 1 from patent US 6291208.
AR169918 GI:17907877
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llarity 90.6%;
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Submitted (30-JUL-1998) Fumiko Arakawa, School of Medicine, Fukuoka
University, First Department of Biochemistry; 7-45-1 Nanakuma,
Jonan Ku, Fukuoka, Fukuoka 814-80, Japan
(E-mail:farakawa@msat.fukuoka-u.ac.jp, Tel:092-801-1011(ex.3246),
Fax:092-801-3600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB016620 405 Dp mRNA linear ROD 27-MAR-2002 Mus musculus mRNA for Immnogloblin light chain variable region,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                          Arakawa,F., Yamamoto,T., Kanda,H., Watanabe,T. and Kuroki,M. CDNA sequence analysis of monoclonal antibody FU-MK-1 specific a transmembrane carcinoma-associated antigen, and construction mouse/human chimeric antibody Hybridoma 18 (2), 131-138 (1999)
                                                                                                                                               GGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCAGATGGAACTA
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                                                                     11 CIGCTCAGATICITGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGTGACATCCAGA
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             DB 10;
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             Score 325.4; DB 1
Pred. No. 2.7e-87;
0; Mismatches 36
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/organism="Mus musculus"
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            74.8%;
90.6%;
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Arakawa,F.
            Query Match 74.8
Best Local Similarity 90.6
Matches 347; Conservative
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Hirama,M., Mizugaki,M. and Goto,J.
Hirama,M., Mizugaki,M. and Goto,J.
Direct Submission
Submitted (09-AUG-2002) Yoshihisa Tomioka, Tohoku University
Hospital, Department of Pharmaceutical Sciences; 1-1, Seiryo-machi,
Aoba-ku, Sendai, Miyagi 980-8574, Japan
Fax:81-22-717-7545)
                                                                                                              AGGITCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                             247 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 306
                                                                                                                                                                                                                                                                                          GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
               7 ATGAGGGTTCCTGCTCACGTTTTTGCTTCTTGTTGCTCTGGTTTCCAGGTACCAGATGT
ATGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT
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Pred. No. 8.3e-85;
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                                                                                                                  72.9%;
94.8%;
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18; Conservative
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2003, 16:05:49; Search time 190.798 Seconds (without alignments)

Fitle: US-08-836-455-1

Perfect score: 435
Sequence: 1 ArGGGGCCCCTGCTCAGAT......CACCATCCAGTAAGCTTGGG 435
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries N_Geneseq_19Jun03:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Murine monoclonal	Antibody 11D10 lig	Mouse 11D10 antibo	Sequence encoding	Mouse light chain	Murine anti-human	Murine 44H104 mab	Segmence encoding
	OI.	AAT85149	AAV83772	AAL51273	AAN30165			AAD32138	AA046084
	BB	18			4			24	14
	Length	435	435	435	450	407	387	387	739
Query	Match	100.0	100.0	100.0	8.06	88.4	74.3	74.3	71.1
	Score	435	435	435	394.8	384.6	323.4	323.4	309.4
Result	No.	-	7	m	4	S	9	7	&
		Query Score Match Length DB ID	Ouery Score Match Length DB ID 435 100.0 435 18 AAT88149	Score Match Length DB ID 435 100.0 435 18 AAT85149 435 100.0 435 20 AAV83772	Ouery Score Match Length DB ID 435 100.0 435 18 AAT85149 435 100.0 435 20 AAV83772 435 100.0 435 25 AAL51273	Ouery Score Match Length DB ID 435 100.0 435 18 AAT85149 435 100.0 435 25 AAV83772 435 100.0 435 25 AAL51273 394.8 90.8 450 4 AAN30165	Ouery Score Match Length DB ID 435 100.0 435 18 AAT85149 435 100.0 435 20 AAV83772 435 100.0 435 25 AAL51273 394.8 90.8 450 4 AAN30165 384.6 88.4 407 21 AAX4548	Ouery Score Match Length DB ID 435 100.0 435 20 AAV83772 435 100.0 435 20 AAV83772 435 100.0 435 25 AAL51273 394.8 90.8 450 4 AAN30165 384.6 88.4 477 21 AAZ49548 323.4 74.3 387 18 AAZ77851	Govery Score Match Length DB ID 435 100.0 435 18 AAT85149 435 100.0 435 20 AAV83772 435 100.0 435 25 AAL51273 394.8 90.8 450 4 AAN30165 384.6 88.4 407 21 AAZ49548 323.4 74.3 387 18 AAZ77851 323.4 74.3 387 24 AAD32138

520C9 anti-c-erbB- 520C9 anti-c-erbB- 520C9 sFV DNA Sequ PESCFV#125-2H HT r PESCFV#125-2H reco Mouse anti-II-IB a Sequence encoding	P4-3 single chain P5-10 single chain 3B10xP4-3 bispecif 520C9 hybridoma VL Light chain variab Light chain va	Filamentous phage IL-2 chimerts anti Fialmentous phage Human coding seque Monoclonal anti-id 3H1 light chain va Anti-idotype anti Murine Mab against Mouse anti-idotyp Antibody 3H1 light	Muzuse Sur anilbody Human ovarian anti 650E2 hybridoma VL Mouses 3H1 antibody Murine anti-human Partial nucleotide DNA encoding the k Mouse derived RT3 Human immunoglobul Human iffRAM-9 immu Murine m166 antibo Mouse derived RT3
AAT36880 AAV21798 AAV63399 AAZ49543 AAZ49542 AAZ49534	AAS97136 AAS97142 AAS97145 AAA38908 AAQ97504 AAQ97510 AAQ97510 AAQ97510	AAC15113 AAC15113 AAC47002 AAH44157 AAT34541 AAT31540 AAT35842 AAC35842 AAC35842 AAC35842 AAC35842	AAA28909 AAL51275 AAC78732 AAC78732 AAC78732 AAA7343 AAA773443 AAA77389 AAS23791 AASS2791
17 20 21 21 21 21	22 2 2 4 4 4 7 1 1 6 1 1	25 25 25 25 25 25 25 25 25 25 25 25 25 2	20 20 20 20 20 20 20 20 20 20
739 739 739 729 711 324	1497 1497 321 321 321 321 432	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1106 1106 1321 444 443 714 714 817 979
71.1 71.1 71.1 70.9 70.7 70.4	699.3 699.3 677.2 66.9 65.9		601.3 601.3 601.0 600.6 600.5 600.2 600.2
309.4 309.4 309.4 308.4 307.4 302	301.4 301.4 301.4 300.2 292.2 291.2 284.4	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	266.8 266.8 266.8 266.8 263.6 263.6 263.6 262.2 262.2 262.2 262.2 262.2 262.2
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ALIGNMENTS

RESULT 1

	5 BP.							Murine monoclonal anti-idiotype antibody 11D10 VL cDNA.		Monoclonal antibody 11D10; anti-idiotype antibody; mucin;	G; tumour; breast cancer; vaccine; ss				alifiers										-			•	
	AAT85149 standard; cDNA; 435 BP.				(updated)	(first entry)		Lonal anti-idic		ntibody 11D10;	at qlobule; HMF				Location/Qualifiers	160	/*tag= a	61435	/*tag= b						96WO-US20757		95US-0575762.	96US-0591965	05C35C0-01150
AAT85149	AAT85149 star		AAT85149;		25-MAR-2003	04-JAN-1998		Murine monocl		Monoclonal ar	human milk fa		Mus musculus.		Key	sig_peptide		mat_peptide			WO9722699-A2.		26-JUN-1997.		19-DEC-1996;		20-DEC-1995;	26-JAN-1996;	13-750-1996.
AAT8514	Π	XX	AC	XX	DT	DT	xx	DE	XX	KW	ΚW	xx	SO	××	FH	FT	FT	FT	FT	××	PN	XX	PD	XX	PF	××	PR	PR	QQ

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                                                              Murine; mouse;
human milk fat
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                                                                                                                                                                                                                                                                                                                                                 12-JUN-1998;
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            16-MAR-1999
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                                                                                                                                                                              This cDNA sequence encodes the light chain variable region VL
(AAW85149) of monoclonal anti-idiotype antibody 11D10 produced by
the particular of monoclonal anti-idiotype antibody 11D10 produced by
the bybridoma cell line AFCC 12020. 11D10 was obtained by immunising
naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype
response. It elicits an immune response against a specific epitope
of a high mol.wt. mucin of human milk fat globule (HMFG). It
induces an immunological response to HMFG in mice, rabbits, monkeys
and patients with advanced HMFG-associated tumours. Pharmaceutical
compositions and vaccines comprising 11D10, 11D10 polypeptides
cand/or 11D10 polynucleotides are claimed. Also claimed are
diagnostic kits and methods of using 11D10, 11D10 polypeptides
associated tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA
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                                                                                                     al anti-idiotype antibody 11D10 - elicits immune response human milk fat globule disease associated tumours,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 435;
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 435; DB 18;
100.0%; Pred. No. 6.8e-128;
ive 0; Mismatches 0;
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                                  Chatterjee M, Chatterjee SK, Foon KA;
                                                                                                                                                      Claim 11; Page 94; 130pp; English.
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Matches 435; Conservative
                                                                                                                             especially breast cancer
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         (KENT ) UNIV KENTUCKY
                                                             WPI; 1997-341690/31
                                                                           P-PSDB; AAW27119
                                                                                                     Monoclonal
against hum
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                                                                          antibody; light chain; variable region; anti-idiotype; ss; globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the coding sequence for the murine antibody 11D10 light chain variable region. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for treating breast tumours.
                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "antibody 11D10 light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_except= (pos:163..165, aa:Thr)
/note= "no stop codon is given at the 3' end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delaying development of, or treating, HMFG-associated tumours - using anti-idiotype antibody 11D10 raised against antibodies to human milk fat globule protein
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Antibody 11D10 light chain variable region coding sequence
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delaying the development, of or treating HMFG/CEA-associated tumours. The present CDNA sequence encodes the light chain variable region of the mouse 11D10 anti-idiotype antibody.
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                                                                                                                                                                       61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTTGGGACAAAGAGTCAGT
                                                                                                                                                                                                                                       GACATCCAGATGACCCCAGTCTCCTTATCTGCCCTCTCTGGGACAAAGAGTCAGT
                                                                                                                                                                                                                                                                                                                                               GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                            241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
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                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nence encoding the leader, variable region and first 16 AAs of constant region of the kappa-chain (light chain) of MOPC41.
                                                                                                                          ö
                                                                                              Length 435;
                                                                                                                           Indels
                                                             Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
                                                                                           Score 435; DB 25;
Pred. No. 6.8e-128;
0; Mismatches 0;
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13..78
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                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 435; Conservative 0
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/praduct= "Mouse 11D10 anti-idiotype antibody light chain
/product= region"
/note= "No stop codon is given"
1..60
fi..43 b
61..43 c
             GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 420
                                                                                                                                                      Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; HMFG; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (EAS). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                     Mouse 11D10 antibody light chain variable region coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                   TCCAGTAAGCTTGGG 435
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                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..435
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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AAL5127
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The present sequence encodes mouse light chain variable region. This recombinant DNA is derived from PCR A which amplifies antibody light chain variable region (VL). The transformant produced using the VL gene was used transform competent E. coli cells. The peptide produced by transformants neutralises interleukin-18. This is useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases which are caused by excessive immunosaction. The peptide has anti-allergic, anti-inflammatory, immunosuppressive, hematopoletic, leukocytopoietic, antialgic, antipyretic and hepatic-function improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA 240
                                                                              Mouse light chain variable region; VL; variable region light chain; interleukin-18; immunopathies; inflammatory discreter; autoimmune disease; mouse; anti-allergic; anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic; antialgic; antipyretic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACATCCAGATGACCCAGTCTCCATATCTGCCTCTCTGGGAGAAGAGTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 407 BP; 96 A; 99 C; 96 G; 116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 384.6; DB 21
Pred. No. 6.7e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanimoto T, Kurimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 28-29; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                           Mouse light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0177580.
98JP-0289044.
98JP-0365023.
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llarity 96.6%;
Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-118341/11.
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393; Conserv
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                                                                                                                                                                                                                                   musculus
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
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                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishida Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activities
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Best Local Si
Matches 393;
                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATITITGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 GACATCCAGATGACCCAGTCTCCATATCTGCCTCTCTGGGAGAAAGAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The pref. vector or plasmid of the invention has a double-stranded DNA seq. coding for a variable region of a light or heavy chain of 1gG, or for a variable region of a light or heavy chain of an immunoglobulin specific for an enzyme or surface protein. The sequence esp. codes for a variable region of a light chain having 95-115 AAs or for a variable region of a heavy chain having 110-125 AAs esp. including the D region of the heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Transformed expression vectors or plasmid(s) - with double stranded DNA sequence coding only for desired part of polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 394.8; DB 4; Length 450;
Pred. No. 4e-115;
0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 450 BP; 108 A; 114 C; 104 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Page 40-41; 68pp; English
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94.9%;
83EP-0001655
                                                         82US-0358414
83US-0558551
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                                                                                                                                                                                                                                      Moore KW, Zaffaroni A;
                                                                                                                                           (SCHE ) SCHERING CORP. (DNAX-) DNAX RES INST.
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                                                                                                                                                                                                                                                                                                                        P-PSDB; AAP30251
10-MAR-1983;
                                                      15-MAR-1982;
05-DEC-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant conjugate antibody molecules comprise a monoclonal antibody specific for a surface structure of antigen presenting cells (APC), genetically modified to contain at least one antigen cells (APC), genetically modified to contain at least one antigen cells (APC), genetically modified to contain at least one antigen cells of delivering the antigen to APC and eliciting an immune response to the antigen. The new conjugates are useful as vaccines and are able to elicit an enhanced immune response without the use of an adjuvant. In a specific example, a conjugate was constructed using the murine anti-human class II monoclonal antibody secreted by hybridoma anti-human class II monoclonal antibody secreted by hybridoma tandemly linked T and B cell epitope derived from HIV MN strain. The present sequence encodes the light chain variable region which was PCR amplified from 44H104 and used in the preparation of a conjugate with antigen CLTB36.
      GAAGATTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
                                                     GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG
                                                                                                                                                                                                                                                           Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.
                                                                                                                                                                                                                                                                                Antibody; light chain; variable region; hybridoma cell line 44H104; immune response; enhance; stimulate; vaccine; immunodiagnosis; antigen delivery; ss.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..387
/*tag= a
/note= "Encodes 44H104 light chain variable region,
Including secretion signal; termination
codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant conjugate antibody mol., modified for delivering an antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or immuno:diagnosis
                                                                                                    361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATC 407
                                                                                                                 Cates GC, Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caterini JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1A; 64pp; English.
                                                                                                                                                                                     BP
                                                                                                                                                                                  AAT77851 standard; cDNA; 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-CA00400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0483576
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-077271/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW22537.
                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9640941-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1996;
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                                                                                                                                                                                                                                   03-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anand NN,
                                                                                                                                                                                                          AAT77851;
                                                     301
                                                                             301
                                                                                                                         361
                                                                                                                                                           RESULT 6
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                                                                                                                                                                                                                                                            CTCACTTGTCGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 180
                                                                                                                                                                                                                                                                                                                                                                              127 CTCACTTGTCGGGCAAGTCAGGAAATTAGTGGTTACTTAACCTGGCTTCAGCAGAAACCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAGAGTCAGT 120
                                                                                                                                          9
                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                        1 ATGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTTGTTTCCAGGTACCAGATGT
                                                                                                                                                                   7 ATGAGGGTTCCTGCTCACGTTTTTGCTTCTTGTTGCTCTTGGTTTCCAGGTACCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; mab; light chain; VL; conjugate antibody; antigen delivery; immune system; vaccine; detecting agent; antibacterial; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag = a //product = Murine 44H104 mab VL" //product = Murine 44H104 mab VL" //transl_except = (pos:277..279, aa:Thr) //ord = "This translation exception occurs while decoding for murine mab VL alternative version (AAE20204); CDS does not include stop codon"
                                                                                           ;
0
                                            Score 323.4; DB 18; Length 387;
Pred. No. 1.8e-92;
); Mismatches 36; Indels 0;
Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine 44H104 mab variable light chain (VL) DNA.
                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACCAAGCTGGAAATAAAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                            74.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0007093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0007093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2002 (first entry)
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /partial
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(BARB/) BARBER B H.
(CATE/) CATES G A.
(CATE/) CATERINI J E.
                                                                  Similarity
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395
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           Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT 120
                                                                                                                                                                                                                                                                                                                                                                CTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA 180
                                                                                                                                                                                                                                                                                                                                                                                                         GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant conjugate antibody, comprising a monoclonal antibody specific for a surface structure of antigen presenting cells genetically modified to contain an antigen molety for the purpose of delivery of the antigen moiety to antigen. Presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable light chain (VL) DNA.
                                                                                                                                                                                                                                                                                                                               7 Argasserrecrecreacerrrresecrretrecreserrecassance
                                                                                                                                                                                                                                                                                                           1 AFGGGGGCCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT
                                                                                                                                                                                                                                                                                        Gaps
                                                                      Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                                                                                                                      Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig; blosynthetic single polypeptide chain binding site; ss.
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                                                                                                                                                                                                                                                                 DB 24; Length 387;
                                                                                                                                                                                                                                                               74.3%; Score 323.4; DB 24; Length 90.6%; Pred. No. 1.8e-92; ive 0; Mismatches 36; Indels
                     MH;
                     Klein
                                                                                                                                                                                                                                             Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
                     Caterini JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence encoding 520C9 sFv protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGACCAAGCTGGAAATAAAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGACCAAGCTGGAGCTGAAA 387
                                                                                                                 Example 1; Fig 1A; 28pp; English.
                    GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                     Cates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ46084 standard; cDNA; 739
                                        WPI; 2002-267519/31.
P-PSDB; AAE20200, AAE20204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
                                                                                                                                                                                                                                                                           Best Local Similarity 90.6
Matches 345; Conservative
                    Barber BH,
(KLEI/) KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
07-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
                    Anand NN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ46084;
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                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                Query Match
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116 TCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGTGACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575 CCAAAAGGTTCAGTGGCAGTCGGTCTGGGTCAGATTATTCTCTCACCATCAGTAGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen - for imaging or treating breast or ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New single chain Fv polypeptide binding to C-erbB-2 tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.3e-88;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGGGGGACCAAGCTGGAAATAAAACGGGCTGAT 390
                                                                                                                                                                                                                                                                                                                                                                                              DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%; Score 309.4;
llarity 95.2%; Pred. No. 6.3
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; pages 60-61; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Oppermann H,
Location/Qualifiers
11..739
/*tag= a
                                                                                                                                                                                                                                                                                                                   (CETU ) CETUS ONCOLOGY CORP. (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
AAT36880
ID AAT36880 standard; CDNA; 739
                                                                                                                                                                                                                                                                  92US-0831967
                                                                                                                                                                                                               93WO-US01055
                                                                                                                                                                                                                                                                                                                                                                                                 Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1993-272889/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR39569
                                                                                                           W09316185-A2
                                                                                                                                                                                                               05-FEB-1993;
                                                                                                                                                                                                                                                                  06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                              Houston LL,
                                                                                                                                                            19-AUG-1993
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574 295

355 634

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construct. This was constructed by connecting the Vh and VI genes with a DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal antibody useful in targeting c-erbB-2 antiben. This dimeric construct can be used in the methods of invention of imaging a preselected antigen expressed in a mammal. The methods are used in magnetic resonance imaging of c-erbB-2 or related antigens in cancer diagnosis. The blosynthetic constructs have enhanced properties as in vivo targetting agents in comparison with intact monoclonal antibodies or their Fab fragments. The antigen with greater apparent avidity, including of an epitope on an antigen with greater apparent avidity, including greater tumour specificity, tumour localisation and tumour retention properties than that of the Fab fragment having the same CDRS as the construct.
                                                                                                                                                         296 AGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Imaging of antigens in vivo - using dimers of single-chain antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of a 520C9 sFv' (single chain Fv)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520C9 anti-c-erbB-2 sFv' dimeric construct gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "520C9 sFv' polypeptide"
                                                                                                                                                                                                                  356 GAGGGGGGCCAAGCTGGAATAAAACGGGCTGAT 390
                                                                                                                                                                                                                                      695 GAGGGGGACCAACCTGGAAATAAAACGGGCTGAT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Columns 33-36; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c-erbB-2; tumour; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                     AAV21798 standard; cDNA; 739
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92US-0831967.
95US-0461838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houston LL, Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-311318/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW53170
                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1998
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05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                          AAV21798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                               RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGTGACATCCAGATGACCCAGTCTCCCTTATCTGCCTCTCTGGGACAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 GATCCGATATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTTGGGAGAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 TCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Variable heavy (VH) and variable light (VL) genes were cloned from a 520C9 hybridoma cDNA library, using probes directed toward the antibody constant and joining regions. A two single chain FV (SFV) gene was constructed by connecting the VH and VL genes with a Ser rich polypeptide linker. The resulting 520C9 two sFV gene, transformed into E. coll, and protein expression vector, addn. of IPTG to the culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A composin. comprising a carrier and the 2 sFv protein prod. can be used for in vivo imaging, and drug targetting experiments. The EsFv protein prod. is a homodimer, in which both fragments target the same antigen, therefore giving greater binding avidity and longer tissue retention times, compared to individual sFv protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compsns. contg. antigen-targetting antibody fragment constructs comprising dimer of single-chain Fv fragments
                                                                                                                                                     520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv; construct; polypeptide linker; C-terminal amino acid sequence; in vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 309.4; DB 17; Length
Pred. No. 6.3e-88;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
                                                                                                             520C9 anti-c-erbB-2 two single chain Fv construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ring DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "START codon absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Columns 33-36; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oppermann H,
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.18;
95.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0133804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0133804
92US-0831967
                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-333194/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW02280
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J7-0CT-1993;
                                                      25-MAR-2003
29-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1993;
06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houston LL,
                                                                                                                                                                                                                                                                                                                                                                                      US5534254-A.
                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1996
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                  AAT36880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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imaging agents, especially to tumours
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391..711
                                                                                                                                                 al Similarity
319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                           176
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                                                                                                                                                                                                                                                                                                                                         962
                                                                                                                                                                                                                                                                                                                                                                                356
                                                                                                                                        Query Match
                                                                                                                                                   Local
                                                                                                                                                            Matches
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AAZ49543
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                                                                                                                                                                                                         634
                                                                                                                                                                                                                                        56 GATGTGACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGACAAAGAG
                                                                               116 TCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGG
                                                                                                                   CCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTG
                                                                                                                                                                                                                              AGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCG
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding single-chain Fv fragment specific for antigens - and having C-terminal tail for crosslinking to form dimer with improved pharmacokinetic properties, used to deliver drugs and
                                               ;
0
                            DB 19; Length 739;
                                               Indels
         G; 193 T; 0 other;
                                               16;
                                                                                                                                                                                                                                                                     GAGGGGGGCCCAAGCTGGAAATAAAACGGGCTGAT 390
                                                                                                                                                                                                                                                                               695 GAGGGGGACCAACCTGGAAATAAAACGGGCTGAT 729
                                                                                                                                                                                                                                                                                                                                                                                                                      520C9 sFv; antigen; tumour cell; antibody 520C9; targeted delivery; antigen-expressing cell; ss.
                            Score 309.4; DB 1 Pred. No. 6.3e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ring
                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFV
        C; 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP. (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= 520C9
                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                        AAV63399 standard; cDNA; 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93US-0133804.
92US-0831967.
95US-0461386.
                           71.18;
95.28;
       A; 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0461386
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   sFv DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houston LL, Huston JS,
         BP; 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-023541/02.
P-PSDB; AAW80424.
                                     Best Local Similarity
Matches 319; Conserv
        Sequence 739
                                                                                                                                                                                                                                                                                                                                                                               28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-FEB-1992;
05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 520C9
                                                                                                                                                                                                                                                                                                                       RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GATGTGACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGACAAAGAG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes an an antibody 520C9 sFV. Variable heavy and light sequences of antibody 7520C9 are connected, together with a serine linker, to produce the present single chain FV gene. The present sequence exemplifies the invention. Dimers of the single chain FV are used for targeted delivery of drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium) to antigen-expressing cells, particularly for treatment or diagnosis of tumours (especially of ovary or breast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     575 CCAAAAGGTTCAGTGGCAGTCGGTCTGGGTCAGATTATTCTCTCACCATCAGTAGCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACATCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pEscFv#125-2H.HT recombinant cDNA, EscFv#125-2H.HT; interleukin-18; immunopathikes; inflammatory disorder; autoimmune disease; mouse; anti-allergic; anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic; antialgic; antipyretic; ss.
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                   71.1%; Score 309.4; DB 20; Length 739; 95.2%; Pred. No. 6.3e-88; 1ve 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*teg= a
/note= "single chain variable region fragment
neutralising IL-18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "Encodes light chain variable region"
                                                                                                                                                                                                                                                                              Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGGGGGCCCAAGCTGGAAATAAAACGGGCTGAT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       695 GAGGGGGACCAACCTGGAAATAAAACGGGCTGAT 729
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/note= "Encodes heavy chain
Example 1; Columns 33-36; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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GGTGTCCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGC 288
                                                                                                                                                                                                                                                             99EP-0304977
                                                                                                                                                                                                                                                                                                      98JP-0365023
                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                               Okura T,
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-118341/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
ses 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY44595
                                                              musculus
                                                                                                                                                                                                                                                            24-JUN-1999;
                                                                                                                                                                                                                                                                                           12-OCT-1998;
22-DEC-1998;
                                                                                                                                                                                                                     EP974600-A2
                                                                                                     mat_peptide
                                                                                                                                                                            mat_peptide
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                                                                                                                                                                                                                                                                                                                                               Nishida Y,
                                                              Mus muscul
Synthetic.
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Matches
                                                                                             Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTAATTATACTGGCTT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTAC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This was used
                                                                                                                                                                                                                                                to transform competent E. coli cells. The peptide produced by transformants designated Escry#125-2H.HT, neutralises interleukin-18. This is useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases which are caused by excessive immunoreaction. The peptide has anti-allergic, anti-inflammatory, immunosuppressive, hematopotetic, leukocytopotetic, antialgic, antipyretic and hepatic-function improving activities. The DNA is also useful for the production of transgenic animals and plants.
                                                                                                                                                                         New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                     CAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                 70.9%; Score 308.4; DB 21; Length 729; llarity 95.2%; Pred. No. 1.3e-87; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                      present sequence is pEscFv#125-2H.HT recombinant cDNA.
                                                                                                                                                                                                                                                                                                                                             Sequence 729 BP; 174 A; 177 C; 192 G; 186 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGTTCGGAGGGGGGACCAAGCTGGAAATAAAAC 382
                                                                                                                          Tanimoto T, Kurimoto M;
                                                                                                                                                                                                                   Claim 13; Page 25-26; 32pp; English
                                                                                                     (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PESCFv#125-2H recombinant cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ49542 standard; cDNA; 711
                                                             98JP-0177580
                                                                      98JP-0289044,
98JP-0365023,
                                        99EP-0304977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                          Nishida Y, Okura T,
                                                                                                                                             WPI; 2000-118341/11.
                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 318; Conserv
                                                                                                                                                        P-PSDB; AAY44596
                                                                                22-DEC-1998;
                                        24-JUN-1999;
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                                                           24 -JUN-1998;
EP974600-A2
                    26-JAN-2000
                                                                      2-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          49
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                                                                                                                                                                                                                                                                                                                                                                                     Matches
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The present sequence is pBscFv#125-2H recombinant cDNA. This was used to transform competent E. coli cells. The peptide produced by transformants designated EscFv#125-2H, neutralises interleukin-1B. This is useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases which are caused by excessive immunoraction. The peptide has anti-allorgic, anti-inflammatory, immunosupressive, hematopoletic, leukocytopoietic, anti-inflammatory antipyretic and hepatic function improving activities. The DNA is also useful for the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAAGAGTCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCT
                           immunopathies; inflammatory disorder; autoimmune disease; mouse; anti-allergic; anti-inflammatory; immunosuppressive; hematopoietic; leukocytopoietic; antialgic; antipyretic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.7%; Score 307.4; DB 21; Length 711; llarity 95.2%; Pred. No. 2.7e-87; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "single chain variable region fragment
neutralising IL-18"
recombinant cDNA; EscFv#125-2H; interleukin-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "Encodes light chain variable region"
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/note- "Encodes heavy chain variable region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanimoto T, Kurimoto
                                                                                                                                                                                                                                                            Socation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 23-24; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgenic animals and plants.
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61 GACATCCAGATGACCCAGTCTCCATCCTTATCTGCCTCTCTGGGACAAAGAGTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present cDNA sequence derived from hybridoma #125-2H, encodes mouse anti-interleukh-18 antibody light chain variable region (VL). It can be used in the production of recombinant monoclonal antibody #125-2HmAb, which is capable of neutralising biological activities of interleukin-18. The antibody has antiinflammatory, immunosuppressive, leucocytopoietic, antiallergic antiaplace, antiallergic and hepatotropic activity and can be used for prevention and treatment of autoimmune diseases, immunopathies and inflammatory disorders caused by excessive immunoreaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL; hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory; immunosuppressive; leucocytopoietic; antialgic; antipathergic; hepatotropic; treatment; autoimmune disease; immunopathy; inflammatory disorder; immunoreaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..324
/*tag= a
/label= Anti-IL-18_antibody_light_chain_variable_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
AGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse anti-IL-18 antibody VL encoding cDNA from hybridoma #125-2H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 306.4; DB 21; Length 324; llarity 96.6%; Pred. No. 4.1e-87; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 324 BP; 83 A; 78 C; 76 G; 87 T; 0 other;
                                                                                                                                                                                                                        349 ACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanimoto T, Kurimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
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98JP-0289044.
98JP-0365023.
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P-PSDB; AAY44587.
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12-OCT-1998;
22-DEC-1998;
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                                                                                                       1 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCCCTCTCTGGGAGAAGAGTCAGT
                                    CTCACTTGTCGGCCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCA
                                                                                                                                            241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                                          c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AAQ46083, AAR39568).
(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New single chain Fv polypeptide binding to 'C-erbB-2 tumour antigen - for imaging or treating breast or ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB;
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                                                                                                                                                                                                                                                  GGGACCAAGCTGGAAATAAAACGG 384
                                                                                                                                                                                                                                                                             GGGACCAAGCTGGCAATAAAACGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour antigen; c-erbB-2; G-FIT;
                                                                                                                                                                                                                                                                                                                                                AAQ46086 standard; cDNA; 1605
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(first entry)
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/*tag=
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07-FEB-1994
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Sequence 1605 BP; 434 A; 354 C; 373 G; 444 T; 0 other;

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Gaps

Best Local Similarity Matches 313; Conserv

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1501 AGCCTTGAGTCTGGAGATTTTGTAGTCTATTACTGTCTACATAGATATCCTGTAC 1560
                                                  49 GGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGA 108
                                                                                                                                                                                                     289 AGCCTTGAGTCTGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTAC
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 Score 302; DB 14; Length 1605;
Pred. No. 1.9e-85;
0; Mismatches 25; Indels 0;
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Query Match 69.4%;
Best Local Similarity 92.7%;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-779-784-11

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US-09-817-853-5

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US-09-924-099-11

US-09-924-099-11

US-09-924-099-11

US-09-924-099-11

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US-09-844-736-3

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sequence 19, Appl sequence 37859, A sequence 1210, Ap sequence 1210, Ap sequence 120, Appl sequence 29, Appl sequence 16, Appl sequence 19, Appl sequence 11, Appl sequence 11	· .	0; Gaps 0
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US-00-918-995-37859 US-09-918-995-37859 US-09-878-178-1210 US-10-046-935-1210 US-10-06-543-1205 US-10-06-543-1205 US-10-06-543-2025 US-08-75-784-20 US-08-75-784-20 US-08-75-784-20 US-09-919-344-7 US-10-156-794-16 US-10-158-646-55 US-09-764-304-9 US-10-158-646-55 US-09-764-304-9 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-195-752-19 US-10-10-244-11 US-10-040-244-11 US-10-040-244-11 US-10-040-244-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13 US-09-844-684-13	ALIGNMENTS 4 4 7 861,294 840 244 Sion 4:0	Mismatches
	SULT 1 Sequence 1, Application US/0986129, Patent No. US20020098190A1 GENERAL THORMATION: GENERAL THORMATION: GENERAL THORMATION: TITLE OF INVENTION: CHATTERJEE APPLICANT: Kenneth A. FOON TITLE OF INVENTION: TUMORS BEARI FILE REFERENCE: 304142000620 CURRENT FAPLICATION NUMBER: US/09 CURRENT FAPLICATION NUMBER: 06/049; PRIOR APPLICATION (1)(435) NAME/KEY: MAL_PEPTIGE LOCATION: (1)(435) NAME/KEY: MAL_PEPTIGE LOCATION: (1)(435) NAME/KEY: MAL_PEPTIGE LOCATION: (1)(435) NAME/KEY: MAL_PEPTIGE LOCATION: (1)(435) DOUGY MATCH	Conservative 0;
266 265 261 261 261 261 261 261 261 261 261 261	SULF 1 Sequence 1, Application Patent No. US20020098196 GENERAL INPORMATION: APPLICANT: Malaya CHATTALE OF INVENITON: CO TITLE OF INVENITOR TITLE OF INVENITOR THE OF INVENITOR TO THE OF INVENITY TO THE OF INVENITOR TO THE OF	435;
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-861-294 Sequence 1, Patent No. GENERAL INF APPLICANT: TITLE OF I TITLE OF I TITLE OF I FILE REFER CURRENT APPL PRIOR FILI PRIOR APPL PRIOR	Matche

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1 AIGGGGGCCCCTGCTCAGATICTIGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT

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	RESULT 3 US-09-924-099-27 Sequence 27, Application US/09924099 Patent No. US20020128450A1 Sequence 27, Application US/09924099 Patent No. US20020128450A1 SEQUENCE INVENDANTION: APPLICANT: NISHIDA, Yoshihiro APPLICANT: NISHIDA, Takanori APPLICANT: NISHIDA, Takanori APPLICANT: TANIMOTO, Massahi TITLE OF INVENINO: PEPTIDE FILE REFERENCE: CURRENT APPLICATION NUMBER: US/09/924,099 CURRENT FILING DATE: 2001-08-08 PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23 PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12 PRIOR PLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98 PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22 PRIOR PLICATION NUMBER: RELIER APPLICATION NUMBER: JP 289,044/98 PRIOR PLICATION NUMBER: EARLIER PILING DATE: 1998-12-22 SEQ ID NOS: 33 SEQ ID NOS: 33 SEQ ID NOS: 33 COCATION: (1)(407) MAME/KEY: CDS LOCATION: (1)(60) US-09-924-099-27	Query Match 88.4%; Score 384.6; DB 10; Length 407; Best Local Similarity 96.6%; Pred. No. 2.6e-119; Action 19; Action 19;
0 0 0 0 0 0 0 0 0 0	RESULT 2 US-10-367-506-1 Sequence 1, Application US/10367506 Publication No. US200301525751 GENERAL INFORMATION: APPLICANT: Melaya CHATTERJEE APPLICANT: Renneth A. FOON TITLE OF INVENTION: TUMORS BEARING HWEG AND CEA ANTIGENS FILE REFERENCE: 304142000620 GURRENT FILING DATE: 2003-02-13 PRIOR FILING DATE: 2003-02-13 PRIOR PAPLICATION NUMBER: 05/09/861,294 PRIOR FILING DATE: 1997-06-11 PRIOR FILING DATE: 1999-06-11 NUMBER OF SEQ ID NOS: 38 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 435 TYPE: DNA ORGANISM: Wus musculus FEATURE: NAME/KEY: CDS NAME/KEY: CDS NAME/KEY: Sig_peptide	FEATURE: TAME/KEY: mat_peptide

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Gaps

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APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0062.NPUSOI.
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEO ID NO 10
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Pred. No. 9e-101;
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   4.6e-115;
     d. No. 4.6e.
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. Sequence 10, Application US/102
; Publication No. US20030138862A1
; GENERAL INFORMATION:
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91.1%;
 96.28;
   Best Local Similarity 96.2
Matches 381; Conservative
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CRGANISM: Mouse
US-10-268-883-10
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                                                    CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAAATTATACTGGCTTCAACAGGAACCA 180
                                                                                                                                                                         GAAGATITIGIAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Miller, David J.
APPLICANT: ASAKURA, KUNIHIKO
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
                                                                                                                                                                                                                                               GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATC 407
                                                                                                                                                                                                                                                                   Length 402;
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1 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AGG-1996
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 26,742
REFERNCE/DOCKET NUMBER: 1199-1-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08779784
Publication No. US20020164325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Ave, STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: ROdriguez, Moses
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nucleic acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Jersey
: USA
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STATE:
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                                                                                                  181 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
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                                                                                                                                                                                                                                                                 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACAACGTTCGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
FILING DATE: 08-AUG-1996
APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/779,784 FILING DATE: 07-JAN-1997 CLASSIFICATION: 424
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOSAS-DOS
SOFTWARE: Patentin Release #1 0.
                                                                                                                                                                                                                                                                                                                                           361 GGGACCAAGCTGGAAATAAAA 381
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Publication No. US20020164325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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STRANDEDNESS:
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                                           AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : CHIMERIC ANTIBODIES FOR DELIVERY OF ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
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COMPUTER: IEM PC COMPATIBLE
OPERATORS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.3%; Score 323.4; DB 9; 90.6%; Pred. No. 1.1e-98; 1ve 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                          367 GGCACCAAGCTGGAAATCAAACGG 390
                                                                                                                                                                                                   361 GGGACCAAGCTGGAAATAAAACGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,09:
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Cates, Michel H
APPLICANT: Rieln, Michel H
TITLE OF INVENTION: CHIMERIC ANT
                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09007093
Patent No. US20020025315A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (416) 595 1163
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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Matches 345; Conserv
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STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Canada
ZIP: M5G 1R7
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US-09-007-093-1
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Length 351;

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ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
Imaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                         DB 8;
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                                                                                                                                          Pred. No. 2e-98;
0; Mismatches
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APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <un>

CLASSIFICATION:

                                                                                                                         Score 322.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Huston, James S. Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
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                                                                                                                       74.2%;
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                                                                                                                                          Best_Local Similarity 95.9
Matches 331; Conservative
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                                      linear
                  STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: c
HYPOTHETICAL: NO
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US-08-779-784-16
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                                    Gaps
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APPLICANT: Asskura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
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Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCC 344
                                  Indels
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWAREN PATENTIN RELEASE #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-37N-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-30G-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
                                    13;
 DB 8;
Score 323.2; DB 8 Pred. No. 1.2e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/08779784 Publication No. US20020164325A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 16:
74.38;
96.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodriguez, Moses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201-487-5800
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LENGTH: 351 base pairs
                                 331; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                Similarity
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Query Match
              Best Local 9
Matches 33
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49 GGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTTGGGA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NISHLEAN, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
APPLICANT: TANIMOTO, Tadao
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT FLILIG DATE: 2001-08-08
PRIOR PELICATION NUMBER: US/09/924,099
CURRENT FLILIG DATE: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP 289,044/98
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                                 Length 729
                     Score 308.4; DB lu; ......
Pred. No. 1.7e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGTTCGGAGGGGGACCAAGCTGGAAATAAAAC 382
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                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                     70.9%;
95.2%;
                                                                          Conservative
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                                   Query Match
Best Local Similarity
Matches 318; Conserv
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hes 317; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-924-099-19
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US-09-924-099-20
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                                                                                                                                                                                                                                                                                                                                                                                               116 TCAGTCTCACTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 AACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 CCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635 AGTCTGAAGATTTTGTAGTCTATTACTGTCTACAATATGCTATTTTTCCGTACACGTTCG 694
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Sequence 20. Application US/09924099

Sequence 20. Application US/09924099

Sequence 20. Application

APPLICANT: NISHIDA, Yoshihiro

APPLICANT: OKURA, Takanori

APPLICANT: TRAIMOTO, Masashi

TITLE OF INVENTION: PEPTIDE

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/924,099

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511

PRIOR PELING DATE: BARLIER FILING DATE: 1999-06-23

PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-3

PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-12

PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-12

PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22

WHOREN OF SEQ ID NOS: 33

SEG ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 GATGTGACATCCAGATGACCCAGTCTCCATCCTTATCTGCCTCTCTTGGGACAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Artificial DNA to code for the amino acid sequence OTHER INFORMATION: SEQ OTHER INFORMATION: 1D NO:10
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                   Length 739;
                                                                                                                                                                                                        /product= "520C9 sFv polypeptide
                                                                                                                                                                                                                                                                                                   Score 309.4; DB 10; Length
Pred. No. 7.7e-94;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 GAGGGGGGCCAAGCTGGAAATAAAACGGGCTGAT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695 GAGGGGGACCAACCTGGAAATAAAACGGGCTGAT 729
                                                                                                                                                                                                                  sequence" , SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-09-887-853-5
             INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERRISTICS:
LENGH: 739 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEFAX: 617-248-7100
                                                                                                                                                                                     LOCATION: 1.729
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                   71.1%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 319; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 20
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CAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCT
                                                        GGTGTCCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGC
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TANIMOTO, Masashi
TILLOO ENVENTION: PEPTIDE
FITLE OF INVENTION: PEPTIDE
FITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/224,099
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR RILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR RILING DATE: EARLIER FILING DATE: 1998-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTTGGGACAAAGAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 306.4; DB 1 Pred. No. 5.5e-93;
                                                                                                                                                                               ACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 381
                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09924099
Patent No. US20020128450A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.4%;
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: NISHIDA, YOSHIHITO
APPLICANT: OKURA, Takanori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.4
Best Local Similarity 96.6
Matches 313; Conservative
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; ORGANISM: Mus musculus
US-09-924-099-11
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RESULT 13

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181 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCCAAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/797,481
FILING DATE: 28-P6-2001
CLASSIFICATION: CURKOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/361,772
FILING DATE: 27-JUL-1999
APPLICATION NUMBER: US 08/579,940
FILING DATE: 28-DEC-1995
FILING DATE: 28-DEC-1994
                                                                                                Kohler, Heinz
Foon, Kenneth A.
Charterjee, Sunil K.
TITLE OF INVENTION: WURINE ANTI-IDIOTYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414200102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 22..447
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               APPLICANT: Chatterjee, Malaya
Sequence 1, Application US/09797481 Patent No. US20010047083A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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	111111 1 1 1 1 1 1 1 1	di d	FILING DATE: April 9, 1997 APPLICATION NUMBER: 05 60/044,455 FILING DATE: April 12, 1996 APPLICATION NUMBER: US 08/631,085. FILING DATE: April 12, 1996 ATTORNEY AGENT INFORMATION: NAME: POlizzi, Catherine M. REGISTRATION NUMBER: 40,130 REFERENCE/DOCKET NUMBER: 304142000402 TELECOMMUNICATION INFORMATION: TELEFRAX: (415) 813-5600 TELEFRX: (415) 494-0792 INFORMATION FOR SEQ ID NO: 3:
Qy 241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCTTGAGTCT 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 14 US-09-844-736-3 ; Sequence 3, Application US/09844736 ; Patent No. US20020041872A1 ; GENERAL INFORMATION: APPLICANT: Chatterjee, Malaya Chatterjee, Sunil K. TITLE OF INVENTION: METHODS OF DELAXING DEVELOPMENT OF CHATTER OF CHATTER OF CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1		SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-844-736-3 Query Match 61.5%; Score 267.6; DB 9; Length 447; Best Local Similarity 76.8%; Pred. No. 7.7e-80; Matches 327; Conservative 0; Mismatches 99; Indels 0; Gaps 0; QY 1 ATGGGGCCCTGCTCAGATTCTTGGGTTCTTGTTGCTCTTGTTTCCAGGTACCAGATGT 60 11

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                                                                                                                                                                                                                                                                                                                                                  142 ATCACTTGCAAGGCGAGTCAGGACATTAATGGTTATTTAAATTGGTTCCAACAAGAACCA 201
                                                                                                                                                                                                                                                                                                                                                                                              181 GATGGAACTATAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 AGGTICAGTGGCAGTGGGATCTGGGCAAGTTTACTCTCTCACCACCACCAGCAGGAATAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGGG 360
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                                                                                                                                                                    Gaps
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                                                                                                                                    Length 447;
                                                                                                                                Score 267.6; DB 14; Length
Pred. No. 7.7e-80;
0; Mismatches 99; Indels
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
JOPOLOGY: linear
US-10-162-396-3
                                                                                                                                Query Match 61.5%;
Best Local Similarity 76.8%;
Matches 327; Conservative
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442 TCCAGT 447
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Search completed: August 30, 2003, 19:50:20 Job time : 161.241 secs

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BG962572 602829953.
BG963548 602831226
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6988.707 Million cell updates/sec
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435
1 ATGGGGGCCCCTGCTCAGAT......CACCATCCAGTAAGCTTGGG 435
                                                                                    August 30, 2003, 16:08:05 ; Search time 1512.79 Seconds
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
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BG962572
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BY083003
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Gapop 10.0 , Gapext 1.0
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em_gss_rod:*
em_gss_phg:*
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gb_gssl:*
gb_gss2:*
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Maximum DB seq length: 2000000000
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gb_htc:*
gb_est3:*
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em_gss_pln:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                            /tissue_type="tumor, metastatic to mammary"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies.
dr. Library constructed by Life Technologies.
linestigator providing samples: Gilbert Smith, NIH"
158 c 150 g 160 t
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                                                                                               GGGCTCCTGCGCAGGTTTTTGGCTTCTTGTTGCTCTTGTTTCCAGGTGCCAGATGTGACA
                                                                                                                                                                                                                                                                                                                                                                 CTTGTCGGGCAAGTCAGGACATTGGTATTAACTTACATTGGCTTCAGCAGGAACCAGATG
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                                                                                                                                                                                                                                                       DB 10; Length 630;
                                                                                                                                                                                                                                                    Score 373.2; DB 10; Length
Pred. No. 4.3e-106;
0; Mismatches 33; Indels
                        /organism="Mus musculus"
/mol_type="mRNA"
/strain='cZECH |
/db_xref='taxon:10090"
/clone='INAGE:4008404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Location/Qualifiers
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Mus musculus
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Best Local Similarity 92.3%;
Matches 393; Conservative
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BG963548 112-JUN-2001 1002831226F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4985791 5',
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/db_xref="taxon:10090"
/clone="IMAGE:4984788"
/clone="bildow (TI phage-resistant)"
/clone_lib="NUL_GAR_CO24"
/note="forgan: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lnl.gov

Plate: LLAM10991 row: i column: 13

High quality sequence stop: 685.

I. 926
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                                                                                                                                                                                                                                                                         . /organism="Mus musculus"
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Mus musculus
                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="FVB/N"
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TCCAGTGAGC 444
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Mus musculus cDNA clone K630040M06 5', mRNA sequence.
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374 bp mRNA linear EST 07-DEC-2003
BY083003 RIKEN full-length enriched, pooled tissues, adult spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 ATCAGGCCTCCTGCTCAGTTTCTTGGCATCTTGTTGCTTGGTTTCCAGGTGCCCAGATGT 75
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                1 (bases 1 to 714)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4985791"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 334; DB 12;
Pred. No. 9.8e-94;
                                                                                                                                                                                                                                    Plate: LLAM10994 row: c column: 08
High quality sequence stop: 712.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
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Matches 370; Conservative
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RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomanau, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Brade, D.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dargarlan, T., Fletcher, C.F., Forrest, J.E., Cousins, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Ming, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maltais, L., Marchina, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., P.A., Majott, D.R., Maltais, L., Warchina, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Red, J.C., Ravasina, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reden, J.C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Tasadale, M., Sakazume, N., Vand, L., Yan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Azakaya, T., Fukuda, S., Hara, A., Hashiuwe, W. Imotani, K., Ishiiayawa, A., Yasunishi, A., Yoshino, M., Materston, R., Lander, R.S., Rogers, J., Birney, E. and Hayashizaki, Y. Rander, M., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sakazume, N., Sakai, M., Materston, R., Lander, R.S., Rogers, J., Birney, E. and Hayashizaki, Y. Sasaki, R., Sakai, R., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fmall: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Normalization and subtraction of cap-trapper-selected cDNAs tprepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                          Mus musculus (house mouse)
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BG518527 874 bp mRNA linear EST 02-APR-2001 602578261F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491798 5', mRNA sequence.
BG518527.1 GI:13513491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 TGAAGATTTTGTAGCCTATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTCGGAGG
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                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The T.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can life through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Hitp://image.llnl.gov
High quality sequence stop: 827.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 827;
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Pred. No. 3.5e-79;
0; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                      1. .827
/organism="Mus musculus"
  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5066931"
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80.7%;
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ATCCAGTGAGC 443
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348; Conserv
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Best Local 8
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                                                                                                                    /clone="refall lucyou"
/clone="refall lucyou"
/clone="lib="RIKEN full-length enriched, pooled tissues,
adult spleen, etc."
/clone=lib="RIKEN full-length enriched, pooled tissues,
adult spleen, etc."
/clone=lib="RiKEN full-length enriched, pooled tissues,
adult stage=adult tissue_type=kidney,sex=male),
(dev_stage=adult,tissue_type=heart,sex=male),
(dev_stage=adult,tissue_type=heart,sex=male),
(dev_stage=adult,tissue_type=stomanch,sex=male),
(dev_stage=adult,tissue_type=stomanch,sex=male),
(dev_stage=adult,tissue_type=stomanch,sex=male),
(dev_stage=adult,tissue_type=stomanch,sex=male),
(dev_stage=14 days embryo,tissue_type=whole body,sex=mix),(dev_stage=17 days embryo,tissue_type=whole body,sex=mix),(dev_stage=15 days pregnant, adult,tissue_type=shnion
/sex=female),(dev_stage=10 days neonate,tissue_type=brain
/sex=mix),(dev_stage=10 days neonate,tissue_type=heart
/sex=mix),
/sex=mix),
/sex=mix),
/sex=mix),
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/sex=mix)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212
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Pred. No. 1.7e-89;
); Mismatches 14; Indels
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                                                       organism="Mus musculus"
                                                                                                           /db_xref="taxon:10090"
  Location/Qualifiers
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                                                                              _type="mrna"
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ilarity 95.9%;
Conservative (
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Matches 328;
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BF579422 891 bp mRNA linear EST 12-DEC-2000 602093833F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208144 5',
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/organism="Mus musculus"
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FvB_NN"
/db_xref="taxon:10090"
/clone="IMAGE:4208144"
/lab_host="DH10B (T1 phage-resistant)"
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NOI_CGAP Library."
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                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 09
High quality sequence stop: 711.
Location/Qualifiers
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 7.5e-79;
0; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordai
Mammalla; Eutheria; Rodent
                                                                                                                                                                         BF579422.1 GI:11653134
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Best Local Similarity 80.7%;
Matches 347; Conservative
                                                                                                                                     mRNA sequence.
BF579422
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                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E I 'Chases I to 874)

E I 'Chases I to 874)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (Inc.

CDNA Library Preparation: Life Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stops: 843.
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//octe="Organ: lung; Vector: pCMV-SPORT6; Site_l: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT_Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
132 c 205 g 203 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                          musculus (house mouse)
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79.38;
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Best Local Similarity 79.3
Matches 341; Conservative
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	QY 301 GAAGATTTGTAGCCTATTACTGTCTACTATTGTCTCCGTAACGTTCGAGGG 350 	OY 361 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTCCCACCA 420	Oy 421 TCCAGTAAGC 430 	SULT 9 580940	LOCUS BF580940 725 bp mRNA linear EST 12-DEC-2000 DEFINITION 602100636F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4224032 5', mRNA sequence.	ACCESSION BF580940 VERSION BF580940.1 GI:11654652 KEYWORDS EST. SOURCE Mus musculus (house mouse)	NISM	Mammalla; Eutherla; Kodentla; 1 (bases 1 to 725) NIH-MGC http://mgc.nci.nih.gov.National Institutes of Health.	JOURNAL Unpublished COMMENT Contact: Robert Strausberg, Ph.D. Emall: cgapbs r@mall.nlh.gov	Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	nttp://image Plate: LLAM9 High quality	source 1/25 /organia="Mus musculus" /mol_type="mRNA" /mof_type="mRNA" /strain="FVB/N"	/db_xrer="Taxon:10090" /clone="IMAGE:4224032" /db_host="DHIOB (TI phage-resistant)" /dlone lth="MIOT Cab Coa"	/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.6 kb. Constructed by Life_	Technologies, Note: this is a NCI_CGAP Library." BASE COUNT 207 a 183 c 159 g 176 t , ORIGIN	Query Match 65.6%; Score 285.2; DB 10; Length 725; Best Local Similarity 80.5%; Pred. No. 2.2e-78; Matches 346; Conservative 0; Mismatches 83; Indels 1; Gaps 1;	OY 1 ATGGGGCCCCTGCTCAGATTCTTGGTTCTTGTTGCTTGTTTCCAGGTACCAGATGT 60 1	OY 61 GACATCCAGATGACCCAGTCTCCATCCTTATCTGCCTCTGGGACAAAGAGTCAGT 120	
OY 361 GGGACCAAGCTGGAAATAAAAGGGGCTGATGCTGCACCAACTGTATCCATCC	Qy 421 TCCAGTAAGC 430 	SULT 8	BF382283 LOCUS LOCUS DEFINITION 602101109F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224267 5', mRNA sequence.		_	A RS		es, Inc. onsortium (LLNL)	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	Figh quali High quali	source I626 /organism="Mus musculus" /mol_type="mRNA"	/db.xref="tvaxn:10090" /db.xref="IMAGE:422467" /lab.hst="IMHOB(T1 phage-resistant)"	/cloue_ling="Nc_CGAP_CGAP" /note="Organ: colony Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.6 kb. Constructed by Life	BASE COUNT 178 a 153 c 137 g 158 t NCI_CGAP LIDIALY." ORIGIN	Ouery Match 65.6%; Score 285.2; DB 10; Length 626; Best Local Similarity 80.5%; Pred. No. 2.1e-78; Matches 346; Conservative 0; Mismatches 83; Indels 1; Gaps 1;	Qy 1 ATGGGGCCCCTGCTCAGATTCTTGGTTCTTGCTTGTTTTCCAGGTACCAGATGT 60 1		121 CTCACTTGTCGGGCAAGTCAGGACTTGGTATTAACTTACACTTGGCACGCAAGTCACCACTTGGTATTAACTTACATTGGCTTCAGCAGGAACCACTAGATCAGAACTCAGCAACTAGAACCAATTAGAACTAACATTAGAACCAAATTAACATTAGAACTAAACTAAAAACAAAAAAAA	181 GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTAGGTTCTGGTGTCCCCAAA	DD 180 GATGGAACTGTTAAACTCCTGATCTATTACACATCAAATTTACATTCAGGGGTCCCATCA 239

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 72)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                      310 ATCACTTGCAGGTCAAGTCAGGACATTAGTAATTAAAACTGGTATCAGCAAACCA
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                                                                                                                                                                                     GATGGAACTATTAAACGCCTGATCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
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/lab_host="DHJDB (T1 phage-resistant)"
/clone_lib="NCI_GGAP_CC24"
/note="Gragan colon; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_GGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13895 row: c column: 15
High quality sequence start: 165
High quality sequence stop: 634.
Location/Qualifiers
I. 1459
//organism="Musm musculus"
//gtrain="FVB/N"
                                    GATGGAACTATTAAACGCCTGAFCTACGCCACATCCAGTTTAGGTTCTGGTGTCCCCAAA
                                                   AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
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Pred. No. 1.6e-77;
0; Mismatches 92;
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13894 row: i column: 15
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                                          Length 762;
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                                          DB 10;
                                         Score 278.8; DB 10;
Pred. No. 2.3e-76;
0; Mismatches 92;
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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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BF581992 772 bp mRNA linear EST 12-DEC-2000 602099448F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4219618 5', mRNA sequence.
BF581992:1 GI:11655613
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LINL at:
http://magg.lln.gov
Plate: LIAM9801 row: o column: 11
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                                                                                                                                                                                                                      Length 901;
                                                                                                                                                                                                                   Score 278; DB 13; Length 9 Pred. No. 4.4e-76; 0; Mismatches 95; Indels
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Best Local Similarity 77.9%;
Matches 335; Conservative (
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1. .830
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/clo
  Found through the I.M.A.G.E. Consortium/LLNL
                         http://image.llnl.gov
Plate: LLAM11638 row: e column: 12
High quality sequence stop: 820.
Location/Qualifiers
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ilarity 77.7%;
Conservative
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Best Local Simi
Matches 334;
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B1455041.1 G1:15245697
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
204 c 175 g 176 t lothers
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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Pred. No. 1.3e-75;
0; Mismatches 77; Indels
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    772
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/mol_type="mRNA"
    /strain="FVB/N"

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ity sequence stop: 715.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.5%;
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Best Local Similarity 80.73
Matches 322; Conservative
  quality
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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BE284224 695 bp mRNA linear EST 13-JUL-2000 601099161F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491798 5',
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Subaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 695)
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Score 276.4; DB 12; Length 830; Pred. No. 1.4e-75; 0; Mismatches 96; Indels 0;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8536 row: i column: 15
High quality sequence stop: 562.
Location/Qualifiers
CCE
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_l: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

182 c anpl 9
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                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
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  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Pred. No. 2.3e-75;
0; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:3491798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 63.4%;
Best Local Similarity 79.1%;
Matches 340; Conservative (
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434 TCCAGTGAGC 443
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ORIGIN
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Search completed: August 30, 2003; 19:44:46 Job time : 1519.79 secs

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August 30, 2003, 22:04:11; Search time 24.8154 Seconds (without alignments) 927.461 Million cell updates/sec
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145
1 MGAPAQILGFLLLEFPGTRC.....IKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                     1107863
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Murine monoclonal	Mouse 11D10 antibo	Antibody 11D10 lig	Murine anti-human	Murine 44H104 mab	Murine 44H104 mab	Anti-idiotype anti	Antibody ABX-CBL 1	Mouse derived RT3
SUMMARIES	D	AAW27119	AA016292	AAW87593	AAW22537	AAE20200	AAE20204	AAR74966	AAY39452	AAW95480
	DB	18	24	20	18	23	23	16	20	20
	Length	145					129			
di	Query e Match Length DB ID	100.0	100.0	62.1	22.8	22.8	22.8	20.7	20.7	20.0
	Score	145	145	90	33	33	33	30	30	29
	Result No.	-	7	m	4	S	9	7	80	6

Mouse derived RT3	Light chain of mon		Light chain of Mlf		Escherichia coli l	Mouse light chain	Sequence of the le	Anti-idiotype mono	MAb 1A7 light chai	Light chain variab	Monoclonal antibod	EscFv#125-2H recom	520C9 anti-c-erbB-	520C9 ant1-c-erbB-	520C9 sFv sequence	Escrv#125-2H.HT re	Sequence of 520C9	P4-14 single chain		3B10xP4-14 bispeci	Sequence of G-FIT.	650E2 hybridoma VL	Anti-bovine prion	Filamentous phage	Chimeric antibody	Mouse monoclonal a	-	Mouse antibody FB3	Mouse antibody F4-	TSH receptor antib	TSH receptor antib	WOW-1 Fab light ch	Amino acid sequenc	m16	Single chain Fv fr
				21 AAY44587	4 AAE34366		K	.7 AAW03199	AAY4920	0 AAY28468						AAY4459		23 AAU72863		3 AAU72872	AAR3957	_	m	2 AAB3509	AAP9303	8 AAW2708	7 AAW1593	6 AAR7545	6 AAR7545	4 ABP967	4	1 AAY9525	1 AAY689	3 ABG31731	.2 AAR15443
				108 2																			112 2		213 1		216 1								
20	20	20	20	20.0	20	20	50	20	20	50	20	20	20	20	20	20	20	20	20	20	20	19	19	19	19	19	19	19	19	19	19	19	19	19	19
29	29	29	29	29	29	29	53	29	29	29	29	29	29	29	29	58	29	29	29	29	29	28	28	28	28	28	28	28	28	. 58	28	28	28	28	28
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

				dy 11D10 VL region	pe antibody; mucin	breast cancer; vac								: :	on I.		"complementarity determining region		0n 2"		
119 AAW27119 standard; Protein; 145 AA.		(updated)	. entry)	Murine monoclonal anti-idiotype antibody 11D10 VL region.	Monoclonal antibody 11D10; anti-idiotype antibody; mucin;	human milk fat globule; HMFG; tumour; breast cancer; vaccine.		Location/Qualifiers	20	/label- Sig_peptide	21145	/label= Mat_protein	.43	4	/note≕ "iramework region	Tabel CDR1		5569	/label= FR2 /note= "framework region 2"		(1250) - (200)
tandard;				oclonal a	antibody	fat glob	ns.	Loc	120	/la	21.	/1a	21.	/la	ou/	/19	ou/	55.	/la	70.	; ;
AAW27119 ID AAW27119 s xx	AAW27119;	25-MAR-2003	04 - JAN - 1998	Murine mon	Monoclonal	human milk	Mus musculus.	Key	Peptide		Protein		Region		Bodion	mod for		Region		Region	

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Mouse 11D10 antibody light chain variable region.
                               (first entry)
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                                                                                                                                                                                                                  WO200292012-A2
                                                                                                                    Mus musculus
                                                                                                                                                                                                                                      21-NOV-2002
           AA016292;
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                                                                                                                                                                                                                                                                                                                                                                          hybridoma cell line ATCC 12020. IDEO was obtained by immunishing hybridoma cell line ATCC 12020. IDEO was obtained by immunishing native mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elloits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides (see also AAT85149-50) are claimed. Also claimed are diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMFG-associated tumours. IlD10 is also used in a claimed method of palliating HMFG-associated disease and in claimed kits to
                                                                                                                                                                                                                                                                                                                                                                   This polypeptide sequence comprises the light chain variable region
                                                                                                                                                                                                                                                                                                     Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                 /label= CDR3
/note= "complementarity determining region 3"
/label= FR1
note- "complementarity determining region 2"
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100.0%; Pred. No. 5.7e-125;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detect or quantify anti-HMFG antibody. (Updated on 25-MAR-2003 to correct PR field.)
 /note-
77.108
/label-FR3
---- "framework region 3"
                                                                                             /note- "framework region 4"
                                                                                                                                                                                                                                                  Foon KA;
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                                                                                                                                                                                           96US-0591965.
96US-0766350.
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                                                                                                                                                                                  95US-0575762
                                                                                                                                                                                                                                                Chatterjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                         especially breast cancer
                                                                                                                                                                                                                            (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                      WPI; 1997-341690/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 145 AA;
                                                                                                                                                                                                                                                                                 N-PSDB; AAT85149
                                                                                                                                                                                                                                                Chatterjee M,
                                                                                                                    WO9722699-A2
                                                                                                                                                            19-DEC-1996;
                                                                                                                                                                                           26-JAN-1996;
13-DEC-1996;
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AAO16292 standard; Protein; 145 AA.

AA016292 ID AA01

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/label= signal_peptide
21..145
/note="Mature murine 11D10 antibody light chain variable
region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for pelaying the development, of or treating HMFG/CEA-associated tumours. The present amino acid sequence represents the light chain variable region of the mouse 11D10 anti-idiotype antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of anti-idiotypic antibodies for human milk fat globules (HMFG) or carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
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Mouse; murine; vaccine; tumour; human milk fat globules; HMFG; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
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100.0%; Pred. No. 5.7e-125;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 145; Conservative
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AAW87593
ID AAW8
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56 LQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115
                                                                                                                        116 YTFGGGTKLEIKRADAAPTVSIFPPSSKLG
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Matches 33; Conserv
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                                                                                                                                                                Murine; mouse; antibody; light chain; variable region; anti-idlotype;
human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the light chain variable region of the murine antibody 11D10. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for treating breast tumours.
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/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "complementarity determining region
                                                                                                                Antibody 11D10 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                 "mature protein"
                                                                                                                                                                                                                                                                                                                                                "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "encoded by TGG'
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= framework_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label = CDR1
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97US-0049540.
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                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                    'note-
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hes 90; Conserva
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                                                                    16-MAR-1999
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Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                          Antibody; light chain; variable region; hybridoma cell line 44H104; immune response; enhance; stimulate; vaccine; immunodiagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant conjugate antibody mol., modified for delivering an antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or
                                                                                                                                                                                                                                     Murine anti-human class II monoclonal antibody 44H104 VL chain.
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100.0%; Pred. No. 2.3e-22;
ive 0; Mismatches 0;
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AAW22537 standard; Protein; 129
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Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
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Note: This sequence SEO. ID. NO:2 is stated to be similar to the sequence shown in fig 1A (AAE20200). However these sequences differ.
                    antigen delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
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                  Murine; mab; light chain; VL; conjugate antibody; anti-
immune system; vaccine; detecting agent; antibacterial
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 23;
Pred. No. 2.3e-22
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                                                                                                                                                                          /note= "Encoded by TAT'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 11-12; 28pp; English
                                                                                                                              Location/Qualifiers
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                               (ANAN/) ANAND N N.
(BARB/) BARBER B H.
(CATE/) CATES G A.
(CATE/) CATERINI J E.
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Best Local Similarity
Matches 33; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                    (BARB/) BARBER B H. (CATE/) CATES G A. (CATE/) CATERINI J I (KLEI/) KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AA;
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                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                     US2002025315-A1
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                    Murine;
                                                                                       Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a monoclonal antibody specific for a surface structure of antigen presenting cells genetically modified to contain an antigen moiety for the purpose of delivery of the antigen moiety to antigen. Presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable
                                                                                                                                                                                                                   Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
immune system; vaccine; detecting agent; antibacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          light chain (VL).
Note: This sequence SEO.ID.NO:2 is stated to be similar to the sequence shown in page 11-12 of the specification (AAE20204).
However these sequences differ.
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100.0%; Pred. No. 2.3e-22;
iive 0; Mismatches 0;
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                                                                                                                                                                          Murine 44H104 mab variable light chain (VL).
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                                         AAE20200 standard; Protein; 129
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N-PSDB; AAD32138.
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                                                                                                                              18-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2002
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                                                                                  AAE20200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATE/)
(KLEI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ANAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BARB/)
                                                                                                                                                                                                                                                                                      Mus sp.
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RESULT 5
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                                                                                                         NAMES OF THE PROPERTY OF THE P
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Gaps

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invention relates to a monoclonal antibody (MAD) with an isotype that fixes complement and a variable region that binds to the epitope on CD147 bound by the IgM MAD ADX-CBL, providing that the antibody is not CBL1. The MAD can selectively kill activated T-cells, activated B-cells or resting or activated monocytes. The products and methods can be used for treating diseases involving activated T-cells or B-cells or monocytes, e.g. graft versus host disease (GVHD), organ transplant rejection diseases (e.g. renal transplant, ocular transplant), cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catalytic; antibody; phage display; immunising; phage expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
                                                     This sequence represents the light chain of the antibody ABX-CXL. The
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inscrting coding into a phage expression vector and isolating the catalytic antibodies
  disease, cancers, autoimmune diseases and inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fitzgerald K, Kenten JH;
Smith R, Titmas RC, Williams RO;
                                                                                                                                                                                                                                                    Length 206;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                 1.9e-19;
                                                                                                                                                                                                                                                    Score 30; DB 20;
Pred. No. 1.9e-19
                                                                                                                                                                                                                                           20.7%; Sco...
100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                                                                       113 SSPYTFGGGTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                 AAW95480 standard; Protein; 92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0273146
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McCafferty J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHISWELL D.
DARSLEY M J.
FITZGERALD K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KENTEN J H.
MARTIN M T.
MCCAFFERTY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-105036/09.
N-PSDB; AAX00879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMITH R.
TITMAS R C.
WILLIAMS R C
                                                                                                                                                                                                                            206 AA;
                                                                                                                                                                                               (e.g. arthritis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prodrug; scFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS5855885-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin MT,
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW95480;
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chiswell
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MCCA/)
(SMIT/)
(TITM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHIS/)
(DARS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILLY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                   AAW95480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia; activated B-cell; monocyte; graft versus host disease; therapy; cancer; organ transplant rejection disease; lymphoma; pancreatic disease; autoimmune disease; inflammatory disease; arthritis; binding site.
                                                                                                                                                                                                                                                                                                   AAR74960-R74969 are clones of the anti-idiotype antibodies Idio3, Idio20, Idio20, Idio27 and Idio33 against a human anticancer monoconal antibody. These antibodies and DNA encoding them are useful in pharmacological, medical and biochemical fields of research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hales J;
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                      Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibody, used for treating e.g. graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Culwell AR, Green LL, Ha
Liu Q, Weber RF, Yang X;
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                                                                                                                                                                                                                                                                                                                                                                                               Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 16; 1
Pred. No. 1.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                               116 YTFGGGTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 YTFGGGTKLEIKRADAAPTVSIFPPSSKLG 141
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
              l..13
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody ABX-CBL light chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corvalan JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipani JA,
Location/Qualifiers
                                                                                                                                                                                                                                                                          Example 5; Page 19; 28pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY39452 standard; Protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                   20.7%; Scor.
100.0%; Pre
                                                                                                      93JP-0272950
                                                                                                                               93JP-0272950
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99US-0244253
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.7
Best Local Similarity 100.
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ivanov VE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blacher RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABGE-) ABGENIX INC.
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                                                                                                                                                                                  WPI; 1995-182987/24
                                                                                                                                                         (HAGI/) HAGIWARA Y.
                                                                                                                                                                                                                                                                                                                                                                    146 AA;
                                                                                                                                                                                               N-PSDB; AAQ90431
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                                                  JP07101999-A
                                                                                                      06-OCT-1993;
                                                                                                                              36-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1999
                                                                            18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39452;
            Peptide
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Mus sp
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                                                                            The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The catalytic antibodies can be isolated by preparing an antigen; optionally immunising an animal with the antigen; generating a antibodies; selecting phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically cot the antigen; screening the selected phage display antibodies; selecting phage display antibodies which bind specifically catalytic activity to substrate; and isolating the catalytic antibodies; where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of light chain pCR pattern C from mouse derived RT3 phage antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; Length 92;
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Smith R, Titmas RC, Wi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.0%; Score 29; DB 100.0%; Pred. No. 8e-ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPKRFSGSRSGSDYSLTISSLESEDFV 76
Example 4; Fig 11; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95476 standard; Protein; 92 AA
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Martin MT, McCafferty J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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FITZGERALD K.
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WILLIAMS R O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCCAFFERTY J. SMITH R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-105036/09.
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MARTIN M T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHISWELL D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-1994;
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14-JUL-1994;
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(DARS/)
(FITZ/)
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The invention relates to methods for producing catalytic antibodies
displayed on a phage. The method comprises: (a) generating a gene library
of antibody-derived domains; (b) inserting coding for the domains into a
phage expression vector; and (c) isolating the catalytic antibodies. The
phage expression vector incorporates a histidine peptide in tandem with a
comprehence, performing an animal with the antigen; generating an
antigen; optionally immunising an animal with the antigen; generating a
cand VL domains from the immunised animal; cloning the VH
completes; selecting phage display antibodies which bind specifically
cantibodies; selecting phage display antibodies which bind specifically
contact the phage expression vector incorporates a histidine peptide in
tandem with a myc peptide. The processes are used to produce catalytic
antibodies, which can be used for in vivo activation of a prodrug. The
present sequence represents a genetic sequence of light chain pattern A
crossent sequence represents a genetic sequence of light chain pattern A
crosses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pathogenic virus; tropism; mucosa; CDR region; monoclonal antibody; respiratory syncytial virus; RSV; WP6 protein; rota virus; RV; viral infection; inhibit; fusion; protection; transcription; antiviral agent; prophylaxis; diagnosis; infection; contamination.
inserting coding into a phage expression vector and isolating the catalytic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide(s) recognising viral epitope with tropism to mucosa useful for, e.g. diagnosing, preventing and treating viral infection(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.0%; Score 29; DB 20; Length 92; 100.0%; Pred. No. 8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain of monoclonal antibody RS-255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPKRFSGSRSGSDYSLTISSLESEDFV 76
                                                                                                                       Example 4; Fig 9A-F; 117pp; English.
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Best Local Similarity 100.0
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-390320/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2758331-A1
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        antigen antibody type reactions, at least 1 epitope of a pathogenic virus having tropism for the mucosa. AAW70905-16 and AAW70929-46 are analogous to CDR regions of monoclonal antibodies specific for RSV. AAW70917-28 are analogous to CDR regions of monoclonal antibodies specific for site III or IV of the VP6 protein of rota virus (RV). The peptides can neutralise viral infections and may also inhibit fusion between infected and uninfected calls or calls and viruses. They provide passive or active uninfected and transcription of the virus, so are useful as antiviral agents or for prophylaxis, in human or veterinary medicine. The peptides can be labelled and used to diagnose infection or contamination by the virus. The peptides are particularly directed against RSV or RS but may also be used against papilloma, adeno, entero, polio, influenza or immune deficiency viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a monoclonal antibody (MAb) (I) that binds to a human breast cancer antigen that is also bound by MAb 454Cll and 520Cg (produced hybridoma ATCC HB8484 and HB8656, respectively). Also described is a hybridoma that produces (I). (I) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma; specific binding assay; affinity purification; drug targeting; toxin targeting; immaging; genetic; therapeutic.
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                      Length 95;
                                                                                                                                                                                                                            0; Indels
 specification describes peptides which recognise,
                                                                                                                                                                                                    20.0%; Score 29; DB 19; 100.0%; Pred. No. 8.2e-19; 1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                  SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
                                                                                                                                                                                                                                                               520C9 hybridoma VL domain SEQ ID NO:26.
                                                                                                                                                                                                                                                                                                                                   AAY90824 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 13; 57pp; English.
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88US-0190778.
84US-0577976.
85US-0690750.
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nes 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-338508/29
                                                                                                                                                                             95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating cancer
                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                           AAY90824;
                                                                                                                                                                             Sequence
                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                            RESULT 12
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and genetic or immunological therapeutics for various cancers. The present sequence represents a VL domain derived from a 520C9 hybridoma, which is used in the exemplification of the present invention.
                                                                                                                                                                                  Gaps
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Clackson TP, Chiswell DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is the light chain of clone MIF encoding an scFv fragment specific for both hen and turkey egg lysozyme (HEL and TEL). The DNA encoding the chain was amplified from a cDNA library prepditom the spleen of an unimmunised mouse. The corresponding heavy chain was also amplified from an existing construct, pSWI-VHDI.3 (Ward et al., 1989). The two fragments were assembled via a linker to prepare an scFv construct which was ligated into the fdCAT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus; g3p; binding; adsorption; gene VIII; diverse repertoire; specific binding pairs; replicable genetic display package.
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                                                                                                                                          Length 107
                                                                                                                                                                                  ;
0
                                                                                                                                      DB 21;
9e-19;
                                                                                                                            20.0%; Score ...
100.0%; Pred. No. 9e-1.
                                                                                                                                                                                                                             76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
                                                                                                                                                                                                                                                    SGVPKRFSGSRSGSDYSLTISSLESEDFV
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, Marks JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
25..34
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 46; Fig 52; 109pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                     AAR21310 standard; Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50..56
/label= CDR2
89..96
/label= CDR3
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90GB-0022845.
90GB-0024503.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McCafferty J, Pope AR, Jd
Jackson RH, Holliger KP,
Winter GP, Bonnert TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1992 (first entry)
                                                                                                                                      Query Match 20.09
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain of M1f clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-056862/07
                                                                                         107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR21310;
                                                                                           Sequence
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Length 108;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              light chain variable region (VL) encoded by cDNA derived from hybridoma 4155-24. The nucleofide sequence is used in the production of recombinant monoclonal antibody #125-24mAb, which is capable of neutralising biological activities of interleukin-18. The antibody has antialized antiantenatory, immunosuppressive, leucocytopoletic, antipyretic, antialiary and hepatotropic activity and can be used for prevention and treatment of autoimmune diseases, immunopathies and inflammatory
                                                                                                                                                                                                                                                                                                                                                                     Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL; hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory; immunosuppressive; leucocytopotetic; antialgic; antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy; inflammatory disorder; immunoreaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present protein sequence is the mouse anti-Interleukin-18 antibody
                                                                                                                                                               Gaps
vector for expression on the surface of fd bacteriophage. In this way, the VL domain was replaced by a library of VL domains to allow for selection of a broader range of antibody specificities. Several clones were isolated which bound to TEL (the parent antibody DI.3 binds exclusively to HEL). The sequences of the light chains of two of these clones, MRI and MRI are given in AAR21310 and AAR21311 see also AAR21260-307, 309-312, AAR22450, AAR22565, AAR22567-81.
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                                                                                                                                      Length 108;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                              Mouse anti-IL-18 antibody light chain variable region.
                                                                                                                                      DB 13; I
9.1e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders caused by excessive immunoreaction.
                                                                                                                                   20.0%; Score 29; DB 100.0%; Pred. No. 9.1:ive 0; Mismatches
                                                                                                                                                                                      SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
                                                                                                                                                                                                  (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                         AAY44587 standard; Protein; 108 AA
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                                                                                                                        Query Match
Best Local Similarity 100.00
These 29; Conservative
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-118341/11.
N-PSDB; AAZ49534.
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                                                                                                             108 AA;
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22-DEC-1998;
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                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                    S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody against S-surface antigen of the hepatitis B virus (HBV). The variable regions of the antibodies are useful against HBV S-surface antigens, e.g. adr, adw, ayr or ayw, particularly for neutralising or removing HBV. They may also be employed to treat or prevent HBV infection. The present sequence is Escherichia coll light
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to light and heavy chain variable regions of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New light and heavy chain variable regions of a monoclonal antibody against the S-surface antigen of the hepatitis B virus (HBV), useful for neutralizing or removing HBV, or for preventing or treating HBV
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         DB 21; L
). 9.1e-19;
cches 0;
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1.1e-18;
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                                                                                                                                                                                                                                                                                                                                 Escherichia coli light chain variable region.
                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 TFGGGTKLEIKRADAAPTVSIFPPSSKLG 130
                                                    Mismatches
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             Score 29;
Pred. No.
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20.0%; bcc.
100.0%; Pre
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/note= "CDR1"
56..62
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                                                                                                                                                                                                                                                                                               (first entry)
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                                                    Conservative
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95..102
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Best Local Similarity
Matches 29; Conserv
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Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                         hepatotropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
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Search completed: August 30, 2003, 22:09:54 Job time: 25.8154 secs

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August 30, 2003, 22:08:56 ; Search time 15.5705 Seconds (Without alignments) 1273.781 Million cell updates/sec
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145
1 MGAPAQILGFLLLEPGTRC.....IKRADAAPTVSIFPPSSKLG 145
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510680 seqs, 136781880 residues
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                                                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

	Description	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 35, Appl	Sequence 7, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 10, Appl	Sequence 6, Appli	Sequence 12, Appl	Sequence 1, Appli	Sequence 11, Appl	74,
SUMMAKIES	Ω	US-09-861-294-2	US-10-367-506-2	US-09-007-093-2	US-09-924-099-1	US-08-779-784-35	US-10-146-305-7	US-09-990-205-2	US-10-153-401-2	US-09-924-099-9	US-09-924-099-10	US-09-887-853-6	US-10-268-883-12	US-10-355-780-1	US-10-268-883-11	US-09-943-906-74
	DB	6	12	σ	10	8	14	10	15	10	10	10	12	12	12	10
	&. Query Match Length DB	145	145	129	108	130	130	149	149	237	243	243	108	112	130	109
,	& . Query Match	100.0	100.0	22.8	20.0	20.0	20.0	20.0	20.0	20.0	20.0	20.0	19.3	19.3	19.3	18.6
	Score	145	145	33	53	29	29	29	29	29	29	29	28	28	28	27
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4.			Sequence 102, App	Sequence 24, Appl	Seguence 4, Appli	Sequence 11, Appl	Sequence 1, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 2, Appli	Sequence 4, Appli	4	Sequence 72, Appl		'n		11	Sequence 2, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 25, Appl	-	3,	Sequence 130, App	Sequence 17, Appl	Sequence 7, Appli	Sequence 21, Appl	Sequence 21, Appl
9 US-09-802-077-4	3 US-U9-8UZ-U96-4 11 mg-00-00E-130-4			12 US-10-281-479A-24		15 US-10-216-484-11	11 US-09-900-766-1	9 US-09-861-294-9	12 US-10-367-506-9	9 US-09-797-481-2	9 US-09-844-736-4	15 US-10-162-396-4	10 US-09-943-906-72	9 US-09-861-294-5	12 US-10-367-506-5	11 US-09-929-665-11	11 US-09-929-546-11	14 US-10-027-770-2	14 US-10-027-770-5	9 US-09-839-447A-2	15 US-10-153-271-2	9 US-09-839-447A-25	15 US-10-153-271-25	9 US-09-756-899A-3	11 US-09-563-222-130	9 US-09-229-200A-17	9 US-09-229-200A-7	11 US-09-929-665-21	11 US-09-929-546-21
124	471	17.4	142	234	238	238	672	33	33	142	142	142	95	23	23	121	121	269	269	129	129	19	19	16	23	108	109	109	109
17.9	. L	Y	17.9	17.9	17.9	17.9	17.9	17.2	17.2	17.2	17.2	17.2	16.6	15.9	15.9	14.5	14.5	13.8	13.8	13.1	13.1	11.7	11.7	11.0	11.0	11.0	11.0	11.0	11.0
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ALIGNMENTS

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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR PILING DATE: EARLIER PILING DATE: 1999-06-23
PRIOR FILING DATE: EARLIER PILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-12
NUMBER OF SEQ ID NOS: 33
                                                            Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 SGVPKRFSGSRSGSDYSLTISSLESEDFV 84
                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                     APPLICATION NUMBER: US/09/007,093
                                          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-779-784-35
Sequence 35, Application US/08779784
                                                                                                                                                                                                                                                     NAME: Stewart, Michael I
REGIZTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFAX: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09924099 Patent No. US20020128450A1
1: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: NISHIDA, YOSHIHITO
APPLICANT: OKURA, TAKANORI
APPLICANT: TANIMOTO, TAGAO
APPLICANT: KURIMOTO, MASASHI
TITLE OF INVENTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 22.8
Best Local Similarity 100.
Matches 33; Conservative
                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Mus musculus
                      COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
  MEDIUM TYPE:
                                                                                                                                FILING DATE
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US-09-007-093-2
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; ORGANISM: Mu:
US-09-924-099-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
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Patent No. US20020025315A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Cates, George A
APPLICANT: Cates, Michel H
APPLICANT: Cates, George A
APPLICANT: Cates, George A
APPLICANT: ALAIN, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                          APPLICANT: MAIAS CHATTERJEE
APPLICANT: MAIAS CHATTERJEE
APPLICANT: MAIAS CHATTERJEE
APPLICANT: Renneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TOWNERS BEARING HAFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/09/861,294
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 145; DB 12;
Pred. No. 6.4e-122;
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STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                  121 GTKLEIKRADAAPTVSIFPPSSKLG 145
                                          121 GTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10367506
Publication No. US20030152575A1
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-367-506-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: Canada
M5G 1R7
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                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim
Matches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                US-10-367-506-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-007-093-2
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Length 108;

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Sequence 2, Application US/09990205

Patent No. US20020150572A1

GENERAL INFORMATION:

APPLICANT: FOON, Kenneth A.

APPLICANT: FOON, Kenneth A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS

FILE REFERENCE: 304142000501

CURRENT APPLICATION NUMBER: US/09/990, 205

CURRENT FILING DATE: 1998-11-16

PRIOR FILING DATE: 1998-11-16

PRIOR FILING DATE: 1998-11-16

PRIOR FILING DATE: 1998-11-17

NUMBER OF SEQ ID NOS: 5

SOSTWARE: PATENTIN VOR: 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
                                                                                                                                                                         Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                      DB 14; L
. 2.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%; Score 29; DB 10; 1000.0%; Pred. No. 2.7e-18; tive 0; Mismatches 0;
                                                                                                                                                                      20.0%; Score 29; DB 100.0%; Pred. No. 2.4
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                                                                                                                                                                                                                                                                                   102 TFGGGTKLEIKRADAAPTVSIFPPSSKLG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TFGGGTKLEIKRADAAPTVSIFPPSSKLG 149
                                                                                                                                                                                                                                                         117 TFGGGTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: WORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10153401 Publication No. US20030114398A1 GENERAL INFORMATION:
                                                                                                                                                                         Query Match 20.09
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 29; Conservative
                                                                                    ; TYPE: PRT; ORGANISM: Escherichia coli
US-10-146-305-7
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Kopatentin 1.71
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus Musculus
US-09-990-205-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
                                                              130
                                                                                                                                                                                                                                                                                                                                                                                     US-09-990-205-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 149
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-153-401-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
                                                                LENGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME CURRENCE: OV17440

CURRENT APPLICATION NUMBER: US/10/146,305

PRIOR RAPPLICATION NUMBER: KR 10-2001-26634

PRIOR FILING DATE: 2002-05-15

PRIOR FILING DATE: 2001-05-16
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                    APPLICANT: Asakura, David J.
TILLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A T.-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                        ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 20-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 20-APR-1994
ATTORNEY/AGENT INFORMATION:
TELEPRAK: 20-1437-5800
TELEPRAK: 201-437-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29; DB 8; Le
Pred. No. 2.4e-18;
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Publication No. US20020173035A1
GENERAL INFORMATION:
APPLICANT: YUHAN CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
Publication No. US20020164325A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                    GENERAL INFORMATION:
APPLICANT: Rodrigu
APPLICANT: Miller,
APPLICANT: Asakura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO FRAGMENT TYPE: N-ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                     07601
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US-10-146-305-7
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ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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CURRENT FILING DATE: 2001-08-08

CURRENT PILING DATE: 2001-08-08

FRICA PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511

PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12

PRIOR PLING DATE: EARLIER FILING DATE: 1998-10-12

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12

PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
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                                                                                                                                                                                                                                  NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.0%; Score 29; DB 100.0%; Pred. No. 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.0%; Score 29; DB 1100.0%; Pred. No. 4.1
                                                                                APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
PAPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/153,401 FILING DATE: 27-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 TFGGGTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 SGVPKRFSGSRSGSDYSLTISSLESEDFV 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                      FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 149 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09924099 Patent No. US20020128450A1
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NISHIDA, YOShihiro
                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 20.0 Best Local Similarity 100. Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                   TELEX: 706141
                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-924-099-9
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) OTHER INFORMATION: Artificially produced peptide in the form of a single other information: chain cother information: variable region fragment (scFv) which neutralizes IL-18 US-09-924-099-10
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                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/338,511
PRIOR PLING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR PLING DATE: EARLIER PILING DATE: 1998-10-12
PRIOR PLING DATE: EARLIER PILING DATE: 1998-10-12
PRIOR PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: J 365,023/98
PRIOR PAPLICATION NUMBER: EARLIER APPLICATION NUMBER: J 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 243;
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Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Le
4.2e-18;
thes 0;
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100.0%; Pred. No. *...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
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FILING DATE: 21-Jun-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/133,804
FILING DATE: <Unknown>
Sequence 10, Application US/09924099
Patent No. US20020128450A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUMTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Huston, James S.
Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09887853 Patent No. US20020168375A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                        APPLICANT: OKURA, TAKANOTI
APPLICANT: TANIMOTO, TAGAO
APPLICANT: KURIMOTO, MASSAH
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
                                                                             APPLICANT: NISHIDA, YOSHINITO APPLICANT: OKURA, Takanori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.0
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 33
SEQ ID NO 10
LENGTH: 243
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Gaps

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Indels

Length 112;

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APPLICANT: TSO, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05892.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williamson, R. Anthony
Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PROUMBER OF SEQUENCES: 86
CORRESPONDERS: ADDRESS:
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 130;
                                                                                                                                                             DB 12; L 1.7e-17;
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Pred. No. 1.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.3%; Sco. 100.0%; Pred. No. 1.1. 0. Mismatches
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                                                                                                                                                                                                                                           76 SGVPKRFSGSRSGSDYSLTISSLESEDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SGVPKRFSGSRSGSDYSLTISSLESEDF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
                                                                                                                                                           Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                 ; OTHER INFORMATION: synthesized peptide US-10-355-780-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
                                                                                                                                                                                                                                                                                                                                                                  US-10-268-883-11
; Sequence 11, Application US/10268883
; Publication No. US20030138862A1
; GENERAL INFORMATION:
                                                                                                                                                             19.3%; Sco
ilarity 100.0%; Po
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 16
SOFWARE: Patentin version 3.1
SEQ ID NO 11
EBNCTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94025
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.3
Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
                                                                                                                                                             Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-943-906-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-268-883-11
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SEQ ID NO 1
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APPLICANT: TSO, J. Yun
APPLICANT: TSO, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-Lina-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882.0062.NPUS0.
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR PELING DATE: 2003-03-26
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: USSN 60/331,965
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                          Length 243;
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Publication No. US20030143224A1

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley

APPLICANT: Williamson, Anthony

APPLICANT: Williamson, Anthony

APPLICANT: Williamson, Anthony

TITLE OF INVENTION: Antibodies Specific for Ungulate Pre-

FILE REFERENCE: UCAL-194

CURRENT FILING DATE: 2003-01-30

PRIOR APPLICATION NUMBER: US/09/627,218B

PRIOR FILING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.3%; Score 28; DB 12; Best Local Similarity 100.0%; Pred. No. 1.6e-17; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         20.0%; Scor.
100.0%; Pred. No. *...
                                                                                                                                                                                                                                                                                                                                                                                                             189 SGVPKRFSGSRSGSDYSLTISSLESEDFV 217
                                                                                                                                                                                                                                                                                                                                                                                      76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
          REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMONICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 SGVPKRFSGSRSGSDYSLTISSLESEDF 103
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-887-853-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-268-883-12
is equence 12, Application US/10268883
publication No. US20030138862A1
GENERAL INFORMATION:
                                                                                                                                                           LENGTH: 243 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                   Query Match 20.0°
Best Local Similarity 100.
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mouse
US-10-268-883-12
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LENGTH: 108
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Gaps ö

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FILING DATE: 30-Aug-2001

CLASSIPICATION: -CURROWN->
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/550,374
FILING DATE: CURROWN->
FILING DATE: CURROWN->
RELIVED TO NUMBER: 08/50,374
FILING DATE: CURROWATION:
NAME: BOAIGCATION NUMBER: 28,807
FELECOMMUNICATION INFORMATION:
TELEFRAX: 415-84-687
FELESTAX: 415-84-687
FELESTAX: CURROWN->
FERESTAX: C
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GenCore version 5.1.6
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OM protein - protein search, using sw model

; Search time 10.2181 Seconds August 30, 2003, 22:07:01 Run on:

(without alignments) 1364.679 Million cell updates/sec

145 1 MGAPAQILGFLLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 145 US-08-836-455-2 Perfect score:

Scoring table: Sequence:

283308 seqs, 96168682 residues OLIGO Gapop 60.0 , Gapext 60.0 Searched:

Total number of hits satisfying chosen parameters: Word size

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Listing first 45

PIR_76:*
1: pir1:*
3: pir2:*
5: pir3:*
: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

kappa chain V r kappa chain V r kappa chain V r kappa chain pre kappa chain V r light chain V r phosph chain (WM chain V chain V chain V chain Ig kappa chai Ig light chai Description kappa kappa kappa kappa kappa kappa kappa kappa light kappa S29593 S68212 S37484 PL0261 PL0260 PL0259 KVMSM4 B28840 DB Query Match Length Score Result Š

light chain kappa chain	ig kappa chain V r Ig kappa chain V r Ig kappa chain V r	kappa chain kappa chain kappa chain	kappa chain kappa chain kappa chain	kappa chain kappa chain	kappa chain kappa chain kappa chain
\$26332 \$26330	S26329 C33936 PL0269	S60066 A27594 K1HU11	S43528 C21056 B21056	S42263 S21668	S24206 S41809 S46370
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103	106	115 116 117	117	117	117 117 120
11.0	0.00	11.0	11.0	11.0	11.0
16	16	16 16	16	16	16 16 16
30 31	33.2 34.3	35 37	38 39 40	412	44 45 45

ALIGNMENTS

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R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Ig Kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-80 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;l-5/Region: framework l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.0%; Score 29; DB 2; Lo ilarity 100.0%; Pred. No. 8.3e-21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
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                                                                                                                                                                                                                                                                                                                                                                                                                           F;32-38/Region: complementarity-determining
F;39-70/Region: framework 3
F;71-79/Region: complementarity-determining
F;80-88/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                F;1-5/Region: framework 1
F;6-16/Region: complementarity-determining
                                                                                                                                                                                                                                                                                                                                                                                                        F;17-31/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                    C; Accession: PL0261
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RESULT 2

- m pre <u>و</u>

Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PLO260
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990
A;Titte: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat A;Reference number: PLO231; MUID:90111618; PMID:2104919

A; Molecule type: mRNA A; Residues: 1-106 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1 F:16-90/Domain: immunoglobulin homology <IMM> F:24-34/Region: complementarity-determining 1

F;50-56/Region: complementarity-determining F;35-49/Region: framework 2

us-08-836-455-2.oli.rpr

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A. Wolecule type: protein
A. Rolecule type: protein
A. Rolecule type: protein
A. Rolecule type: protein
A. Rolecule s. 23-49, 18, 51-53, LSB', 57-58, ZZ', 61-62, 'BZ', 65-76, 'B', 78-108, 110-130 <GRA
A. Experimental source: Bence Jones protein MOPC 41
C. Genetics:
A. Introns: 19,1
A. Introns: 19,1
A. Introns: 19,1
A. Introns: 19,1
A. Introns: 10,1
A. Introns a specific second in the subunits associate into C. Superfamily: immunoglobulin homology
C. Reywords: alternative initiators; heterotetramer; immunoglobulin
F.; 1-22,Domain: signal sequence #status experimental <SIG2>
F.; 2-22,Domain: signal sequence #status experimental <SIG2>
F.; 3-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F.; 38-112/Domain: immunoglobulin homology <ALMA>
F.; 45-110/Disulfide bonds: #status predicted
        R;Gray, W.R.; Dreyer, W.J.; Hood, L. Science 155, 465-467, 1967 A;Title: Mechanism of antibody synthesis: size differences between mouse kappa chains A;Title: Mechanism of antibody synthesis: PMID:4162931 A;Reference number: A94239; MUID:67056897; PMID:4162931
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1062
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Datc: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S1762
C;Accession: T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 8-82/Domain: immunoglobulin homology <IMM>
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
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Pred. No. 1.1e-20;
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100.0%; Pred. No....
0; Mismatches
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A;Status: nucleic acid sequence not shown
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Matches 29; Conservative
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28; Conservative
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A; Residues: 1-91 <CLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: immunoglobulin
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Matches 2
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N;Contains: Ig kappa chain precursor V region VK41
S;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999
C;Accession: A93211; B93211; A93815; A94239; A01922; A01923
R;Seldman, J.G.; Max, E.E.; Leder, P.
R;Seldman, J.G.; Max, E.E.; Leder, P.
A;Title: A Rappa-immunoglobulin gene is formed by site-specific recombination without fu
A;Reference number: A93211; MUID:79221900; PMID:111146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues; 1-117 < VK41>
A; Residues; 1-117 < VK41>
A; Cross-references: GB: J00866; NID: 952127; PIDN: CAA24186.1; PID: 9575660
A; Note: the sequences were determined from the differentiated gene MOPC 41 and the germ!
B; Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A; Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors A; Reference number: A93815; MUID: 77148916; PMID: 403522
A; Accession: A93815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Spacies: Musculus (house mouse)
(Spacies: Musculus Musculus (house)
(Spacies: Musculus Musculus (house)
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A;Residues: 1-33 <BUR>
A;Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
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                                                                                                                                                                                     Length 106;
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Best Local Similarity 100.0%; Pred. No. 9.7e-21;
Matches 29; Conservative 0; Mismatches 0;
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Pred. No. 9.7e-21;
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                                                                                                                                                                                                                                                                                                                                                76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
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F;57-88/Region: framework 3
F;88-97/Region: complementarity-determining
F;98-106/Region: framework 4
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A;Residues: 1-130 <PC41>
A;Accession: B93211
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A,Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-densi
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-densi
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>
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A;Title: Cloning and characterization of CDNAS coding for heavy and light chains of A;Reference number: PC4202; MUID:97082978; PMID:8964510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-225 < DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                         A;Molecule type: mRNÅ
A;Residues: 1-214 <TAK>
A;Cross-references: EMBL:D29668
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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       A; Reference number: S68211; MUID:96085223; PMID:7498516
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0; Mismatches 0;
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                                   A, Accession: S68212
A, Status: preliminary; nucleic acid sequence not
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Best Local Similarity 100.6
Matches 27; Conservative
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Best Local Similarity 100.
Matches 26; Conservative
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submitted to the EMBL Data
A; Reference number: S37483
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S37484
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S38865
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Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic acti
A;Reference number: A47271; MUID:93165660; PMID:8094556
A;Accession: B47271
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A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                nitrophenyl phosphonate-specific antibody 48G7 light chain VJ - synthetic (fragment)
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C'Bate: 06-14n-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C'Bate: 06-14n-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C'Bate: 06-14n-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
R'Seymour, R.
Submitted to the EMBL Data Library, February 1991
A'Reference number: $29593
A'Reference number: $29593
A'Reference preluminary
A'Relus: preluminary
A'Relus: preluminary
A'Relus: Preluminary
A'Relus: Relus: Relus
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A;Note: parts of this sequence were determined by protein sequencing
F;24-89/Disulfide bonds: #status predicted
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9.2e-20;
                                                                  ore 28; DB 2; L
red. No. 8.5e-20;
Mismatches 0:
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llarity 100.0%; Pred. No. 9.2
Conservative 0; Mismatches
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                                                                                                                                                                                                                                           SGVPKRFSGSRSGSDYSLTISSLESEDF 84
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                      Score 28;
Pred. No.
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                                                 19.3%; Scur.
100.0%; Pred
0; N
                                                                                                                                     Conservative
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                                                                      Query Match
Best Local Similarity
Matches 28; Conserva
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Best Local Simi
Matches 28;
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Matches 22
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A, Experimental source: strain BALB/c, cell line RP93 hybridoma cell A, More: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132 A, Note: the nucleotide sequence shown is inconsistent with authors' translation because ect except for four positions shown above C; Comment: The protein is an anti-phosphorylcholine antibody. C; Superfamily: immunoglobulin V region; immunoglobulin homology
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L. Exp. Med. 167, 954-973, 1988
A;Title: Point mutations cause the somatic diversification of 1gM and 1gG2a antiphosphor A;Reference number: JL0029; MUID:88171315; PMID:3127529
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0445
E;Raluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Fitle: A general method for chimerization of monoclonal antibodies by inve
A;Reference number: PN044; MUID:93138402; PMID:1339379
A;Reference rumber: PN0445
A;Reference number: Carrier (MIC)
A;Reference number: Carrier (MIC)
A;Reference number: Carrier (MIC)
A;Reference (MIC)
A;Re
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                              A;Accession: S38865
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-219 <KIP>
A;Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 1.5e-17;
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Best Local Similarity
Matches 26; Conserv
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A; Residues: 1-225 <CHI>
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R;Kaluza, B; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polym
A;Reference number: PNO444; MUID:93138402; PMID:1339379
A;Accession: PNO446
A;Wolecule type: mRNA
A;Residues: 1-140 <KAL>
A;Cross-references: GB:L02345
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>
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F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-140/Product: Ig light chain Kappa-2 V region #status predicted <MAT>
F:36-114/Pomain: immunoglobulin homology <IMM-
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                                                                                                                                                                   Length 128
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Pred. No. 7.9e-14;
0; Mismatches 0;
                                                                                                                                                                   15.2%; Score 22; DB 2; Ld 100.0%; Pred. No. 7.3e-14; Ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 TFGGGTKLEIKRADAAPTVSIF 138
                                                                                                                                                                                                                                                                             117 TFGGGTKLEIKRADAAPTVSIF 138
                                                                                                                                                                                                                                                                                                             C; Superfamily: immunoglobulin V region;
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100.0%; Pre
                                                                                                                                                                                                                         22; Conservative
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 30, 2003, 22:04:41; Search time 8.75839 Seconds (without alignments) 778.553 Million cell updates/sec Run on:

US-08-836-455-2 145 1 MGAPAQILGFLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 145 Title: '
Perfect score:
Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

127863 seqs, 47026705 residues Searched:

0 Word size :

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	163	P01641 mus musculu	homo	уошо	рошо	mus m	P01593 homo sapien	homo	homo	homo	рошо	homo	homo	homo	homo	mus m	P01652 mus musculu	mns	mns	P01630 mus musculu		ratt	mns	mus	P01662 mus musculu	P01664 mus musculu	P01613 homo sapien	P01629 mus musculu	P01655 mus musculu	P01634 mus musculu	mus	mus m	P01605 homo sapien
SUMMARIES	ID	S	KV5H_MOUSE	KV1I_HUMAN	KV1W_HUMAN	KV1X_HUMAN	KAC_MOUSE	KV1A_HUMAN	KV1B_HUMAN	KV1G_HUMAN	KV1H_HUMAN	KV10_HUMAN	KV1P_HUMAN	KV1Q_HUMAN	KV1R_HUMAN	KV1Y_HUMAN	KV5Q_MOUSE	KV5S_MOUSE	KV5T_MOUSE	KV2E_MOUSE	KV2F_MOUSE	KACA_RAT	KACB_RAT	KV3D_MOUSE	KV3H_MOUSE	KV3J_MOUSE	KV3L_MOUSE	KV1U_HUMAN	KV2D_MOUSE	KV3B_MOUSE	KV5B_MOUSE	KV6A_MOUSE	KV6D_MOUSE	KV IM_HUMAN
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42 12 8.3 113 1 KV2C_MOUSE P01631 mus musculu 43 12 8.3 149 1 KV5A_MOUSE P01631 mus musculu 44 11 7.6 108 1 KV5R_MOUSE P01651 mus musculu 45 11 7.6 108 1 KV5R_MOUSE P01651 mus musculu ALIGNMENTS
ESULT 1
TYSIC_MOUSE STANDARD; PRT; 130 AA.

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conversion
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P04431;
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                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-81064681; Pubmed-6777049;
MEDLINE-81064681; Pubmed-6777049;
MEDLINE-81064681; Pubmed-6777049;
MEDLINE-81064681; Pubmed-6777049;
"Variation in the crossover point of kappa immunoglobulin gene V-J recombination: evidence from a cryptic gene.";
                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAPPA CHAIN V-V REGION MOPC 173B.
  MISSING (IN 25% OF THE MOLECULES).
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Pred. No. 2.3e-10;
0; Mismatches 0; Indels
                                        Length 130
                                                          0; Indels
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                    14311 MW; SEFEOFE71D5F1BEC CRC64;
                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
1-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region MOPC 173B precursor.
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                                                                                                                                                117 AA
                                                                                      SIMILARITY
                                                                             76 SGVPKRFSGSRSGSDYSLTISSLESEDFV 104
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100.0%; Pre
0;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                EMBL; K00880; AAA39031.1; -. PIR; A01924; KVMS3B.
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                                                                                                                                                STANDARD;
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                                                                                                                                                                                                        Mus musculus (Mouse)
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117
117 AA;
                    130 AA;
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                                                                                                                                               KV5H_MOUSE
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VARIANT
NON_TER
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KV11_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                         Bentley D.L., Rabbitts T.H.; "Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes and a pseudogene."; Nature 288:730-733(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
21-JUL-1986 (Rel. 01, Created)
1-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1998 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17 kappa chain V-I region HK101 precursor (Fragment).
18 kappa chain V-I region HK101 precursor (Fragment).
19 kappa chain V-I region HK101 precursor (Pragment).
10 kappa chain V-I region HK101 precursor (Pragment).
11 kappa chain V-I region HK101 precursor (Pragment).
12 kappa chain V-I region HK101 precursor (Pragment).
13 kappa chain V-I region HK101 precursor (Pragment).
14 kappa chain V-I region HK101 precursor (Pragment).
15 kappa chain V-I region HK101 precursor (Pragment).
16 kappa chain V-I region HK101 precursor (Pragment).
17 kappa chain V-I region HK101 precursor (Pragment).
18 kappa chain V-I region HK101 precursor (Pragment).
19 kappa chain V-I region HK101 precursor (Pragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83129397; PubMed-6402305; Mentley D.L., Rabbitts T.H.; Perlution of immunoglobulin, y genes: evidence indicating that "Evolution of immunoglobulin, y genes recently duplicated human V kappa sequences have diverged by gene
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FRAMEWORK-1.
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red. No. 2e-08;
Mismatches 0; Indels
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EMBL; K01324; AAA58932.1; --
EMBL; V00558; CAA23824.1; --
PIN; A01881; K1HU11.
HSSP; P01607; 1REI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:ammune response; NAS.
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Pred. No.
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100.0%; Pre
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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117 1
117 AA;
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FRAMEWORK - 2
                                                                                                                                                                                                       EMBL; X00966; CAA25478.1; ALT_TERM.
PIR; A01884; K1HUDI.
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    MEDLINE=85014148; PubMed=6091049;
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Immunoglobulin V region; Signal.
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SMART; SM00406; IGV; 1.
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129 1
129 AA;
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Matches 16; Conserv
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ID KAC_MOUSE
AC P01837;
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SEQUENCE
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                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                               MEDLINE-85014148; PubMed-6091049;
Klobeck H.G., Combriato G., Zachau H.G.;
"Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PIR; A01883; KIHUWK.
HSSP; P01607; IREL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005857; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_HO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16; DB 1; LA Pred. No. 2.2e-08;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Walker precursor.
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Daudi precursor.
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Immunoglobulin V region; Signal.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its wase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Klobeck H.G., Combriato G., Zachau H.G.;
firmunoglobulin genes of the Kappa light chain type from two human
lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=73053310; PubMed=4638343;
Svasti J., Milstein C.;
"The complete aming acid sequence of a mouse kappa light chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Biochem. J. 126:837-850(1972).
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COMPLEMENTARITY-DETERMINING-1.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_N-V.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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KV1B_HUMAN
P01594;
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                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-81191915; PubMed-62262318;
MAX E.B., Maizel J.V. Jr., Leder P.;
MAX E.B., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
J. Biol. Chem. 256:5116-5120(1981).
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILINE-68329081; Pubmed-3138116;
de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
"Expression in non-lymphoid cells of mouse recombinant immunoglobulin
directed against the tumour marker human placental alkaline
                                                                                                                                                                                                                                                                                                 MEDLINE-81198949; PubMed=6785724; Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.; "DNA sequence of the constant gene region of the mouse immunoglobulin
                                                                                                          SEQUENCE FROM N.A.
MEDLINE-82059477; PubMed=6170937;
Hamlyn p.H., Gait M.J., Milstein C.;
Hamlyn p.H., Gait M.J., Milstein C.;
"Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
Nucleic Acids Res. 9:4485-4494(1981).
                                   Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem. 176:287-295(1988).
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            AND REVISIONS TO 53-59.
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                                                                                                                                                                                                                                                                                                                                          kappa chain.";
Nucleic Acids Res. 9:971-981(1981).
                      MEDLINE-79084137; PubMed-103625;
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PDB; 25C8; 09-JUL-99.
MGD; MGI:96495; Igk-C.
INTERPO; IPR007110; Ig-11ke.
INTERPO; IPR003597; Ig_C1.
INTERPO; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
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SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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03-JUN-95.
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"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";

"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";

"I biol. Chem. 244:3550-3560[469].

"I BIOL. Chem. 244:3550-3560[469].

"I MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

"I MISCELLANEOUS: THE IS IS A BENCE-JONES PROTEIN.

BIR, A01861; KIHUMG.

HSSP; PO1607; 1REI.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0005576; c:extracellular; NAS.

GO; GO:0005576; c:extracellular; NAS.

GO; GO:0005576; p:immune response; NAS.

InterPro; IPR001306; Ig_MC.

InterPro; IPR003506; Ig_W.

RIMERPRO; IPR003506; Ig_W.

RIMERPRO; SMOUGO; IGY: 1.

Pfam; PR00147; ig; 1.

RIMERPRO; SMOUGO; IGV: 1.

RIMERPRO; SMORT; SMOUGO; IGV: 1.

RIMERPRO; PRS00815; IG_LIKE; 1.
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1-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g kappa chain V-I region AU.
1g kappa chain V-I region AU.
1d kappa chain V-I region AU.
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
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Pred. No. 1.7e-06;
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               Score 14; DB 1; Le
Pred. No. 1.7e-06;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-I region AG.
Homo sapiens (Human).
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9.7%; Scc...
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Best Local Similarity 100.
Matches 14; Conservative
                                                        14; Conservative
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35
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108
AA;
                                   Similarity
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Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
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HSSP; PO1607; IRET.
GO; GO:0005576; Cartracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0008955; P:immune response; NAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
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100.0%;
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SMART; SM00406; IGv; 1.
PROSTTE; PS50895; IG_LIKE; 1.
Immunoglobulin V region.
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Mammalia; Eutheria; Primates;
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Best Local Similarity
                                                        MACROGLOBULIN
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Laure C.J., Matanabe S., Hilschmann N.;
The primary structure of a monoclonal IgM-immunoglobulin
(macroglobulin Gal.), I. The amino acid sequence of the L-chain of kappa-type, subgroup I.";
                                                MEDLINE=72189444; PubMed=5028201; Schiechl H., Hilschmann N.; "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
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Mono sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00047; 1g; 1.
SMART: SW00406; 1Gv; 1.
PROSITE; PS50835; 1G_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN
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Pred. No. 1.7e-06;
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                                                                                                                                             Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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100.0%; Pre
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                                                                                                                            protein Au).
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P01599;
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subgroups.";
subgroups.";
- Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
- I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
- I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
R SOS BOSO52: JUTIC.
R GO: GO:0005957; F:antigen binding activity; NAS.
R GO: GO:0005957; F:antigen binding activity; NAS.
R GO: GO:0005957; F:antigen binding activity; NAS.
R GO: GO:0006955; F:antigen binding activity; NAS.
R GO: GO:0006955; F:antigen binding activity; NAS.
R InterPro; IPR007100; Ig-like.
R InterPro; IPR003706; Ig-MC.
R InterPro; IPR003706; Ig-MC.
R Ffam: FF00047; Ig: 1.
R WARR; SM00406; IGy: 1.
R PROSITE: PS50855; IG-LIKE: 1.
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Watanabe S., Hilschmann N.;
"The primary structure of a monoclonal kappa-type immunoglobulin I
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
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COMPLEMENTARITY - DETERMINING - 1.
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Pred. No. 1.7e-06;
Mismatches 0; Indels
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Catarrhini; Hominidae; Homo.
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21 DIOMIOSPSSLSAS 34
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  Local Similarity
nes 14; Conser
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P01608;
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Homo sapiens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Palm W., Hilschmann N.;
"The primary structure of a crystalline monoclonal immunoglobulin
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        FRAMEWORK - 3.
COMPLEMENTARITY - DETERMINING - 3.
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COMPLEMENTARITY - DETERMINING - 3.
FRAMEWORK - 4.
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                                                        Length 108;
                                                       9.7%; Score 14; DB 1; Length 108
100.0%; Pred. No. 1.7e-06;
tive 0; Mismatches 0; Indels
                                          11671 MW; 08D3A6160D8D0618 CRC64;
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                    108 AA
                            BY SIMILARITY.
                    FRAMEWORK - 4
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                                                                                           DIQMTQSPSSLSAS 14
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PDB; IAR2; 12-NOV-97.
PDB; IBWW; 29-DEC-99.
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                                          108 AA;
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Best Local Similarity
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Gaps
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Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franck F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
-1- MISCELLANBOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-68362076; PubMed-5595110;
Hilschmann N.;
"Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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                                                   Length 108;
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11902 MW; 9E8143E1188BCE2A CRC64;
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PIR: A91638; KIHURY.
HISSP: P80362; LWTL.
GO: GO: 1005576; C: extracellular; NAS.
GO: GO: 0005576; P: immune response; NAS.
InterPro: IPR007110; Iq-like.
InterPro: IPR003065; Ig-MHC.
InterPro: IPR003596; Ig-WHC.
                                                   Score 14; DB 1; Le
Pred. No. 1.7e-06;
0; Mismatches 0;
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SMART: SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immoglobulin V region; Bence-Jones protein.
DOMAIN 1 23 FRAMEWORK-1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-I region Roy.
Homo sapiens (Human).
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                                  9.7%; Scc.
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108 AA.

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KV1Y_HUMAN
P80362;
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P01610;
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Eulitz M., Hilschmann N.;
"The primary structure of a human immunoglobulin L-chain of kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides and the complete anno acid sequence.";
Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
-!-MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-I region Scw.
Homo sapiens (Human)
18 kappa chain V-I region Scw.
Homo sapiens (Human)
19 kappa chain V-I region Scw.
Mammalia: Butheria: Mordata; Craniata; Vertebrata; Euteleostomi;
MCBI_TaxiD=9606;
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           COMPLEMENTARITY - DETERMINING - 2.
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                            COMPLEMENTARITY - DETERMINING - 3.
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Pred. No. 1.7e-06;
                                                                                      Query Match 9.7%; Score 14; DB 1; Length 108; Best Local Similarity 100.0%; Pred. No. 1.7e-06; Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                    11782 MW; F5ACEDE5A313DF3A CRC64;
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HSSP; PO1607; 1REI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005575; C:extracellular; NAS.
GO; GO:0005955; P:lamuue response; NAS.
InterPro: IPR003006; Ig_AMC.
InterPro: IPR003006; Ig_AMC.
InterPro: IPR003096; Ig_V.
Ffam; FF00047; Iq; I.
SMART; SM00406; IGv; I.
PROSITE; PSS0835; IG_LIKE; I.
Immunoglobulin V region; Bence-Jones protein.
DOMAIN
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-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
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                     FRAMEWORK - 3.
  FRAMEWORK - 2
                                        FRAMEWORK - 4
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                                                                                                                                                                                                      PRT;
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                                                                                                                                          1 DIQMTQSPSSLSAS 14
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                                                                                                                                21 DIQMTQSPSSLSAS 34
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108 AA;
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Best Local Similarity
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1 DIQMTQSPSSLSAS 14

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Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-!- MISCELLANGOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
PIR; A01876; K1HUWE.
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MEDLINE-95086080; PubMed-7993911;
Huang D.-B., Chang C.-H., Anisworth C., Bruenger A.T., Eulitz M.,
Solomon A., Stevens F.J., Schiffer M.;
"Comparison of crystal structures of two homologous proteins:
21-JUL-1986 (Rel. 01, Created)
15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
17 kappa chain V-I region WEA.
18 kappa chain V-I region KeA.
18 kappa chain V-I region WEA.
19 kappa chain V-I region WEA.
10 kappa chain V-I region WEA.
11 kappa chain V-I region WEA.
12 kappa chain V-I region WEA.
13 kappa chain V-I region WEA.
14 kappa chain V-I region WEA.
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18 kappa chain V-I 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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COMPLEMENTARITY-DETERMINING-1.
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Pred. No. 1.7e-06;
); Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11840 MW; 9249B61F0945618C CRC64;
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GO: GO:0005576; C:extracellular; NAS.
GO: GO:0003823; F:antigen binding activity; NAS.
GO: GO:0006955; P:immune response; NAS.
InterPro: IPR007110; Ig-like.
InterPro: IPR003065; Ig_MHC.
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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Monoclonal antibody.
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RAPPA chain V-I region WAT.
Homo sapiens (Human)
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100.0%; Pre
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structural origin of altered domain interactions in immunoglobulin light-chain dimers."; Blochemistry 33:14848-14857(1994).
                                                                                                    SEQUENCE OF 1-35.
MEDLINE-81267384; PubMed-6167731;
MEDLINE-81267384; PubMed-6167731;
Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
Popp R.A., Solomon A.;
"Characterization and preliminary crystallographic data on the VL-
"A Nol. Biol. 147:185-193(1981).
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PDB: IWIL: 01-NOV-94.
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SPRam; PR00047; 1g; 1.
SPRART; SM000406; Ig_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein; 3D-structure.
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COMPLEMENTARITY-DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.

BY SIMILARITY.
TN -> SD (IN REF. 2).
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COMPLEMENTARITY - DETERMINING - 2,
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108 108
108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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Best Local Similarity 100.
Matches 14; Conservative
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Foon K.A., Chatterjee S.K.;
Foon K.A., Chatterjee S.K.;
Foon sisting of an anti-idiotype antibody mimicking a breast cancer-
associated antigen and the cytokine GM-CSF.";
Hybridoma 18:193-202(1999).
BMEL, ARISTA121;
ARISSL20.1;
InterPro: IPR00710; 19-11ke.
InterPro: IPR003006; 19-MC.
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Q925S9 (TEMBLE) 19, Created)
01-DEC-2001 (TEMBLE) 19, Last seque
01-MR-2003 (TEMBLE) 23, Last anno
Immunoglobulin light chain (Fragment)
Mus musculus (Mouse).
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Q96PF6
Q9JL82
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0920E9
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Q9XPG5
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STRAIN~BALB/C;
MEDLINE-99306687; Pubmed-10380019;
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PROSITE; PS50835; IG_LIKE; 1.
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\begin{array}{c} \texttt{Opp} \\ \texttt{up} \\ \texttt{v} \\ \texttt{op} \\ \texttt{op} \\ \texttt{up} \\ \texttt{v} \\ \texttt{v
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1 MGAPAQILGFLLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 145
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Q9rci6
Q8rcp0
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          summaries
                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VCIG
Q9R1A5
Q8R062
Q8VCP0
Q99M37
Q8K1F3
Q8K1F1
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Q91WF8
Q91W12
                                                                                                                                                                                                                                                                                                                                                                                       OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8K0F8
Q91WS9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_mhc:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                     US-08-836-455-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sb_fund1:*
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Match 1
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199.3
177.9
177.9
157.2
157.2
1157.2
111.7
111.0
111.0
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288
286
222
222
222
117
117
116
116
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                                                             OM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                              Run on:
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111
113
113
114
115
115
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62 62

Gaps

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Length 239;

Q8VC55

RESULT 2 Q8VC55

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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.8 kDa protein (Fragment).
Hypothetical 25.8 kDa protein (Fragment).
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC013496; AAH13496.1;
InterPro; IFR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.9%; Score 26; DB 11; Length 23
100.0%; Pred. No. 1.3e-18;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001);
InterPro: JPR003006; Ig_MHC.
InterPro: JPR003596; Ig_V.
Pfam; PF00047; Ig; SMART; SM00406; IGv; 1.
                                             D7BE84398AA341F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA; 25781 MW; B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kDa protein.
                                                                                       Query Match
19.3%; Score 28; DB 11; 18est Local Similarity 100.0%; Pred. No. 1.1e-20; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AA
                                                                                                                                                                                                                                                                                                                                                  233 AA
                                                                                                                                                                                117 TFGGGTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 TFGGGTKLEIKRADAAPTVSIFPPSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00406; ĬĠv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein NON_TER 1 SEQUENCE 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; 1g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8VCI6
Q8VCI6;
                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
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                     Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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| Strausberg R. |
| Strausberg R. |
| Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. |
| Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. |
| Strausberg R. |
| InterPro: IPR001399; Ig. |
| InterPro: IPR003599; Ig. |
| InterPro: IPR003596; Ig. |
| InterPro: IPR003596; Ig. |
| InterPro: IPR003596; Ig. |
| SMRRT: SM00407; IG.; 1. |
| SMRRT: SM00406; IG.; 1. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Colon:
Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021781; AAH21781.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfan: PF00047; 1g: 2.
SMART; SM00406; 1GV; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 28; DB 11; I
100.0%; Pred. No. 1.1e-20;
11ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                            239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 PYTFGGGTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 PYTFGGGTKLEIKRADAAPTVSIFPPSS 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                               KLEIK 127
                                                                                                                                                          123 KLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                            123
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Matches

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OBKOF8; Q8K0F8

RESULT 3 Q8K0F8

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Gaps

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Length 233;

Gaps

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RESULT 6

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 15.2%; Score 22; DB 11; Length 234; Best Local Similarity 100.0%; Pred. No. 1.9e-14; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          Length 234;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1; -.
HSSP; P01679; 2FBJ.
InterPro; IPR007110; Ig-like.
·InterPro; IPR003006; Ig-MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Colon;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; EC019474; AAH19474.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003996; Ig_V.
                   InterPro; IPR003596; Ig_v.
Pfam; PE00047, 19; 2.
SMART; SMO406; ICv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein: PS50857 MW; 4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 234 Aa; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26, 3 kDa protein.
Mus musculus (Mouse)
                                                                                                                                                                                        DB 11; L
1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AA
                                                                                                                                                                                     Query Match 15.2%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                              121 GTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                         121 GTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
  InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8VCP0;
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Q99M37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNas encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFv).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI52371; AAD40242.1;
HSSP; P01679; ZFBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Pred. No. 1.8e-14;
                                                                              Query Match 17.9%; Score 26; DB 11; Length 238; Best Local Similarity 100.0%; Pred. No. 1.3e-18; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Colon;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1; -
InterPro; IPR007110; Ig-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23922 MW; 52BA205FDE995E2A CRC64;
                                         35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TIEMBLEEL. 21, Created)
01-JUN-2002 (TIEMBLEEL. 21, Last sequence update)
01-MAR-2003 (TIEMBLEEL. 23, Last annotation update)
Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                       214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 15.2%; Score 22; DB Local Similarity 100.0%; Pred. No. 1.8 nes 22; Conservative 0; Mismatches
                                                                                                                                                                                        121 TFGGGTKLEIKRADAAPTVSIFPPSS 146
                                                                                                                                                                  117 TFGGGTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GTKLEIKRADAAPTVSIFPPSS 122
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro: IPR007110; Ig-11ke.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Ffam: PF00047; Ig; 2.
SWART; SW0406; IGv. 1.
PROSITE; PS00359; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                   Hypothetical protein.
SEQUENCE 238 AA; 26224 MW;
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 2
214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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NON_TER
SEQUENCE
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Q8R062;
                                                                                                                                                                                                                                                                                                              Q9R1A5
Q9R1A5;
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Q8R062
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUE-Hyperimmunized spleen;

A Zhou Y.-X. Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.

"Innate proteolytic antibodies: Failed D-VIPase response to the D-
re entantiomer of VIP and identification of L-VIPase VL domains.";

L Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R InterPro: IPR001599; Ig.

R InterPro: IPR001599; Ig.

R InterPro: IPR003006; Ig.Mrc.

R InterPro: IPR003006; Ig.Mrc.

R Fami PF00047; ig; I.

R SMART; SM00409; IG; I.

R SMART; SM00406; IG; I.

R SMART; SM00406; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Pau "Innate proteolytic antibodies: Failed D-VIPase response to the entantiomer of VIP and identification of L-VIPase VL domains.";
                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 11; Length 112;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                 Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF516285; AAM64203.1; -.
Interpro; IPR07110; Ig-1ike.
Interpro; IPR077110; Ig-1ike.
Interpro; IPR073596; Ig_MHC.
Interpro; IPR003596; Ig_W.
FF00047; Ig; I.
SMART; SMO0409; IG; I.
SMART; SMO0409; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AA; 11901 MW; F6644663201AA239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annocation update)
Anti-VIPase light chain variable region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                      11.7%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 AA.
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100.0%; Pred
0; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 TFGGGTKLEIKRADAAP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 TFGGGTKLEIKRADAAP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 TFGGGTKLEIKRADAAP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 TFGGGTKLEIKRADAAP 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                           PROSITE; PS50835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VDD0 PRELIMINARY;
Q8VDD0;
10-MAR-2002 (TEMBLE-1. 20,
01-MAR-2002 (TEMBLE-1. 20),
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.9
Matches 17; Conservative
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Matches 17; Conservative
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SEQUENCE
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                                                                                                                                                                                                                               Gaps
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Labou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
Innate proteolytic antibodies: Failed D-VIPase response to the D-
entantiomer of VIP and identification of L-VIPase VL domains.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF516282; AAM64200.1; -.
InterPro: IPR003199; Ig.
InterPro: IPR003110; Ig-like.
InterPro: IPR003106; Ig-W.
Ffam; PF00047; ig: I.
SWART; SM00409; IG; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse),
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Walsaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                               Indels
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                                                            PROSTTE; PS50835; IG_LIKE; 2. PROSTTE; PS00290; IG_MHC; 1. Hypothetical protein. SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AA; 12017 MW; 22DD75B5414CDB18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-07T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
                                                                                                                                                                              Score 22; DB 11; I Pred. No. 1.9e-14;
                                                                                                                                                              15.2%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                                                                                  121 GTKLEIKRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                              94 PYTEGGGTKLEIKRADAAP 112
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Conservative 0;
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InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 2.
                                                                                                                                                                              Ouery Match 15.28
Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                         Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Search completed: August 30, 2003, 22:11:18 Job time : 23.3825 secs
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                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                  Length 134;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC028540; AAH28540.1; -... InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_W.
                                                                                                                                                                              Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AJ416331; CAC94866.1; -. InterPro; IPR007110; Ig-like. InterPro; IPR003065; Ig_MHC. InterPro; IPR003596; Ig_WHC.
                                                                                                      Chernajovsky Y., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AA; 14525 MW; CFDF8E2236E2D0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-MOG 212 variable light chain (Fragment).
ANTI-MOG KAPPA.
                                                                                                                                                                                                                                                                                                11.7%; Score 17; DB 11; I 100.0%; Pred. No. 1.9e-09; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 16; DB 11; I larity 100.0%; Pred. No. 3.4e-08; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                     'Targeting T cells to the CNS.";
                                                                                                                                                                                                                                                                                                                                          117 TFGGGTKLEIKRADAAP 133
                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 KRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 KRADAAPTVSIFPPSS 142
                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                 STRAIN-BALB/c;
Sembi P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                                                              STRAIN-BALB/C;
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                  Query Match
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Q8R028;
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Gaps
                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kba protein.
Hypothetical 25.9 kba protein.
Buks musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Pred. No. 3.4e-08;
0; Mismatches 0; Indels
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015292; AAH15292.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR0047; ig; 2.
InterPro; IPR00465; Ribosomal_S2.
Ffam; PF00447; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00929; IG_MHC; 1.
PROSITE; PS00929; IRBOSOMAL_S2_1; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
234 AA
PRT;
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Matches 16; Conservative
PRELIMINARY;
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Sun Aug 31 18:17:27 2003
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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MUSIGKCMA
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MUSIKCC
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-Q-/cgn2_1/USPFO_spool/US0883645/runat_29082003_132901_22281/app_query.fasta_11.654
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-EGAPORT-120 -WARN TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                     August 30, 2003, 22:10:26 ; Bearch time 2967.15 Seconds (without alignments) 1999.191 Million cell updates/sec
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1 MGAPAQILGFLLLEFPGTRC.....IKRADAAPTVSIFPPSSKLG 145
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                   nucleic search, using frame_plus_p2n model
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Maximum Match 1008
Listing first 45 summaries
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X0217 M. musculus X0217 M. musculus X0217 M. musculus AB089681 Was musculus AB089681 Sequence AR122008 Sequence AR163749 Mus muscu AR163749 Mus muscu AR07981 Sequence AR66770 Mus muscu AR07981 Sequence 5 E54967 Peptide. 1/103643 Sequence 4 10783 Sequence 4 10783 Sequence 4 10783 Sequence 4 X7455 Mouse Ica Ge AX256284 Sequence AX36302 Sequence AX256302 Sequence AX56302 Sequence AX56302 Sequence AX56302 Sequence AX5644 Human mon BD01554 Human mon BD01554 Human mon

L48667 Mus musculu S65921 anti-colore AC122260 Mus muscu AF003293 Mus muscu X82890 M.musculus

AX256296 Sequence

A17963 Variable re E54975 Peptide. 1/ E54976 Peptide. 1/

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AR164505 Sequence BD085737 Methods o

Description

AB017434 Mus muscu

AF045495 Mus muscu AF045510 Mus muscu AB016620 Mus muscu J00565 Mus musculu V00808 Part of the X02177 M.musculus

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GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
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          Chatterjee_M. and Foon,K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11010
Patent: JP 2001523269-A 1 20-NOV-2001;
FTHE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PD 2001523269-A/1
PD 12-UNN-1998 JP 1999503252
PR 13-JUN-1998 US 60/049540,11-JUN-1998 US 09/096244 PI
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PN JP 2001523269-A/1
PD 20-NOV-2001
PF 12-UNV-1998 JP 1999503252
PR 13-UNN-1997 US 60/049540,11-JUN-1998 US
MALAYA CHATTERJEE, KENNETH A FOON
PC AGIK39/395,AGIK39/39//CO7K16/42
CC Strandedness: Single;
CC Topology: Linear;
CC Methods of delaying development of HMFG-ass
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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HMFG-associated tumors using
            PAT 17-0CT-2001
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                                                                                                 1 (bases 1 to 435)
Chatterjee, M. and Foon, K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11D10
Patent: US 6274143-A 1 14-AUG-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer
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PAT 31-JAN-2002
     61 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAAGAGTCAGT 120
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Nishida,T., Okura,T., Tanimoto,T. and Kurimoto,M.
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                       C12N15/09, A61K31/00, A61K39/395, A61K48/00, C07K16/24, C12P21/08, C12N15/00
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(1). (407)
Location (1). (60).
Location/Qualifiers
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HAYASHIBARA BLOCHEM LAB INC
MAS musculus (mouse)
PN JP 2000236884-A/15
PD 05-SEP-2000
PP 24-JUN-1999 JP 1999177846
                                                                                                                           DNA
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                                                                                       E54981 407
Peptide. E54981 E54981 G:18629719
JP 200023684-A.15.
Mus musculus (house mouse)
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                                                        GlyThrLysLeuGluIleLys
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/product="immunoglobulin light chain"
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/product="immunoglobulin light chain"
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ASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESED
FVAXYCLQYASSPYTFGGGTKLEIK"

93 c 89 g 109 t
  AF124721 381 bp mRNA linear ROD 22-MAY-2001 Mus musculus immnogloblin light chain mRNA, partial cds.
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Tripathi, P.K., Oin, H., Bhattacharya-Chatterjee, M., Ceriani, R.L., Foon, K.A. and Chatterjee, S.K.
Construction and characterization of a chimeric fusion protein cancer-associated antigen and the cytokine GM-CSF Hybridoma 18 (2), 193-202 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                                                                                                                                         2 (bases 1 to 381)
Chatterjee_S.K. and Tripathi,P.K.
Chatterjee_S.K. and Tripathi,P.K.
Submission
Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
Location/Qualifiers
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    >381
/note="anti-idiotype antibody 11D10; mimics a breast
cancer-associated antigen, human fat globule (HMFG)"

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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                       Mus musculus (house mouse)
Mus musculus
                                        AF124721.1 GI:14164546
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Query Match:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eu (bases 1 to 381)
S O'Connor.K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
L Unpublished
S O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
S O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
L Direct Submission
L Submitted (02-FBB-1988) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marian Marian Marka Linear ROD 28-FEB-1998 Mar Marian antibody kappa Light Ar045508 (IGK) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC04536.1"
/db_xref="GI:2906100"
/db_xref="GI:290610
                                          81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
                                                                                                                                                                                                                                                                                                                                   GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 126
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                                                                                                                                         /cell_line="spleen cell hybridoma"
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/chromosome="6"
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Mus musculus
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/codon_start=1
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346. .>381
/gene="IgK"
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61. .345
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1. .>381
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CRASQDIGSSLNWLQQEPDGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLES
EDFVDYYCLQYASSPYTFGGGTKLEIKR"
                                                                                                                                                                                                                                                          MUSIKCC 390 bp mRNA linear ROD 24-JUL-1997
Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.
L41880
                                             GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 39).
Asakura, K., Miller, D. J., Pogulis, R. J., Pease, L. R. and Rodriguez, M. Oligodendrocyte-reactive Ol, O4, and HNK-1 monoclonal antibodies are encoded by germline immunoglobulin genes
Brain Res. Mol. Brain Res. 34 (2), 283-293 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-JUL-1997) Immunology, Mayo Clinic, 200 First Street Sw. Rochester, Mn 55905, USA Coriginal source text: Was musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
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67. .>390
/product="immunoglobulin kappa chain"
a 90 c 95 g 109 t
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Matches:
Conservative:
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/organia="Mus musculus"
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/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="hybridoma HNK-1"
1. 390
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Mus musculus (house mouse)
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Asakura, K.
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1. 60
61. >384
/product="anti-IL-18 IgG Light chain"
92 c 91 g 110 t
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Mus musculus dC4 anti-poly(dC) monoclonal antibody kappa light
Chain variable region, (IgK) mRNA, partial cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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O'Connor.K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Direct Submission
Submitted (02-FEB-1998) Biochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
Location/Qualifiers
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O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
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Mus musculus
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Light chain"
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                                                                                                                                                                                                          Direct Submission
Submitted (02-SEP-1988) Yoshihiro Nishida, Hayashibara Biochemical
Submitted (02-SEP-1988) Yoshihiro Nishida, Hayashibara Biochemical
Laboratories, Inc., Fujisaki Institute; 675-1, Fujisaki, Okayama,
Okayama 702-806, Japan (E-mali:fujihigo, harenet.or.jp,
Tel:+81-86-276-3141, Fax:+81-86-276-6885)
Location/Qualifiers
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/product="variable region precursor of anti-IL-18 IgG
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Mus musculus (house mouse)
Mus musculus
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variable region precursor
IgG Light chain.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musns.
E 1 (bases 1 to 381)
Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
L Unpublished
E 2 (bases 1 to 381)
S O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
Direct Submission
L Submitted (02-FEB-1989) Blochemistry, Tufts University School of Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
                                                                                                                                                                                                                                                                                                                                                                                       /translation="MARPAQIEGELLILEPGTRCDIQMTQSPSSLSASLGERVSLTCR
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1. .60
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/protein_id="AAC04538.1"
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                       Mus musculus (house mouse)
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/gene="lgK"
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/gene="lgK"
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1. .60
/ gene="IgK"
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/gene="IgK"
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/gene="IgK"
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Mus musculus 6C9 monoclonal antibody kappa light chain variable
region, (IGK) mRNA, partial cds.
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/organism="Mus musculus"
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/translation="MRAPAQILGFLLLWFPGIRCDIKMTQSPSSLSASLGERVSLTCR
ASQEISGYLSWLQQKPDGTVKRLITYAASTLHSGVPKRFSGSRSGSDYSLTISSLESDD
FADDYTCLQVASDPWTFGGGTKLEIK"
                                                                                                                                                                                                                                                                                                                             Arakawa,F., Yamamoto,T., Kanda,H., Watanabe,T. and Kuroki,M. cDNA sequence analysis of monoclonal antibody FU-MK-1 specific for a transmembrane carcinoma-associated antigen, and construction of a mouse/human chimeric antibody
Hybridoma 18 (2), 131-138 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-JUL-1998) Fumiko Arakawa, School of Medicine, Fukuoka
University, First Department of Blochemistry; 7-45-1 Nanakuma,
Jonan-ku, Fukuoka, Fukuoka 814-80, Japan
(E-mall:farakawaémsat.fukuoka-u.ac.jp, Tel:092-801-1011(ex.3246),
Fax:092-801-3600)
                                                                                                                                                                      AB016620 405 bp mRNA linear ROD 27-MAR-2002 Mus musculus mRNA for Immnoglobiin light chain variable region,
                          241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/note="the hybridoma producing anti-GA733-2 monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"Immnogloblin light chain variable region"
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/db_xref-"GI:3395671"
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Immoogloblin light chain variable region.
Mus musculus (house mouse)
Mus musculus
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'note="PCR primer region"
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Mus musculus immunoglobulin kappa chain variable region (Igk) gene, acons 1 and 2.
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J00565.1 GI:196531
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Seidman, JG., Max, E.E. and Leder, P.
A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation
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20
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Gough, M.M., Cory, S. and Adams, J.M.
Identical 3' non-coding sequences in five mouse Ig kappa chain mRNAs favour a unique C kappa gene
Nature 281 (5730), 394-396 (1979)
                                                                                                                                                                                                                                                                                                                                                                                                          MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys
                      11 ATGAGGCCCCTGCTCAGATTCTTGCTTCTTGTTGTTCTTGTTCCAGGTATTAGATGT
                                                                                                                                                                                        41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
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                                                                                          21 AsplieglnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer
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544 CTTGAGTCTGAAGATTTTGTAGACTATTACTGTCTACAATATGCTAGTTCTCCGTGGACG 603
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join(120. .173,302. .>637)
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altering of the site of transcription initiation. the deletion moves transcription initiation from approximately 30 bp 5' to the initiation codon to about 20 bp 5'. for part of the vk41 constant gene and part of the 3' flank see cmusigkac2> and cmusigkac2> and emisigkac3> respectively. for the germline joining jl region see cmusigkac3> for other rearranged kappa genes see loci beginning cmusigkac> and supsigkac3> expermline kappa variable genes see loci beginning cmusigkac> in the sites table cdr-complementarity determining region and fr=framework region.
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Conservative:
Mismatches:
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/rearranged
|Join(119. 173,302. 312)
| /gene="lgk"
| /gene="lgk"
| /number=1
| /fw. 301
| /gene="lgk"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/cell_line="MOPC41"
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/gene="Igk"
/number=2
596. .597
/gene="Igk"
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part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41). VOOR08 JOD55 VOOR08 JOS5 VOOR08 JOS5 VOOR08 JOS5 WORD JOS5 WORD JOS5 WORD JOS5 WORD JOS5 WORD WAS MUSCULUS (house mouse)
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/product-inmunoglobulin kappa"
/protein_id="cA24190.1"
/db_xref="GI:577074"
/db_xref="GI:577074"
/db_xref="GI:5770074"
/db_xref="G
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Seidman, J. G., Max, E.E. and Leder, P. A Kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation Nature 280 (5721), 370-375 (1979)
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AUTHORS
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M.musculus mRNA for 1gG kappa light chain (partial) Gloop 1.
X02177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Immunoglobulin G kappa light chain"
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                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 380)
Darsley,M.J. and Rees,A.R.
Nucleotide sequences of five anti-lysozyme monoclonal antibodies
BMBO J. 4 (2), 393-398 (1985)
2410256
                                                      X02177.1 GI:51894
gamma-immunoglobulin; Ig light chain; immunoglobulin; joining
region; variable region.
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//product="variable region of IgG kappa light chain"
//note="hypervariable region CDRI"
189. 212
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a 93 c 89 g 110 t
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306. .332

/note="hypervariable region CDR3"

326. .364

/product="joining region of IgG kappa light chain"

365. .>380
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107
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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541.00
89.60%
85.60%
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Best Local Similarity:
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VERSION
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AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                   RESULT 13
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerAspTyrSerLeuThrIleSerSerLeuGluSerGluAspPheValAlaTyrTyrCys 108
                                                                                                                                                                   305
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 381)

Darsley, M.J. and Rees, A. R.

Nucleotide sequences of five anti-lysozyme monoclonal antibodies 85257466
2410256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerSerLeuSerAlaSerLeuGlyGlnArgValSerLeuThrCysArgAlaSerGlnAsp
GCCTTCTTGTTGCTCTGGTTTCCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 TCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCTGAAGATTTTGCAGACTATTACTGT
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366. .>381
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a 92 c 89 g 110 t

    .326
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    .144
    note-"hypervariable region CDRI"

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Hirama, M., Mizugaki, M. and Goto, J.

Direct Submission
Submitted (09-MG-2002) Yoshihisa Tomicka, Tohoku University
Hospital, Department of Pharmaceutical Sciences; 1-1, Sciryo-machi, Aoba ku, Sendai, Miyagi 980-8874, Japan
(E-mail:ytomicka@sm.rim.or.jp, Tel:81-22-717-7543,
                                                                                                                                                                           SerGlySerAspTyrSerLeuThrIleSerSerLeuGluSerGluAspPheValAlaTyr 106
                                                                                                                                                                                                                                                                                                                                                                   TyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGlyGlyThrLysLeuGluIle 126
                                                                                                                                                                                                                                                                                                                                                                               Tomioka,Y., Kato,Y., Tsuruta,L.R., Kudo,Y., Hishinuma,T., Itoh,K., Hirama,M., Goto,J. and Mizugaki,M. Characterization of anti-glycyrrhetic acid monoclonal antibody
                                                                                                                                                                                                                                                                        86
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                             67 LeulleTyrAlaThrSerSerLeuGlySerGlyValProLysArgPheSerGlySerArg
                     381
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB089681.1 GI:28316363
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                  1.32e-45
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                                       Percent Similarity:
Best Local Similarity:
Query Match:
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AUTHORS
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AB089681
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AUTHORS
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                                                                                                                                                                                                                                                                       /product="anti-glycyrrhetic acid antibody GA102 light chain"
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106
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Matches:
Conservative:
Mismatches:
Indels:
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ne : 2969.15 secs
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86 c 83
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                                                                                                                                                                   533.00
94.928
89.838
72.038
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Best Local Similarity:
Query Match:
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments)
1795.608 Million cell updates/sec
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1 MGAPAQILGFLLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 145
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OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Xgapop 10.0 , Xgapext (
Xgapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Command line parameters:

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| SIDSI/gggdatb/geneseqfn-embl/Nal986.DAT:*
| SIDSI/ggdatb/geneseqfn-embl/Nal988.DAT:*
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and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	ery	Length	DB		scription
1	7	100.0	435	18	AAT8514	Murine monoclonal
010	740	100.0	435	20	AAV83772	Antibody 11D10 11g
n 4	740		4 30	7	AALS12/3 AAN30165	Sequence encoding
· ທ	633		407	21	7	Mouse light chain
9	527		387.	18	AAT77851	a)
7	527		387	24	AAD32138	Murine 44H104 mab
œ (507		739	14	AAQ46084	Sequence encoding
ي د	507		739	17	AAT36880	520C9 anti-c-erbB-
11	507	9 9	739	250	AAV63399	520C9 all LI-C-ELDB*
12	506		324	21	AAZ49534	Mouse anti-IL-18 a
13	505		756	24	AAS97136	P4-3 single chain
14	505	68.2	1497	24	AAS97145	cP4-3 bisp
15	503		432	12	AAQ15114	IL-2 chimeric anti
16	503		438	22	AAH41157	
17	502	67.8	711	21	AAZ49542	-2H
87 -	202		129	77	AAZ49543	SSCFV#125-2
F C	700	67.0	132	124	AAS9/142	TI-2 chimeric anti
2,5	495		1605	14	AAOA KOBK	CILLINEI IC
22	492		321	21	AAA38908	520C9 hybridoma VL
23	492		439	18	AAT73443	Human immunoglobul
24	492	66.5	4	20	AAZ21995	
25	486		∞ ∘	18	AAT78825	Kappa light chain
26	486		3819	13	AAV39266	Plasmid pLC6G5 nuc
77	4 2		חפ	2 5	AAZZZUZU	Nucleotide sequenc
8 0 0 7	484.0	60.0	/3/	4 L	AAD31829 AAC78732	Murine anti-human
30	482		817	21	AAA27389	Human IGFAM-9 1mmu
31	481		-	21	AAA46899	DNA encoding the k
32	481		19035	13	AAV61794	Traget plasmid Man
33	479	64.7	456	22	AAC66996	Filamentous phage
3.4	4/9		x 0	77	AAC6/002	Flalmentous phage
35	4.4		T000	4 5	-	Human anti-HBS 119
37	473		4/6	* -	AACS74/3	MODOCIONAL ANTI-10
. ee	471		447	17	_	٠
39	471		447	18	m	Anti-idiotype anti
40	471		447	21	4	Murine MAb against
41	471		447	22	Н	ᅻ
42	471		447	24	S.	ďy
43	471		4	24	327	3H1 an
44	468	63.2	321	16	975	Light chain variab
45		63.2	321	16	20	Light chain variab
					ALIGNMENTS	

Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss. Murine monoclonal anti-idiotype antibody 11D10 VL cDNA. AATB5149 standard; cDNA; 435 BP. (updated)
(first entry) 25-MAR-2003 04-JAN-1998 AAT85149; RESULT 1 AAT85149 EXEXTENT

Location/Qualifiers Key

Mus musculus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
                                                                                                                                                                                                                                                                                                                          Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the coding sequence for the murine antibody 11D10 light chain variable region. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for treating breast tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a /*tag= a //tagouct= antibody 11D10 light chain variable region" //transl_except= (pos:163..165, aa.Thr) //note= "no stop codon is given at the 3' end of the
                             241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delaying development of, or treating, HWFG-associated tumours using anti-idiotype antibody 11D10 raised against antibodies
                                                                                                                                                                                                                                                                                                 Antibody 11D10 light chain variable region coding seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
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13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
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                                                                                                                                                                                                                                                                                                                                                                         This cDNA sequence encodes the light chain variable region VL (AAM85149) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10 anti-iMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFC). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are and alagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMFG-
                                                                                                                                                                                                                                                                                                    response
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tumours,
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Mismatches:
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                                                                                                                                                                                                                             Chatterjee M, Chatterjee SK,
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96US-0591965.
96US-0766350.
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                                                                                                                                                                                                          21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
                                                                                     Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
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The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for anti-idiotypic antibody for treating HMFG/CEA-associated tumours. The present cDNA sequence encodes the light chain variable region of the mouse 11D10 anti-idiotype antibody.
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                                                                                                                                                                                               Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g. breast tumor) in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 other;
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17-MAY-2002; 2002WO-US15840
                                  17-MAY-2001; 2001US-0861294
                                                                     (KENT ) UNIV KENTUCKY RES
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P-PSDB; AAO16292.
                                                                                                         Chatterjee M, Foon
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Query Match:
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No.:
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us-08-836-455-2.p2n.rng

100

258

80

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120

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99 GACATCCAGATGACCCCAGTCTCCCTTATCTGCCTCTCTGGGAGAAAGAGTCAGT 138
                                                     Mouse light chain variable region; VL; variable region light chain; therleukin-18; immunopathise; inflammatory disorder; autoimmune disease; mouse; anti-allergic; anti-inflammatory; immunosuppressive; hematopoletic; leukocytopoietic; antialgic; antipyretic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
                                                                                                      ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer
                                                                                                                                                        LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                         AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys
                                                                                                                                                                                            GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mouse light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse light chain variable region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanimoto T,
                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                   AAZ49548 standard; cDNA; 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99EP-0304977
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98JP-0365023,
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                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...407
                                                                                                                                                                                                                                                                                           SerSerLys 143
                                                                                                                                                                                                                                                                                                          Okura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-118341/11.
P-PSDB; AAY44599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The pref. vector or plasmid of the invention has a double-stranded DNA seq. coding for a variable region of a light or heavy chain of night, or for a variable region of a light or heavy chain of an immunoglobulin specific for an enzyme or surface protein. The sequence esp. codes for a variable region of a light chain having 95-115 AAs or for a variable region of a heavy chain having 110-125 AAs esp. including the D region of the heavy chain.
                                                                                        Sequence encoding the leader, variable region and first 16 AAs of the constant region of the kappa-chain (light chain) of MOPC41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transformed expression vectors or plasmid(s) - with double stranded DNA sequence coding only for desired part of polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 450 BP; 108 A; 114 C; 104 G; 124 T; 0 other;
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131
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Matches:
Conservative:
Mismatches:
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/product= constant region
                                                                                                                                                                                                                                                      variable region
                                                                                                                             Diagnosis; therapy; immunoglobulin; ss
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                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 40-41; 68pp; English.
                                                                                                                                                                                                       /*tag= a
/product= leader
             AAN30165 standard; DNA; 450 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.61e-54
662.00
95.10%
91.61%
89.46%
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83US-0558551.
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                                                               (first entry)
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                                                                                                                                                                                                       /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                              (SCHE ) SCHERING CORP. (DNAX-) DNAX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1983-772290/39.
P-PSDB; AAP30251.
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                                                                                                                                                       Homo sapiens
                                                               25-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                  10-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-1982;
05-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                                                                               EP88994-A.
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                                       AAN30165;
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Query Match:
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AAN30165
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101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                  07-JUN-1996;
                             WO9640941-A1
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                                               19-DEC-1996
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                                                                                                                                                                                                                                                                                                                                  GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes mouse light chain variable region. This recombinant DNA is derived from PCR A which amplifies antibody light chain variable region (VL). The transformant produced using the VL gene was used transform competent E. coli cells. The peptide produced by transformants neutralises interleukin-18. This is useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases which are caused by excessive immunoracaction. The peptide has anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoletic, antilalgic, antilpyretic and hepatic-function improving
                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                   40
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                                                                                                                                                                                                                                           \tt MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys
                                                                                                                                                                                                                                                       GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCTCTGGGAGAAGAGTCAGT
                                                                                                                                                                                                                                                                                                                                                               61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys
                                                                                                                                                                                                                                                                                                                                                                         ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; light chain; variable region; hybridoma cell line 44H104; immune response; enhance; stimulate; vaccine; immunodiagnosis; antigen delivery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Encodes 44H104 light chain variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrVal 135
                                                                                                                                                      407
1125
2
8
8
0
                                                                                                                          Sequence 407 BP; 96 A; 99 C; 96 G; 116 T; 0 other;
                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                          (1-407)
Example 1; Page 28-29; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                          US-08-836-455-2 (1-145) x AAZ49548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT77851 standard; cDNA; 387
                                                                                                                                                     2.3e-51
633.00
94.07%
92.59%
85.54%
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                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                            Alignment Scores:
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                                                                                                         activities
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126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel recombinant conjugate antibody molecules comprise a monocional antibody specific for a surface structure of antigen presenting cells (APC), genetically modified to contain at least one antigen exclusively at one or more preselected sites. The conjugate is capable of delivering the antigen to APC and eliciting an immune response to the antigen. The new conjugates are useful as vaccines and are able to elicit an enhanced immune response without the use of an adjuvant. In a specific example, a conjugate was constructed using the murine anti-human class II monoclonal antibody secreted by hybridoma 44H104. The peptide CITB36 was chosen as antigen; it consists of a tandemly linked T and B cell epitope derived from HIV MN strain. The present sequence encodes the light chain variable region which was PCR amplified from 44H104 and used in the preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer
including secretion signal; termination codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant conjugate antibody mol., modified for delivering a antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines o
                                                                                                                                                                                                                                                                                                Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387
103
7
17
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                Cates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-836-455-2 (1-145) x AAT77851 (1-387)
                                                                                                                                                                                                                                                                                                Caterini JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conjugate with antigen CLTB36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 A; 95 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.39e-41
527.00
86.61%
81.10%
                                                                                                                                                           96WO-CA00400.
                                                                                                                                                                                                                                                   (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                Anand NN, Barber BH,
                                                                                                                                                                                                                                                                                                                                         WPI; 1997-077271/07.
P-PSDB; AAW22537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 387 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immuno:diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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99 40

20

9

186

100

Mus sp

Key

AAD32138

RESULT 7

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        ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThr11eSerSerLeuGluSer

                                                                                      MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys
                                                                                                                                            AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer
                                                                                                                                                                                                      LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                 247 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig; single polypeptide chain binding site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New single chain Fv polypeptide binding to C-erbb-2 tumour antigen - for imaging or treating breast or ovarian cancer etc.
 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ring DB
   Mismatches:
                Indels:
                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oppermann H,
                                                         US-08-836-455-2 (1-145) x AAD32138 (1-387)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding 52009 sFv protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..739
                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyThrLysLeuGluIleLys 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS ONCOLOGY CORP.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ46084 standard; cDNA; 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93WO-US01055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-0831967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
81.10%
71.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-272889/34.
P-PSDB; AAR39569.
 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single chain
biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9316185-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
07-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ46084;
                                                                                                                                            21
                                                                                                                                                                                                      41
                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                         187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ46084
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Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a recombinant conjugate antibody, comprisin a monoclonal antibody specific for a surface structure of antigen for senting cells genetically modified to contain an antigen moiety for the purpose of delivery of the antigen moiety to antigen. Presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable
                                                                                                                                                                                                                                             Murine; mab; light chain; VL; conjugate antibody; antigen delivery;
immuné system; vaccine; detecting agent; antibacterial; gene; ds.
                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Murine 44H104 mab VL"
/transl_except= (pos:277..279, aa:Thr)
/note= "This translation exception occurs while
decoding for murine mab VL alternative version
                                                                                                                                                                                                                                                                                                                                                                                                                       (AAE20204); CDS does not include stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387
103
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 112 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
                                                                                                                                                                                                                  Murine 44H104 mab variable light chain (VL) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caterini JE,
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..387
                                           GlyThrLysLeuGluIleLys 127
                                                         Cates GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1A; 28pp; English.
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                                                                                                                                BP
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527.00
86.61%
                                                                                                                             AAD32138 standard; DNA; 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0007093
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                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATES G A. CATERINI J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anand NN, Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting agent. The light chain (VL) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-267519/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BARBER B H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ANAN/) ANAND N N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 387 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002025315-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-1998;
                                                                                                                                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                          121
                                                                                                                                                          AAD32138;
                                                                     367
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(CATE/)
(CATE/)
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07-OCT-1993;
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                      US5534254-A
                                                            09-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
                               c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells, such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isoleterric pt. of about 5.3 (see AAQ6603, ARN39568). A single chain FV (sFV) is a covalently linked VH-VL heterodimer which is expressed from a peptide-encoding linker. Such linker sequences are set forth in AA residues 116-135 in AAR39569, which includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084 for the 520C9 monoclonal antibody, a single chain polypetide can be produced having a mithody for a c-erbB-2 related antigen. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 AsplieGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv; construct; polypeptide linker; C-terminal amino acid sequence; in vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time; ss.
                                                                                                                                                                                                                                                                                              Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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1..732
/*tag= a
/note= "START codon absent"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Disclosure; pages 60-61; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-836-455-2 (1-145) x AAQ46084 (1-739)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                      3.95e-39
507.00
93.64%
91.82%
68.51%
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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29-OCT-1996
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110 AAT36890

XX AC

XX XX

XX 25-1v

DT 25-1v

XX CODE

XX CODE

XW CODE

XW LIDD

XX LOS

XX CODE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGTTCAGTGGCAGTCGGTCTGGGTCAGATTATTCTCTCACCATCAGTAGCCTTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                               Variable heavy (VH) and variable light (VL) genes were cloned from a 520C9 hybridoma cDNA library, using probes directed toward the antibody constant and joining regions. A two single chain Fv (SFV) gene was constructed by connecting the VH and VL genes with a Ser rich polypeptide linker. The resulting 520C9 two SFV gene, transformed into E. coll, and protein expression vector, transformed into E. coll, and protein expression induced by the addn. of IPPG to the culture medium. A companion comprising a carrier and the 2 SFV protein prod. can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used for in vivo imaging, and drug targetting experiments. The S FV protein prod. is a homodimer, in which both fragments target the same antigen, therefore giving greater binding avidity and longer tissue retention times, compared to individual sFV protein
                                                                                                                                                                                                                                                                                         Compsns. contg. antigen-targetting antibody fragment constructs comprising dimer of single-chain Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              739
101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                               Ring DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyThrLysLeuGluIleLysArgAlaAsp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
                                                                                                                                                                                                                                                                                                                                                       Example 1; Columns 33-36; 30pp; English.
                                                                                                                                                                               Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-836-455-2 (1-145) x AAT36880 (1-739)
                                                                                                                                   (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.95e-39
507.00
93.64%
91.82%
68.51%
93US-0133804
                                           93US-0133804
                                                                  92US-0831967
                                                                                                                                                                               Houston LL, Huston JS,
                                                                                                              (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                    WPI; 1996-333194/33.
P-PSDB; AAW02280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
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AAV21798

RESULT 10

Mus sp

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GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                                                                                                                    LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding single-chain Fv fragment specific for antigens - and having C-terminal tail for crosslinking to form dimer with improved pharmacokinetic properties, used to deliver drugs and imaging agents, especially to tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52009 sFv; antigen; tumour cell; antibody 52009; targeted delivery; antigen-expressing cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                  GlyThrLysLeuGluIleLysArgAlaAsp 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Columns 33-36; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       700 GGGACCAACCTGGAAATAAAACGGGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= 520C9 sFv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
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(CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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92US-0831967.
95US-0461386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV63399 standard; cDNA; 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0461386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520C9 sFv DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-023541/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5837846-A.
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05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-1998
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                                                                41
                                                                                                   091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Imaging of antigens in vivo - using dimers of single-chain antibody
                                                                                                                                                                                                                                             Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer; c-erbB-2; tumour; diagnosis; ss.
                                                                                                                                                                                                         520C9 anti-c-erbB-2 sFv' dimeric construct gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 739 BP; 188 A; 177 C; 181 G; 193 T; 0 other;
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/product= "520C9 sFv' polypeptide"
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Matches:
Conservative:
Mismatches:
Indels:
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        GGGACCAACCTGGAAATAAAACGGGCTGAT 729
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                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oppermann
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                                                                                     BP
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507.00
93.64%
.91.82%
68.51%
                                                                                   CDNA; 739
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92US-0831967.
95US-0461838.
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                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-311318/27.
                                                                                   AAV21798 standard;
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Best Local Similarity:
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06-FEB-1992;
05-JUN-1995;
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                                                                                                                                                                  16-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1998
                                                                                                                                                                                                                                                                                                     Synthetic.
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The present sequence encodes an an antibody 520C9 sFV. Variable heavy and light sequences of antibody 7520C9 are connected, together with a serine linker, to produce the present single chain FV gene. The present sequence exemplifies the invention. Dimers of the single chain FV are used for targeted delivery of drugs or imaging agents (e.g. cytotoxins,
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AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40

US-08-836-455-2 (1-145) x AAV21798 (1-739)

Query Match:

Ring DB;

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459
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                                                                                                                                                                                                                                                                                                        GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL; hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18; antiliflammatory; immunosuppressive; leucocytopoietic; antialgic; antipatotropic; treatment; autoimmune disease; immunopathy; inflammatory disorder; immunoreaction; ss.
                                                                                                                                               40
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/label= Anti-IL-18_antibody_light_chain_variable_region
                                                                                                                                                                                                 AsplleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer
                                                                                                                                                         LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                  ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrlleSerSerLeuGluSer
                                                                                                                                                                                                                                                                            prodrugs or 99m-technetium) to antigen-expressing cells, particularly for treatment or diagnosis of tumours (especially of ovary or breast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse anti-IL-18 antibody VL encoding cDNA from hybridoma #125-2H
                             0 other;
                                                          739
101
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                             181 G; 193 T;
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1..324
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                            188 A; 177 C;
                                                                                                                           x AAV63399
                                                                                                                                                                                                                                                                                                                                                                                                     AAZ49534 standard; cDNA; 324
                                                      3.95e-39
507.00
93.64%
91.82%
68.51%
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98JP-0365023
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                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                             BP;
                            Sequence 739
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mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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22-DEC-1998;
                                                Alignment Scores:
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The present cDNA sequence derived from hybridoma #125-2H, encodes mouse anti-Interleukin-18 antibody 11ght chain variable region (VL). It can be used in the production of recombinant monoclonal antibody #125-2HmAb, which is capable of neutralising biological activities of interleukin-18. The antibody has antiinflammatory; immunosuppressive, leucocytopoietic, antialisty, antigoredic, antialisty and can be used for prevention and treatment of autoimmune diseases, immunopathies and inflammatory disorders caused by excessive immunoreaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic blle duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds; helminth; cytostatic; antimicrobial; immunomodulatory; P4-2; P4-3; P4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
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                                                                                    New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys
                                                                                                                                                                                                                                                                                                               83 A; 78 C; 76 G; 87 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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               Kurimoto
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              Tanimoto T,
                                                                                                                                               Claim 11; Page 21; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
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506.00
94.44%
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              Okura T,
                                        WPI; 2000-118341/11
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                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                Sequence 324 BP;
                                                        P-PSDB; AAY44587
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Pred. No.:
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            Nishida Y,
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, casophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, laryn, breast, ovariy, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protatoza or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent autoimmune hepatitis. The sequences represent DNA encoding the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                   Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases
P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
                                                                                                                                                                                                                                                                                         Kischel R;
                                                                                                                                                                                                                                                                                         Lutterbuese R, Borschert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 756 BP; 184 A; 180 C; 204 G; 188 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Fig 16; 114pp; English.
                                                                                                                                                                     26-MAR-2001; 2001WO-EP03414.
                                                                                                                                                                                                           24-MAR-2000; 2000EP-0106467
                                                                                                                                                                                                                                                                                     Riethmueller G,
Hofmeister R;
                                                                                                                                                                                                                                                                                                                                             WPI; 2002-055119/07.
P-PSDB; AAU72862.
                                                                                                                                                                                                                                                 (KUFE/) KUFER P.
                                                                                         WO200171005-A2
                                                       Homo sapiens.
                                                                                                                               27-SEP-2001
                                                                                                                                                                                                                                                                                     Kufer P,
Mayer M,
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507
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                                                                                                                        GlnGlnGluProAspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySer
                                                                                                                                                      756
100
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9
       Length:
Matches:
Conservative:
Mismatches:
                                        Indels:
                                                               US-08-836-455-2 (1-145) x AAS97136 (1-756)
      6.27e-39
505.00
92.24%
86.21%
68.24%
                               Best Local Similarity:
                       Percent Similarity:
Aliqnment Scores:
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                                        Query Match:
DB:
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Sequence 1497 BP; 364 A; 358 C; 407 G; 368 T; 0 other;

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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated cas a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, cosophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, cary, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larged or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple conditis, goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. The sequences represent DNA encoding the copy propertions.
                                                                                                                                                                                                                                                                     Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; malanoma; myeloma; resroma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds; pelminth; cytostatic; antimicrobial; immunomodulatory; p4-2; p4-3; p4-14; p4-15; p5-2; p5-3; p5-9; p5-10; p5-11; p5-23; 3Bloxp4-3; 3Bloxp4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKGZD receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borschert K, Kischel R;
Riethmueller G, Lutterbuese R, Hofmeister R;
                                                                                                                                                                                                                                     3B10xP4-3 bispecific single chain Fv DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 16; 114pp; English.
                                                                                                                  AAS97145 standard; DNA; 1497 BP
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                                                                                                                                                                                              (first entry)
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Mayer M,
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us-08-836-455-2.p2n.rng

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New recombinant DNA encoding chimeric antibody - with human constant and non-human variable regions, esp. directed against
                            Disclosure; Page 11; 24pp; German
              interleukin 2 receptor
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                                                                                                                         37 GlnArgValSerLeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeu 56
                                                                   GlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGly
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     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                         Gaps:
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/*tag= a
/*tag= b
61..432
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                                                                                                                                                                                                                                                                                                                    Interleukin-2; immunosuppressant
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                                                     US-08-836-455-2 (1-145) x AAS97145
   1.38e-38
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86.21%
68.24%
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                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                 Chimeric Homo sapiens.
Chimeric Mus musculus.
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P-PSDB; AAR15322.
                  Percent Similarity:
Best Local Similarity:
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16-MAR-1992
Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSerGluAspPheVal 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 LysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLysArgPheSerGly
The sequence encodes the interleukin-2 (IL-2) chimeric antibody chain clone 447. Antibodies against IL-2 receptors are useful as immunosuppressants, and are much less immunogenic than mouse or rat antibodies. The DNA sequence provides much higher yields of chimeric antibodies than known methods. See also AAQ15114-Q15118 (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                        Sequence 432 BP; 106 A; 102 C; 104 G; 120 T; 0 other;
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Matches:
Conservative:
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Indels:
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ne : 218.987 secs
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Best Local Similarity:
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sequence 11, Appl
Sequence 19, Appl
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Sequence 11, Appl
Sequence 110, Appl
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Sequence 16, Appl
Sequence 17, Appl
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Sequence 9, Appli
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APPLICANT: Malaya CHATTERJEE
APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: 05/09/861,294
CURRENT FILING DATE: 2001-05-17
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FESTSEQ for Windows Version 4.0
                  US-08-779-784-5

US-10-268-883-10

US-09-784-15

US-08-779-784-16

US-08-779-784-116

US-09-924-099-13

US-09-924-099-13

US-09-924-099-13

US-09-924-099-13

US-09-919-344-7

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US-09-737-88-18

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Patent No. US20020098190A1
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-MODEL-frame+ph.model.-DEV=xlh
-MODEL-frame+ph.model.-DEV=xlh
-OG-/Cgn2_1/USPTO_spool/USO8836455/runat_29082003_132902_22302/app_query.fasta_1.654
-OG-/Cgn2_1/USPTO_spool/USO8836455/runat_29082003_132902_22302/app_query.fasta_1.654
-OB-Published_Applications_NA -OFMT-fastap -SUFFIX-P2n.rnpb -MINMATH=0.1
-LOOPEXT=0 -UNIS=bits -STRAT=1 -END--1 -NATRIX-blosum62
-LOOPEXT=0 -UNIS=bits -STRAT=1 -END--1 -NATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-20 -OTMENACON-ECO -THR_MAX-100
-MAXLEN-2000000000 -USER-ENS08836455_GCGN 1 1_271_Grunat_29082003_132902_22302
-NCPU-6 -ICDPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORS=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEDQT-120 -WARN TIMEDQT-30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5
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an or equal to the score of the result being printed,
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6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                   nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: NISHIDA, YOShihiro
           LOCATION: (1)...(435)
FRATURE:
NAME/KEY: SIG_PEPTIGE
LOCATION: (1)...(60)
FRATURE:
                                                                     ; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-10-367-506-1
                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                      Alignment Scores:
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US-09-924-099-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Malaya CHATTERJEE
APPLICANT: Reneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TOWORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT APPLICATION NUMBER: US/09/861,294
PRIOR RILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 05/049,540
PRIOR PILING DATE: 1997-06-13
PRIOR PELLICATION NUMBER: 09/096,244
PRIOR PILING DATE: 1997-06-13
PRIOR PILING DATE: 1997-06-13
SPRIOR PILING DATE: 1908-06-11
SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                 435
145
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                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                 US-08-836-455-2 (1-145) x US-09-861-294-1 (1-435)
                                                                                 Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 TCCAGTAAGCTTGGG 435
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740.00
100.00%
100.00%
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NAME/KEY: sig_peptide
LOCATION: (1)...(60)
NAME/KEY: mat_peptide
LOCATION: (61)...(435)
                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                     Alignment Scores:
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US-10-367-506-1
                                            US-09-861-294-1
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DB:
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GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
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CURRENT FILING DATE: 2001-08-08
FIROR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
  435
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Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08779784
Publication No. US20020164325A1
Publication No. US20020164325A1
Publicant: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kuniniko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrVal 135
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
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Matches:
Conservative:
Mismatches:
Indels:
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SYSTEM: PC-DOS/MS-DOS
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92.59%
85.54%
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MEDIUM TYPE: Floppy
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CITY: Hackensack
STATE: New Jersey
                                     ORGANISM: Mus musculus
FEATURE:
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                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                        Alignment Scores:
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LENGTH: 407
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           TYPE: DNA
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Matches:
                                                   PRIOR APPLICATION DATA

PRIOR APPLICATION DATA

PRIOR APPLICATION NUMBER: US 08/692,084

FILING DATE: 08-40G-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/236,520

FILING DATE: 29-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: JACKSON ESQ., DAVIG A.

REGISTRATION NUMBER: 1199-1-001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: 201-487-5800

TELEPHONE: SO1-487-1684

INFORMATION FOR SEQ ID NO: 5:
CLASSIFICATION: 424
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Publication No. US20030138862A1
GENERAL INFORMATION:
APPLICANT: Tso, J. Yun
APPLICANT: Green, Jennifer Macphate
                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
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616.00
95.45%
92.42%
83.24%
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity:
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US-10-268-883-10
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TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof FILE REFERENCE: 05882.0062.NPUS01
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: USSN 60/329,178
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-21
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
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Publication No. US20020164325a1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ROdriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
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Mismatches:
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Matches:
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Best Local Similarity:
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US-08-779-784-16
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                                                                                                                                                       SEQ ID NO 10
LENGTH: 390
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67 GACATICCAGATGACCCAGTCTCCATCTCTCTCTCTCTCTGGGAGAAGAGTTCAGT 126
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COMPUTER: FIOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN 1997
CLASSIFICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATORNEY/AGENT INFORMATION:
NAME: 20-APR-1994
ATORNEY/AGENT INFORMATION:
TELECOMMULICATION NUMBER: 1199-1-001 CIPA
TELECOMMULICATION NUMBER: 1199-1-001 CIPA
TELECOMMULICATION NUMBER: 1199-1-001 CIPA
TELECOMMULICATION NUMBER: 1199-1-001 CIPA
TELECOMMULICATION SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
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106
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Mismatches:
Indels:
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Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.41e-58
532.00
94.78%
92.17%
71.89%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 351 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Query Match:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro 60
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                                                                                                                                                                                                                 APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMBRIC ANTIBODIES FOR DELIVERY OF
TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 20
                    101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerPro 115
                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                             Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-UUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-765
TELECOMMUNICATION INPORMATION:
                                                                                                                                     Sequence 1, Application US/09007093
Patent No. US20020005315A1
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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86.61%
81.10%
71.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity:
Query Match:
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CITY: Toronto
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STATE: OI
COUNTRY:
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                  PROMOTION OF CENTRAL NERVOUS SYSTEM REWYELINATION USING MONOCLONAL AUTOANTIBODIES
      TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTITLE OF INVENTION: REMYELINATION USING MONOCLONAL AU NUMBER OF SEQUENCES: 37
ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, 4th STREET: Floor CITY: Hackensack
                                                                                                                                                                                                                              COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE-DOCKET NUMBER: 1199-1-001 CIPA TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION: 424
PROF APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
APPLICANT: Asakura, Kunihiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 17:
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532.00
94.78%
92.17%
71.89%
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201-343-1684
                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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Best Local Similarity:
Query Match:
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US-08-779-784-17
                                                                                                                                                                                                                 07601
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Percent Similarity: 93.64% Conservative: 2 Best Local Similarity: 91.82% Mismatches: 7 Query Match: 68.51% Indels: 0 DB: 10 Gaps: 0	US-08-836-455-2 (1-145) x US-09-887-853-5 (1-739) QY 21 ASplieGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40	41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro	61 AspGlyThrileLysArgLeulleTyrAlaThrSerSerLeuGlySerGlyValProLys 	Oy 81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100	Oy 101 GluaspPheValalaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120	Qy 121 GlyThrLysLeuGluIleLysArgAlaAsp 130	OU GGGACLGGAAAIRAACGGGCIGAA	US-09-924-099-11 ; Sequence 11, Application US/09924099 ; Patent No US-000-00198450A1	GENERAL INFORMATION: ; APPLICANT: NISHIDA, Yoshihiro		; APPLICANT: KURIMOTO, Masashi ; TITLE OF INVENTION: PEPTIDE	. 660,78	; PRIOR APPLICATION NUMBER: EMELIER APPLICATION NUMBER: 09/338,511 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98	; PRIOR FILING DATE: BARLIER FILING DATE: 1998-10-12 ; PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: J98 DPIOR FILING DATE: PAPLIFE FILING DATE: 1998-12-29	; NUMBER OF SEQ ID NOS: 33	; INGTH: 324 ; TYPE: DNA ; OPGENTEN. MICE MILE MILE MILE MILE MILE MILE MILE MIL	-11	ment Scores: 4.25e-55 Length:	Score: 506.00 Matches: 100 Percent Similarity: 94.44\$ Conservative: 2 Best Local Similarity: 92.59\$ Mismatches: 6	68.38% Indels: 10 Gaps:	US-08-836-455-2 (1-145) x US-09-924-099-11 (1-324)	Oy 21 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerLeuGlyGlnArgValSer 40	41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
Qy 61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80 	ThrileSer accarcagc	307 GAAGATTTTGCAGACT 121 GlythrLysLeuGlu	DD 367 GGGACCAAGCTGGAGCTGAAA 387 RESULT 9 US-09-887-853-5	<pre>; Sequence 5, Application US/09887853 ; Patent No. US20020168375A1 ; GENERAL INYORMATION: ; APPLICANT: Huston, James S.</pre>	mann	; TITLE OF INVENTION: Blosynthetic Binding Proteins For Imaging; NUMBER OF SEQUENCES: 11	STREET: Exchange Place, 53 State Street.	COUNTY: Boston STATE: Massachusetts COUNTRY: ISA		MEDIUM TYPE: Floppy disk COMPUTER: IBM PC companies COMPUTER: DEAD COMPANIES COMPUTER: COMPANIES COMPUTER: COMPANIES COMPUTER: COMPANIES COMPUTER: COMPANIES COMPANIES COMPUTER: COMPANIES CO) OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 HIDDENN ADDITIONAL NAME.	CONTENT AFFLICATION NUMBER: US/09/887,853 FILING DATE: 21-Jun-2001	; CLASSIFICATION CONROWN> ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/08/133,804	: FILING DATE: <unknown> : ATTORNEY/AGENT INFORMATION: : NAME: Kellev. Rohin D</unknown>	REGISTRATION NUMBER: 34,637 REFERENCE/DOCKET NUMBER: 2054/22	TELECOMMUNICATION INFORMATION: TELEPHONE: 617-248-7477 TELEPHONE:	INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:	LENGTH: 739 base pairs	STRANDEDENESS: SINGLE TOPOLOGY: linear MOLECULE TYPE: CDNA	; FEATURE: ; CDS	; LCCATION: 1729 ; CTHEN INFORMATION: /product= "520C9 sFv polypeptide : commons"	3EQUE -853-	Alignment Scores: Pred. No.: 9.53e-55 Length: 739 Score: 507.00 Matches: 101

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SerLeuGluSerGluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyr 116
                   Alignment Scores:
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                                                                                                           GluaspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                                                                                                       CTCACTTGTCGGGCAAGTCAGGACATTGGTAGTAAATTATACTGGCTTCAACAGGAACCA 120
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                                                                                                                                                                                                      Sequence 19, Application US/09924099
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Tadao
APPLICANT: TALIMOTO, Masashi
TILE OF INVENTON: PEPTIDE
CURRENT TRIING DATE: 2001-08-08
CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; PRIOR SEQ ID NOS: 33
; SEQ ID NO 19
; LENTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnGlnGluProAspGlyThr1leLysArgLeuIleTyrAlaThrSerSerLeuGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      499 CAACAGGAACCAGATGGAACTITITAAACGCCIGATCTACGCCACATCCAGTTTAGATTCT
                                                                ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                      GlyThrLysLeuGluIleLysArg 128
                                                                                                                                                                           324
                                                                                                                                                                CTHER INFORMATION: Artificial DNA OTHER INFORMATION: SEQ CTHER INFORMATION: ID NO:9 US-09-924-099-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.89e-54
502.00
91.89%
90.09%
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Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Artificial DNA to code for the amino acid sequence OTHER INFORMATION: SEQ OTHER INFORMATION: ID NO:10 US-09-924-099-20
                                                                                                                                                                                                                                                                                                                                                                     JP 289,044/98
                                                                                                                                                                                     APPLICANT: NUMBLIA, TOSHIHITO
APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT FILING DATE: 2001-08-08
PRIOR PELING DATE: EARLIER APPLICATION NUMBER: 09/;
PRIOR PILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR PELING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-2
NUMBER OF SEQ ID NOS: 33
SEQ ID NOS: 33
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Mismatches:
Indels:
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                                  117 ThrPheGlyGlyGlyThrLysLeuGluIleLys 127
                                                                   679 ACGTTCGGAGGGGGACCAAGCTGGCAATAAAA 711
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                                                                                                                                     Sequence 20, Application US/09924099; Patent No. US20020128450A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 ATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTCTTTAGCCTGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 GAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTAACCCTCCGGTCACTTTCGGC
                                                APPLICANT: Pyle, Ruth A.
APPLICANT: Tu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.543
CURRENT APPLICATION NUMBER: US/09/919,344
CURRENT FILING DATE: 2001-07-30
SUTMERN FILING DATE: 2001-07-30
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                               737
97
16
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1
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Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-836-455-2 (1-145) x US-09-919-344-7 (1-737)
                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: 669, 685, 718, 722
; OTHER INFORMATION: n = A,T,C or G
US-09-919-344-7
           Sequence 7, Application US/09919344
Patent No. US20020137911A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             6.71e-52
484.50
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67.36%
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                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-919-344-7
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Sequence 29, Application US/09859053
Fatent No. US20020102658a1
GENERAL INFORMATION:
APPLICANT: Taula, Ratsunari
APPLICANT: Taula, Ratsunari
APPLICANT: Teula, Ratsunari
APPLICANT: Hori, No. US20020102658aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT APPLICATION NUMBER: US 2001-09508
FRIOR PRILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
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96
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Mismatches:
Indels:
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                                                                                                                                                                                                                                       Length:
Matches:
FILE REFERENCE: PC23019A
CURRENY PAPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
SOFTWANE: PATCHILI VOS: 2.1
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67.13%
65.00%
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                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-153-382-18
                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                       Alignment Scores:
Pred. No.:
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                                                                                                                   SEQ ID NO 18
LENGTH: 714
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81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
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95
15
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Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                               Length:
Matches:
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 974
                                                                                                                                                                                                        2.78e-50
473.00
76.92%
66.43%
63.92%
                                                                   | FEATURE:
| NAME/KEY: 5'UTR
| LOCATION: (1) ... (38)
| LOCATION: (39) ... (76)
| LOCATION: (39) ... (76)
| NAME/KEY: 3'UTR
| LOCATION: (750) ... (974)
| NAME/KEY: 319_Peptide
| LOCATION: (39) ... (104)
| US-09-859-053-29
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                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                  Alignment Scores:
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Search completed: August 31, 2003, 01:08:46 Job time : 194.198 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

August 30, 2003, 22:11:21; Search time 1744.87 Seconds (without alignments) 2019.725 Million cell updates/sec Run on:

US-08-836-455-2 740 I MGAPAQILGFLLLEFPGTRC.....IKRADAAPTVSIFPPSSKLG 145 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

22781392 seqs, 12152238056 residues Searched:

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-MODEL-framet-pZn.model.-DEV-Xlh
-MODEL-framet-pZn.model.-DEV-Xlh
-DB-EST-OFMT-fastap -SUFFIX-PZn.rst -MINNATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-DLIS -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-PCT -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-PCO -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-USO8836455_GCGN_1_13596_Grunat_29082001_132902_22290 -NCPU-6 -ICPU-3
-NO_MAAP -LARGEQUERY -NEG_2CORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

EST:* Database :

em_esthum:* em_estin:* em_estba:* em_estpl:* em_estro:* em_estmu:* em_estov:* gb_est1:*
gb_est2: gb_est3: em_htc:* gb_htc:

em_gss_hum:* em_estfun: em_gss_inv: em_estom:* gb_est4: gb_est5:

em_gss_fun:* em_gss_mam:* em_gss_mus:*

em_gss_pln:

em_gss_rod:* em_gss_phg:* em_gss_vrl:* gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	138788 60	G963548 602	X083003 BYO	G518527 602	52061 602	3422 601	4806 601	56818 602	79422 602	18407 AGE	31992 602	34224 601	3114 602	13305 AGE	11988 602	30940 602	57342 AGE	9120 601	BF663472 602	1430 Homc	8543 602	35164 AGE	31143 602	6230 602	57218 602	76253 602	16490 nic	36053 AGE	55041 603	34937 AGE	32283 602	20231 AGE	0//00 AGE	27410 60300	DETRI AGENC	36552 AGENCOU	58128 AGENCOU	36281 BX33628	58542 AGENCOU	34807 AGENCOU	56527 AGENCOU	36236 AG	17347 AGENCOI	DOWNER ASSESSED
рв гр	10 BF1387	2 BG96354	BY08300	0 BG51852	2 BI15206	0 BF12342	0 BF14480	0 BG75681	0 BF57942	3 BQ91840	0 BF58199	0 BE28422	2 BI10311	3 BQ94330	0 BG34198	0 BF58094	4 CB95734	0 BF12912	0 BF66347	HSM07043	0 BG51854	4 CB98516	0 BG43114	0 BF97623	0 BG75721	0 BF97625	4 CA94649	4 CB98605	2 BI45504	4 CB98493	0 BF58228	4 (890620	CB95//0	2 BR01991	3 BO70678	4 CB98655	4 CB95812	3 BX33628	4 CB95854	4 CB98480	4 CB95652	4 CB98623	A CB9873A	* C (0.590 *
% Query Match Length I	.1 630	3.0 71	1.1 37	9.7 87	8.8 82	8.4 66	8.1 76	7.6 88	7.4 89	7.2 145	6.4 77	6.2 69	6.1 70	6.1 90	6.1 96	5.7 72	5.4 78	5.3 91	5.3 110	5.1 46	5.1 68	5.0 76	5.0 81	4.9	4.7 103	4.6 99	4.5 65	4.5 79	4.5	4.5 97	4.3	0/0	4.3	1.1	7. 00	3.9	3 9 74	3.9	3.9 76	3.8 83	3.6 74	3.6 78	3 6 70	0.0
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ALIGNMENTS

BF138788 630 bp mRNA linear EST 24-OCT-2000 601780387F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008404 5', BF138788.1 GI:10977828 mRNA sequence. BF138788 LOCUS VERSION KEYWORDS SOURCE ORGANISM ACCESSION RESULT 1 BF138788

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630) REFERENCE

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mRNA sequence.
BG962572
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Best Local Similarity:
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9242 row: n column: 21
High quality sequence stop: 628.
Location/Qualifiers
I. 630
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Site_2: SalI; transgenic model WNT-1, expression driven by
MMY-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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    AUTHORS
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BG962572 926 bp mRNA linear EST 12-JUN-2001 602829953F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4984788 5',
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HH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10991 row: 1 column: 13
High quality sequence stop: 685.
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Mus musculus
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91.61%
81.82%
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102

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us-08-836-455-2.p2n.rst

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Nus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Musculus
(CE (bazaki,Y.); Euruno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Noganit,A., Schonbach,C.,
Gojobori,T., Balake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani
L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
A., Frazer,K.S., Gasterland,T., Gariboldi,M., Gissi,C., Godzik,A.,
Jarvis,E.D., Kanaj,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M.,
Jarvis,E.D., Kanaj,A., Kawaji,H., Kawasawa,Y., Redzierski,R.M.,
Jarvis,E.D., Kanaj,A., Kavaji,H., Kawasawa,Y., Redzierski,R.M.,
Jarvis,E.D., Ranai,A., Kavochkin,I.V., Lee,Y., Lehhard,B., Lyons
Y., Magoshima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G.,
Pesole,G., Petrovsky,N., Pillai,R., Pontlus,J.U., Qi,D.,
Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring
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Watanabe,Y., Walls,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa
A.M., Shimada,K., Saltana,R., Shinshawa,Y., Kawai,J., Yang,L., Xang,L., Xang,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3/4 bp mRNA linear EST 07-DEC-2002 BY083003 RIKEN full-length enriched, pooled tissues, adult spleen, etc. Mus musculus cDNA clone K630040M06 5', mRNA sequence. BY083003
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                         43 CysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluProAspGly
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AUTHORS
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GluaspPheValalyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
                                              315 GAAGATTTTGCAGACTATTACTGTCTACAATATGCTAATTATCCGTGGACGTTCGGTGGA 374
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/clone_lib="NCI_CGAP_CO24"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I. M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G. E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10994 row: c column: 08
High quality sequence stop: 712.
Location/Qualifiers
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Mus musculus
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/strain="FVB/N"
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435 TCCAGTGAG 443
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BG518527 86127 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491798 5', BG518527 BG518527
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM8536 row: i column: 15
High quality sequence stop: 843.
High quality sequence stop: 843.
Location/Qualifiers
cce //organism="Mus musculus"
                                                     81 ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
                                                                                                                                                                                                                                                                                                         /clone_lib="NCL_CGAP_Lu29"
/clone_lib="NCL_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
     93 GACATCCAGATGACCCAGTCTCCATCCTCCTTATCTGCCTCTCTGGGAGAAGAGTCAGT 152
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                         101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSer 114
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/strain="CZECH II"
/db_xref="taxon:10090"
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/Clone_inb="RKKEN"

dult spleen, etc."

dult spleen, etc."

/clone_inb="RKKEN"

/core="dev_stage=adult, tissue_type=spleen,sex=male),

/core_stage=adult, tissue_type=kidney,sex=male),

/cov_stage=adult, tissue_type=hart,sex=male),

/cov_stage=adult, tissue_type=hart,sex=male),

/cov_stage=adult, tissue_type=colon,sex=male),

/cov_stage=adult, tissue_type=colon,sex=male),

/cov_stage=adult, tissue_type=colon,sex=male),

/cov_stage=adult, tissue_type=colon,sex=male),

/cov_stage=adult, tissue_type=stomach,sex=male),

/cov_stage=13 days embryo, tissue_type=whole body,sex=mix

//cov_stage=16 days embryo, tissue_type=whole body,sex=mix

//cov_stage=16 days embryo, tissue_type=whole body,sex=mix

//cov_stage=16 days pregnant, adult,tissue_type=mnion

//cov_stage=16 days pregnant, adult,tissue_type=bnzin

//cov_stage=16 days pregnant, adult,tissue_type=bnzin

//cov_stage=16 days pregnant, adult,tissue_type=bnzin

//cov_stage=16 days pregnant, adult,tissue_type=bnzin

//cov_stage=16 days pregnant, adult, tissue_type=bnzin
                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues visit our web site (http://genome.gsc.riken.go.jp) for
                                                                         Email: genome-reagesc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Alzawa,K., Arimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Arimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
     Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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,sex=mix),(dev_stage=10 days neonate,tissue_type=heart
,sex=mix)"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
                                                                334
                                                                                                                                                                                                                                                                                                                         101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
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NIH-WGC http://mgc.nci.nih.gov/.
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Stem cell origin."
   MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArqCys
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                                                                                                                                                                                           61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
row: h column: 04
High quality sequence stop: 827.
Location/Qualifiers
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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Mus musculus
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B1152061
B1152061.1 GI:14612062
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BI152061
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BF123422 669 bp mRNA linear EST 24-OCT-2000 601760623F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4023749 5', BF123422
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                           8 LeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCysAspIleGlnMetThrGlnSer
                                                                                                                                                                                                                                                                                                                            28 ProSerSerLeuSerAlaSerLeuGlyGlnArgValSerLeuThrCysArgAlaSerGln
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLAM9282 row: n column: 06
High quality sequence stop: 649.
samples: Gilbert Smith, NIH"
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/mol_type="mRNA"
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Gilbert Smith, Ph.D.
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Matches:
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/clone_lib="NCI_CGAP_Lu30"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9278 row: 1 column: 22
High quality sequence stop: 677.
Location/Qualifiers
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Matches:
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BG756818.1 GI:14067471
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/organism="mRNA"
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Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                     BF579422 891 bp mRNA linear EST 12-DEC-2000 602093833F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208144 5',
      61 AspGlyThrIleLysArgLeuIleTyrAlaThrSerSerLeuGlySerGlyValProLys 80
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9712 row: a column: 09
High quality sequence stop: 711.
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                       1..86 //organism="Momo saplens"
/mol_type="mrNa"
/mol_type="mrNa"
/db_xxef="texon:9606"
/clone="IMAGE:8850686"
/tlssue_type="primary B-cells from tonsils (cell line)"
/tab_host="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/rlone="organ: B-cells, Vector: poTB7; Site_1: XhoI;
Site_2: ECORI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGG(5). Size-selected >500bp
for average insert size 1 8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

11 a 258 c 219 g 197 t 1 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://mage.lini.gov
Plate: LiCM1692 row: e column: 23
High quality sequence stop: 864.
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                                                        NIH-MGC http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity:
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BF581992 772 bp mRNA linear EST 12-DEC-2000 602099448F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4219618 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="INAGE:4219618"
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/clone_lib="NCI_GGAP_C024"
/note="Grgan colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_GGAP Library."
204 c 175 g 176 t I others
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contract: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.o.column: 11
                                                                                                                                                                  101 GluaspPheValalaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly
                                                                                                                                                                                                                                                                                                                                                                                            1 MetGlyAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProGlyThrArgCys
                                  190 ATGATGTCCTCTGCTCCTTGGTCTCCTGTTGCTCTTTTCTAGGTTCCAGATGT
                                                                                                                                                 41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuH1sTrpLeuGlnGlnGluPro
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/organism="Mus musculus"
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Location/Qualifiers
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/db_xref="taxon:10090"
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Mus musculus
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BF581992
BF581992.1 GI:11655613
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BF581992
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Riam.gos. row: c column: 15
High quality sequence start: 165
High quality sequence stop: 634.
                                                                                                                              101 GluAspPheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGly 120
311
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lb="NOI_GGAP_COS4"
/note="Organ colon; Vector: pGWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NOI_GGAP Library."

441 c 306 g 315 t 4 others
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/organisme"Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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/clone="IMAGE:6397382"
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/UB DP MRNA linear EST 26-JUN-2001 5', mRNA sequence.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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//note="Organ: lung: Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                  mammary
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                  t
                  metastatic
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               /tissue_type="spontaneous tumor,
Stem cell origin."
/lab_host="DH108"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
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Mismatches:
Indels:
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Matches:
 /clone="IMAGE:3491798"
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TATCGTTACCTTCCGTGGACGTTCGGTGGAGGCACCAAGTTGGAAATCAAACGGGCTGAT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 TyrAlaSerSerProTyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAsp 130
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NIH-WGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8536 row: i column: 15
High quality sequence stop: 562.
Location/Onalifiers
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                                                                                                                 Gaps:
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                                        3.29e-45
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="INAGE:5044690"
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Site_2: Sal1; Cloned unidirectionally. Primer: Ollgo dr.
Average insert size 1.75 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library. |"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Tryte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
llate: LLAMI122 row: i column: 11
High quality sequence stop: 706.
Location/Qualifiers
1.708
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Matches:
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NOI_GGAP Library."
1 243 c 199 g 227 t 1 others
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 901)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIAM13894 row: i column: 15
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Tissue Procurement: The Cepko Laboratory
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AF137626
MMU55588
MUSIGKAFT
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MUSIGKAFT
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-MODEL-frame+_p2n.model -DEV-x1h
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-Q-/cgn2_1/USPTO_spool_/US08836455/runat_29082003_132953_23045/app_query_fasta_1.654
-DB-GenEmbl -QFWT-fastap -SUFFIX--P2noll.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -START-1 :END--1 -MATRIX-oligo -TRANS-humand0.cdi -LIST-45
-DCALIGN-200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFWT-pto
-NORM-ext - HEAPSIZE-500 -WAINLEN-0 -WAXLEN-200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORESO -WAIT - DSPBLOCK+100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT-60 -DELEXT-7
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1999.191 Million cell updates/sec
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                                                                                          August 31, 2003, 00:02:06; Search time 2967.15 Seconds
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1 MGAPAQILGFLLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG
             GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                OM protein - nucleic search, using frame_plus_p2n model
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), Ygapext 6
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AR083800 Sequence AR198719 Sequence AR275319 Sequence AB050082 Mus muscu

E54981 Peptide. 1/ U88675 Mus musculu

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Chatterjee, M. and Foon, K.A.

S Chatterjee, M. and Foon, K.A.

Methods of delaying development of HMFG-associated tumors using anti-tidotype antibody 11010.

L Patent: UP 2001523269-A.1 20-NOV-2001;

THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PN JP 2001523269-A/1
PD 20-NOV-2001
PF 12-UNI-1997 US 60/049540,11-JUN-1998 US 09/096244 PI
MALAYA CHATTERJEE, KENNETH A FOON
PC A61X39/395, A61X39/399/CO7K16/42
CC Strandedness: Single;
CC Topology: Linear;
CC Methods of delaying development of HMFG-associated tumors CC
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Key Location/Qualifiers
CDS 1. 435
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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          PAT 17-0CT-2001
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                                                                Unknown.
Unknown.
Unclassified.
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Unclassified.
Unclassified.
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Chatterjee,M. and Foon,K.A.
Chatterjee,M. and Foon,K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11D10
Patent: US 6274143-A 1 14-AUG-2001;
Footinf/Qualifiers
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BD085737.1 GI:22631347
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                                                                                                                                                                                                                                                                                    PAT :17-DEC-2001
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Anand, N.N., Barber, B.H., Cates, G.C., Caterini, J.E. and Klein, M.H.
Chimeric antibodies for delivery of antigens to selected cells of
the immune system
Patent: US 6291208-A 1 18-SEP-2001;
Location/Qualifiers
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MARRY M BENDIG
C12N15/709, A61R39/395, A61P1/00, A61P29/00, A61P37/00, C07K16/46,
C12N17/15,
C12N1/19, C12N1/21, C12N5/10, G01N33/53, G01N33/531//C12P21/08, E
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synthetic construct
artificial sequences.
1 (bases 1 to 515)
Ponasu,P.D., Linglar,D., Jones,T.S., Newman,W., Saldanha,H. and
Bendig,M.M.
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Patent: JP 2001507210-A 3 05-JUN-2001;
ROIKOSITE INC
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Matches:
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Sequence 1 from patent US 6291208.
AR169918
AR169918.1 GI:17907877
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15-AUG-1996 US 08/700737
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95 c 90 q
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/product="immunoglobulin light chain"
/product="immunoglobulin light chain"
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/db_xref="G1:14164547
ROD 22-MAY-2001 cds.
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Chatterjee,S.K. and Tripathi,P.K.
Direct Submission
Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 PheValAlaTyrTyrCysLeuGlnTyrAlaSerSerProTyrThrPheGlyGlyGlyThr 122
                                                                                                                                                                                                               Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 381)
Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,R.L., Foon, K.A. and Chatterjee,S.K.
Construction and characterization of a chimeric fusion protein cancer-associated anti-diotype antibody minicking a breast Hybridoma 18 (2), 193-202 (1999)
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/note="anti-idiotype antibody 11D10; mimics a breast
cancer-associated antigen, human fat globule (HMFG)"
               AF124721 381 bp mRNA linear
Mus musculus immnogloblin light chain mRNA, partial
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/organism="Mus musculus"
/organism="Mus"
/ol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
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                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
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PAT 06-FEB-1997
                                 region of Idio17,
106. 153
/note='CDR1 of light chain variable region of
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                                                                                                                                                                                                                     e 154. .198
/note-Fragment 2 of light chain variable region of Idio17, 199; .219
                   /note='Fragment 1 of light chain variable
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132991.
132991.1 GI:1823782
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/organism="Mus musculus"
/mol_type="genomic RNA"
/db_txref="taxon:10090"
12 0 102
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/organism='Mus musculus'
/tissue_type='spleen'
/clone='17KB1'
1. .39
40. .438
/note='1.ight chain variable region of mouse antildiotype
antibody named Idio17 against CLN-IgG FT
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Eukaryotania
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 438)
Hagiwara, H. and Aozuka, Y.
AMINO ACID SEQUENCE OF ANTI-IDIOTYPE ANTIBODY TO ANTI-CANCER HUMAN
MONOCLOMAL ANTIBODY AND DNA BASE SEQUENCE CODING FOR THE SAME
PATENT: JP 1995101999-A 7 18-APR-1995;
Mus musculus (mouse)
PD 1895101999-A/7
PD 18-APR-1995
PD 18-APR-1995
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CO7K16/42,C12N5/10,C12N15/02,C12N15/09,C12P21/08,(C12P21/08,
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Matches:
Conservative:
Mismatches:
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
128 c 132 g 149 t
                                                                         Location/Qualifiers
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Location/Qualifiers
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               C12N5/00
Strandedness: Double;
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JP 1995101999-A/7.
Mus musculus (house mouse)
Mus musculus
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hypothetical: No;
                                                      Topology: Linear;
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Mus musculus VL2C mRNA for anti-A/dT antibody, partial cds. AB050084.1 GI:19909943
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/product-1d-"BABB/1196.1"
/db.xref-"c1:19909944"
/translation-"METDTLLLWVLLLWVPGSTGDIVLTQSPASLAVSLGORATISYR
ASSNSYGTSGYSYMHWNQARPQCPPRLLIYLWSNLESGYPARRSGSGTDFTLNIHPV
EEEDDAATYCQHIRELYTEGGGTKLEIKRADAAPTVSIFPPSSKLG"
117 9 104 t
                                         116 TyrThrPheGlyGlyGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAsPaTaTla71 135
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                 as immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; Minami 2-2, Ogata, Akita
010-0444, Japan (F-mail:Kitagawa@ari.akita-pu.ac.jp,
UKL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
Fax:81-185-45-2678)
                                                                                                                                                                                                                                                                                                                                                           Kitagawa,Y. and Stollar,B.D.
Comparison of poly(A).poly(dT) and poly(I) poly(dC) if it he induction of antibodies to RNA-DNA hybrids Mol. Immunol. 19 (3), 413-420 (1982)
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Indels:
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                                                                                                     Length:
Matches:
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    453
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="BALB/c"

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/gene="VL2C"
9. >452
/gene="VL2C"
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             US-08-836-455-2 (1-145) x AB050077 (1-452)
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ASKSVSTSGYSYSWHWNQOKPGOPPRLLIYLVSNLESGYPARFGGSGSGTDFTLNIHPV
EBEDAATYYCQHIRELYTFGGGTKLEIKRADAAPTVSIFPPSSKLG"
                                                                                                                                                                                                                                                            AB050077 452 bp mRNA linear ROD 02-APR-2002 Mus musculus VL10G1 mRNA for anti-dsRNA (RDV-RNA) antibody, partial
                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural University, Biotechnology Institute; minami 2-2, Ogata, Akita 010-0444, Japana (E-mail:kitagawa@egri.akita-pu.ac.jp, URL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400), Fax:81-185-45-2678)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kitagawa,Y., Matsumoto,T., Okuhara,E. and Shikata,E.
Immunogenicity of rice dwarf virus-ribonucleic acid
Tohoku J. Exp. Med. 122 (4), 337-343 (1977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="anti-dsRNA (RDV-RNA) antibody"
/protein_id="BAB87189.1"
/db_xref="GI:19909930"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Published Only in Database (2002)
3 (absoluted to 452)
Kitagawa,Y.
           Mismatches:
Indels:
                                                                                                                                                                  136 SerIlePheProProSerSerLysLeuGly 145
                                                                                                                                                                                  /db_xref="taxon:10090"
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1. .452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                          Gaps:
                                                                      US-08-836-455-2 (1-145) x I32991 (1-438)
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                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
Mus musculus
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/gene="VL10G1"
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Percent Similarity:
Best Local Similarity:
Query Match:
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ROD 25-JUL-2002

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Percent Similarity:
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Query Match:
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/prodict="immunoglobulin kappa-chain"
/protein_id="AAA38889.1"
/db_xref="G1:466307"
/translation="MGIRASOIQVEVEVELMLSGVDGDIVMTQSHKFMSTSVGDRVS
ITCRASODVSTAVARYQQKPGQSPKLLIYSASYRYTGVPDRFTGSGGGTDFTFTISSV
QAEDLAVYYCHQHYSSPYTFGGGTKLEIKRADAAPTVSIFPPSS"
                                                                                                                                                                                                                                                                                            2 (bases 1 to 456)
Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies
for NMR studies
                                                                                                                    ROD 26-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                             Original source text: Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.

Draft entry and computer-readable sequence [2] kindly submitted by G.Rule, 20-JUL-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTA 422
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 56)
Rule,G.S.
Unpublished (1988)
                                                                                                         MUSIGKCNK

Mouse Ig rearranged kappa-chain mRNA, clone AN12K.
M19914 J03832
M19914.1 GI:197035
C-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)
88234486
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114 c 108 g 116 t
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Matches:
Conservative:
Mismatches:
Indels:
                           133 ProThrValSerIlePheProProSerSer 142
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/db_xref="taxon:10090"
/cell_type="mature B cell"
19. .>456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .456 /organism="Mus musculus"
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/strain="BALB/c"
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Best Local Similarity:
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mat_peptide
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                                                                                    RESULT 10
MUSIGKCNK
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Z (bases 1 to 218)
Yamagishi, H.
Direct Submission
Submitted (02-021-1990) Yamagishi H., Dept of Biophysics Faculty of Science Kyoto University, Sakyo-ku Kyoto 606, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="Caa38556.1"
| Dax xrei="G1:21998640"
| /translation="G0PPDG1R" | YATSSLDSGVPKRFSGSRSGSDYSLTISSLES
| EDFVDYYCLQIASSPFTFGSGTKLEIKR"
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Harada, K. and Yamagishi, H. Lack of feedback inhibition of V kappa gene rearrangement by J. Exp. Med. 173 (2), 409-415 (1991)
Mouse rearranged kappa immunoglobulin light chain (V,J).
X54757
X54757.1 GI:21998639
IG light chain; immunoglobulin.
Mus musculus (house mouse)
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Matches:
Conservative:
Mismatches:
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/note="J kappa gene segment"
/a c 48 g 62 t
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/tissue_type="spleen"
/clone_lib="lambda gtll"
                                                                                                                                                                                                                                                                                                                                                                                                                  1. .218
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="BALB/c-nu/nu"
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<1. .>218
/note="Ig light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="MSI-N102"
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LOCUS
DEFINITION
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(bases 1 to 276)
Smith, R., McCafferty, J., Chiswell, D., Darsley, M.J., Fitzgerald, K.,
Kenten, J. H., Martin, M.T., Titmas, R.C. and Williams, R.O.
Ksolation and production of catalytic antibodies using phage
technology
Patent: US 5855885-A 44 05-JAN-1999;
Location/Qualifiers
                                                                                                                                                           B cell selection and allelic exclusion of an anti-DNA Ig transgene
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Roark, J.H., Kuntz, C.L., Nguyen, K.A., Mandik, L., Cattermole, M. and Erikson, J.
                                                                                                                                                                                                                                                                                                                    Direct Submission Submission Bossica H. Roark, Wistar Institute, 3601 Submitted (15-FEB-1995) Jessica H. Roark, Wistar Institute, 3601 Spruce St., Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                         1. 273 memoral description of the control of the co
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J. Immunol. 154 (9), 4444-4455 (1995)
95238942
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Sequence 44 from patent US 5855885.
AR026090.1 GI:5936930
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    Mus musculus (house mouse)
Mus musculus
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2 (bases 1 to 273)
Roark,J.H.
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AR026090
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                                                                                                                                                                                                                                                                                                                                                     Jurect Submission
Submitted (02-0CT-1990) Yamaqishi H., Dept of Biophysics Faculty of
Science Kyoto University, Sakyo-ku Kyoto 606, Japan
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 269)
Harada,K. and Yamagishi,H.
Lack of feedback inhibition of V kappa gene rearrangement by productively rearranged alleles
J. Exp. Med. 173 (2), 409-415 (1991)
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Ig light chain; immunoglobulin.
Mus musculus (house mouse)
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Yamagishi, H.
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PAT 29-SEP-1999

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PAT 29-SEP-1999
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Smith,R., McCafferty,J., Chiswell,D., Darsley,M.J., Fitzgerald,K.,
Kenten,J.H., Martin,M.T., Titmas,R.C. and Williams,R.O.
Isolation and production of catalytic antibodies using phage
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Patent: US 5855885-A 52 05-JAN-1999;
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AR026094
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Copyright (c) 1993 - 2003 Compugen Ltd.
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19 29 20.0 729 13 AAA49543 ppsscFv#125-2N 20 20.0 739 14 AAA496084 52009 anti-o- 21 29 20.0 739 17 AA73680 52009 anti-o- 22 20.0 739 19 AAV7339 52009 anti-o- 23 20.0 739 19 AAV7339 52009 anti-o- 23 20.0 739 20 AAV7339 5200 52009 anti-o- 24 20 20.0 771 24 AAS97142 52009 anti-o- 25 29 20.0 1497 24 AAS97142 52009 anti-o- 26 29 20.0 1497 24 AAS97142 52009 anti-o- 27 20 20.0 1497 24 AAS97142 52009 anti-o- 28 19.3 456 22 AAC66996 650E2 hybrido 28 19.3 651 21 AAA4396 650E2 hybrido 28 19.3 652 17 AA74346 AAM000 650E2 hybrido 28 19.3 652 17 AA74346 AAM000 771 AA74346 31 28 19.3 654 25 ACC44909 700 AM000 771 AA7600 700 AM000 700 700 700 700 700 700 700 700 700	18	29		\vdash		AAZ49542	pEscFv#125-2H rec
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Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss. KW XX XX XX YX FH

Location/Qualifiers Mus musculus Key ~

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241 AGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATCAGCAGCCTTGAGTCT 300
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                                                                                                                                                                                                                                                  This cDNA sequence encodes the light chain variable region VL (AAW85149) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATCC 12020. 11D10 was obtained by immunising nealve with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice. Tabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are and/or 11D10 polynucleotides, including methods of treating HMFG-associated tumours.
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                                                                                                                                                    Chatterjee M, Chatterjee SK,
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GlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSerIlePheProPro 140
                                                                                                                                        Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss;
human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
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                                                          ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer
                                                                                                                                                                                                                                                                                                                      Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA, 11D10; 3H1; HWFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                                                                                           Mouse 11D10 antibody light chain variable region coding sequence.
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The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for EA (e.g. 3H1). The method is useful for present cDNA sequence encodes the interior of the involves the interior of the involves associated tumours. The mouse 11D10 anti-idiotype antibody.
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                                                                                                                                                                          Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA) associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g. breast tumor) in humans
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                                                                                                                                                                                                                                                            Disclosure; Fig 1; 98pp; English.
                                                             (KENT ) UNIV KENTUCKY RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145
17-MAY-2002; 2002WO-US15840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145.00
100.00%
100.00%
                             17-MAY-2001; 2001US-0861294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chatterjee M, Foon KA;
                                                                                                                            WPI; 2003-129216/12.
P-PSDB; AA016292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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AAT77851;

AAT77851

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49 TITCCAGGTACCAGATGTGACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCCTCT 108
                                                                                                                                                                                                                                                                           Murine; mab; light chain; VL; conjugate antibody; antigen delivery; immune system; vaccine; detecting agent; antibacterial; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_except= (pos:277..279, aa:Thr)
/note= "This translation exception occurs while
decoding for murine mab VL alternative version
(AAE20204); CDS does not include stop codon"
                                                                  CTGGGACAAGAGTCAGTCTCACTTGTCGGGCAAGTCAG 147
                                  35 LeuGlyGlnArgValSerLeuThrCysArgAlaSerGln 47
                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Murine 44H104 mab_VL"
                                                                                                                                                                                                                                          Murine 44H104 mab variable light chain (VL) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cates GA, Caterini JE,
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 1A; 28pp; English.
                                                                                                                                        AAD32138 standard; DNA; 387 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0007093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0007093
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P-PSDB; AAE20200, AAE20204.
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'partial
                                                                                                                                                                                                                                                                                                                                                                               1..387
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BARB/) BARBER B H.
(CATE/) CATES G A.
(CATE/) CATERINI J E.
(KLEI/) KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anand NN, Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            light chain (VL) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ANAN/) ANAND N N. (BARB/) BARBER B H. (CATE/) CATES G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002025315-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-1998;
                                                                                                                                                                                                          18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2002.
                                                                    109
                                                                                                                                                                        AAD32138;
                                                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                        RESULT
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                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel recombinant conjugate antibody molecules comprise a monoclonal antibody specific for a surface structure of antigen presenting cells (ARC), genetically modified to contain at least one antigen exclusively at one or more preselected sites. The conjugate is capable of delivering the antigen to ARC and eliciting an immune response to the antigen. The new conjugates are useful as vaccines and are able to elicit an enhanced immune response without the use of an adjuvant. In a specific example, a conjugate was constructed using the murine anti-human class II monoclonal antibody secreted by hybridoma attandemly linked T and B cell epitope derived from HIV MN strain. The present sequence encodes the light chain variable region which was PCR amphilited from 44H104 and used in the preparation of a
                                                                                                                    Murine anti-human class II monoclonal antibody 44H104 VL chain cDNA.
                                                                                                                                                    Antibody; light chain; variable region; hybridoma cell line 44H104; immune response; enhance; stimulate; vaccine; immunodiagnosis;
                                                                                                                                                                                                                                                                                       /*tag= a
/note= "Encodes 44H104 light chain variable region,
including secretion signal; termination
codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant conjugate antibody mol., modified for delivering an antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein MH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cates GC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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                                                                                                                                                                                                                                                         ocation/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1A; 64pp; English.
                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conjugate with antigen CLTB36
            AAT77851 standard; cDNA; 387
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33.00
100.00%
100.00%
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                                                                                  03-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                          antigen delivery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-077271/07.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immuno:diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW22537
                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996;
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WO9640941-A1

19-DEC-1996.

07-JUN-1995;

Mus musculus

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The invention relates to a recombinant conjugate antibody, comprising
Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                        a monoclonal antibody specific for a surface structure of antigen presenting cells genetically modified to contain an antigen moiety for the purpose of delivery of the antigen moiety to antigen-presenting cells of the immune system. The conjugate antibody is 'formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
33
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 387 BP; 90 A; 95 C; 90 G; 112 T; 0 other;
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Matches:
Conservative:
Mismatches:
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33.00
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Best Local Similarity:
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34

12

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Alignment Scores:

Pred. No.:

Score:

Query Match:

Klein MH;

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construct chimeric, humanised Act-1 antibodies, which contain murine
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                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                      AAQ90431;
                                                                                                                                                                                                                                                                                                                                                                                                                                   sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus
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                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                         AAQ90431
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                                                              PheProGlyThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSer 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the consensus nucleotide sequence comprising the variable region of murine Act-1 antibody determined from several independent mouse light chain variable region clones. Act-1 is active against human alpha-beta7 integrin. Muscosal adressin cell adhesion molecule-1 (MadCAM-1) is a ligand of this particular integrin. The Act-1 antibody inteferes with alpha-beta7 integrin blinding to MadCAM-1, which is present of high endothelial venules in mucosal lymph nodes. Variable regions were amplified from pla encoding Act-1 using degenerate PCR primers Avy20083-84. The degeneracy of the PCR primers produced several different sequences, of which the present sequence is a consensus sequence. The present sequence was used to
                                                                                                                                                                                                                                      Mouse; Act-1 antibody; human alpha4-beta7 integrin;
Muscosal adressin cell adhesion molecule-1; MadCAM-1;
humanised antibody; murine antigen binding region; inhibition;
leukocyte infiltration of tissue; treatment; inflammatory disease;
inflammatory bowel disease; ss.
                                                                                                                                                                                                                   Consensus DNA sequence of the murine variable light chain region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised immunoglobulin reactive with alpha-4-beta-7 integrin used for treating inflammatory disease, pancreatitis, diabetes, asthma, graft versus host disease and sarcoidosis
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                                                                                                                                                                                                                                                                                                                                                         codon given"
 Indels:
          Gaps:
                             US-08-836-455-2 (1-145) x AAD32138 (1-387)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 145pp; English.
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                                                                                                                                                        BP.
                                                                                                                                                       AAV20086 standard; DNA; 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US13884.
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/note= "no :
16..75
/*tag= b
76..435
/*tag= c
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                                                                                                                                                                                               (first entry)
22.76%
24
                                                                                                                                                                                                                                                                                                                                    6..435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-159172/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW53817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO9806248-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .5-AUG-1996;
                                                                                                                                                                                                14-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                     sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bendig MM,
Saldanha J;
                                                  15
                                                                                                                                                                           AAV20086;
                                                                                                               601
Query Match:
                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                    RESULT 6
                                                                                                                                               AAV20086
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                                                                                                               g
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antigen binding regions. The humanised immunoglobulin can be used to inhibit the interaction of cells bearing alpha4-beta7 with cells bearing a ligand for alpha4-beta7. It can be used for inhibiting leukocyte infiltration of tissues, e.g. for treating inflammatory diseases such as inflammatory bowel disease. The immunoglobulin can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ90425-Q90434 are DNA molecules encoding anti-idiotype antibodies Idio3, Idio17, Idio20, Idio27 and Idio33 against a human articancer monoconal antibody. These artibodies and BNA encoding them are useful in pharmacological, medical and biochemical fields of research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel anti-idiotype antibody against an human anticancer monoclonal antibody - and DNA sequences encoding the antibody, useful in pharmacology, medicine and biochemical fields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin; complementarity determining region, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-idiotype_antibody_Idio17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding anti-idiotype antibody Idio17 clone 17KB1.
                                                                                                                                                                                       Sequence 535 BP; 126 A; 128 C; 132 G; 149 T; 0 other;
                                                                                                                                                                                                                                                                 535
31
0
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 GTATCCATCTTCCCACCATCCAGTAAGCTTGGG 465
                                                                                                                                                                                                                                                                                              Matches:
                                                                                                                                                                                                                                                                   Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-836-455-2 (1-145) x AAV20086 (1-535)
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1.438
/*tag= a
                                                                                                                                       detection, isolation and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ90431 standard; DNA; 438
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1.39
/*tag= b
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                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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us-08-836-455-2.p2noli.rng

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MCCAFFERTY J
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MARTIN M T.
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                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                prodrug; scFV; ss.
                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1994;
                                                                                                                                                      Aliqnment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JAN-1999
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                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                             RESULT
ò
                                                                                                116 TyrThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrVal 135
                                                                                                         Catalytic; antibody; phage display; immunising; phage expression vector; prodrug; scFV; ss.
                                                                                                                                                                                                                        Mouse derived RT3 phage antibody light chain pattern C genetic sequence.
                                                                                                                                                                                                                                                                                            /*tag= a
/note= "the start and stop codons are not indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fitzgerald K, Kenten JH;
Smith R, Titmas RC, Williams RO;
     Sequence 438 BP; 104 A; 120 C; 112 G; 102 T; 0 other;
                             438
30
0
0
0
                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                            Indels:
                                                                                 US-08-836-455-2 (1-145) x AAQ90431 (1-438)
                                                                                                                                                                                                                                                                         Location/Qualifiers
1..276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Fig 11; 117pp; English.
                                                                                                                                                                           AAX00879 standard; DNA; 276 BP
                          1.48e-18
30.00
100.00%
100.00%
20.69%
                                                                                                                                                                                                                                                                                                                                                94US-0273146.
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                                                                                                                                                                                                         29-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Darsley MJ,
McCafferty J,
                                                                                                                                                                                                                                                                                                                                                                                              DARSLEY M J.
FITZGERALD K.
KENTËN J H.
MARTIN M T.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITH R.
TITMAS R C.
WILLIAMS R O.
                                                                                                                                                                                                                                                                                                                                                                                                                             MCCAFFERTY J.
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                                                                                                                                                                                                                                                                                                                                                                                        CHISWELL D.
                                                    Best Local Similarity:
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                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                 14-JUL-1994;
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14-JUL-1994;
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                     Alignment Scores:
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                                                                                                                                                                                          AAX00879;
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(MCCA/) I
(SMIT/) S
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9
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The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating agene library of antibody-derived domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a mitigen; optionally immunising an animal with the antigen; generating an antigen; optionally immunising an animal with the antigen; generating at library of VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically cot the antigen: screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies, where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a prodrug. The present sequence represents a genetic sequence of light chain pCR pattern C from mouse derived RT3 phage antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catalytic; antibody; phage display; immunising; phage expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse derived RT3 phage antibody light chain pattern A genetic sequence.
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/note= "the start and stop codons are not indicated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 276 BP; 67 A; 65 .C; 64 G; 80 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX00875 standard; DNA; 276 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DARSLEY M J.
FITZGERALD K.
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                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods for producing catalytic antibodies displayed on a phage. The method comprises: (a) generating a gene library of antibody-dearlyed domains; (b) inserting coding for the domains into a phage expression vector; and (c) isolating the catalytic antibodies. The phage expression vector incorporates a histidine peptide in tandem with a cutient optionally immunising an animal with the antigen; generating a library of VH and VL domains from the immunised animal; cloning the VH and VL domains from the immunised animal; cloning the VH and VL domains into a phage expression vector to generate phage display antibodies; selecting phage display antibodies which bind specifically to the antigen; screening the selected phage display antibodies for catalytic activity to substrate; and isolating the catalytic antibodies; where the phage expression vector incorporates a histidine peptide in tandem with a myc peptide. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a product of antibodies, which can be used for in vivo activation of a producy. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a producy. The processes are used to produce catalytic antibodies, which can be used for in vivo activation of a producy. The
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                                                                                                                                                                                                                Production of catalytic antibodies displayed on bacteriophages - comprises generating a gene library of antibody-derived domains inserting coding into a phage expression vector and isolating the catalytic antibodies
                                                                                   Fitzgerald K, Kenten JH;
Smith R, Titmas RC, Williams RO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 276 BP; 68 A; 65 C; 63 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from mouse derived RT3 phage antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-836-455-2 (1-145) x AAX00875 (1-276)
                                                                                                                                                                                                                                                                                                                            Example 4; Fig 9A-F; 117pp; English.
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                                                                          MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                   Darsley MJ
McCafferty
(SMIT/) SMITH R.
(TITM/) TITMAS R C.
(WILL/) WILLIAMS R O.
                                                                                                                                               WPI; 1999-105036/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
                                                                                                                                                                      P-PSDB; AAW95476
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                                                                                Chiswell D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6054561-A.
                                                                                                         Martin MT,
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binds to a human breast cancer antigen that is also bound by MAD 454C11 and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also described is a hybridoma that produces (I). (I) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence encodes a VL domain derived from a 520C9 hybridoma, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL; hybridoma #125-2H; mouse; monoclonal antibody #125-2HmAb; interleukin-18; antiinflammatory; immunosuppressive; leucocytopoietic; antialgic; antipyretic; antiallergic; hepatotropic; treatment; autoimmune disease; immunopathy; inflammatory disorder; immunoreaction; ss.
                                                                                                                                                                                                                                                                                                            Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a monoclonal antibody (MAb) (I) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse anti-IL-18 antibody VL encoding cDNA from hybridoma #125-2H
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 13; 57pp; English.
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                                                                     86US-0842476.
88US-0190778.
84US-0577976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.24e-18
29.00
                                                                                                                              85US-0690750.
94US-0288981.
                                   95US-0483749
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                                                                                                                                                                                        (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                   2000-338508/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
                                                                                                                                                                                                                                                                   WPI; 2000-338508,
P-PSDB; AAY90824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 321 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                         08-MAY-1988;
08-FEB-1984;
                                                                                                                              11-JAN-1985
25-APR-2000
                                                                         21-MAR-1986
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                                                                                                                                                                                                                           Ring DB;
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DB:
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2002WO-KR00905.
                                                                                                   16-MAY-2001; 2001KR-0026634
                                                                                                                                                                                                                                                                                                                         chain variable region cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                            WPI; 2003-140281/13.
                                                                                                                       (YUHA-) YUHAN CORP
                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                       P-PSDB; AAE34366
                                        WO200292819-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
Synthetic.
                                                                                15-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                            21-NOV-2002
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                                                                                                                                           Lee JW,
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present cDNA sequence derived from hybridoma #125-2H, encodes mouse anti-Interleukin-18 antibody light chain variable region (VL). It can be used in the production of recombinant monoclonal antibody #125-2HmAb, which is capable of neutralising biological activities of interleukin-18. The antibody has antiinflammatory, immunosuppressive, leucocytopoletic, antiallypretic, antiallergic and hepatotroppic activity and can be used for prevention and treatment of autoimmune diseases, immunopathies and inflammatory disorders caused by excessive immunoreaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-surface antigen; Hepatitis B virus; HBV; therapy; infection; virucide;
 /*tag= a
/label= Anti-IL-18_antibody_light_chain_variable_region
                                                                                                                                                                                                   New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle
                                                                                                                                                                                                                                                                                                                                                                                    880000
880000
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Matches:
Conservative:
                                                                                                                                                   Tanimoto T, Kurimoto M;
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                                                                                                                               (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                        Claim 11; Page 21; 36pp; English.
                                                                                        98JP-0177580.
98JP-0289044.
98JP-0365023.
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29.00
100.00%
100.00%
20.00%
                                                                     99EP-0304977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatotropic; gene; ss.
                                                                                                                                                   Okura T,
                                                                                                                                                                     WPI; 2000-118341/11.
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                                                                                                                                                                                                                                                                                                                                                     Sequence 324 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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                                                                     24-JUN-1999;
                                                                                        24-JUN-1998;
12-OCT-1998;
                                                                                                            22-DEC-1998;
                              EP974600-A2
                                                 26-JAN-2000
                                                                                                                                                  Nishida Y,
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/product= "Escherichia coli light chain variable region"
/note= "CDS does not include start and stop codon"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to light and heavy chain variable regions of a monoclonal antibody against S-surface antigen of the hepatitis B virus (HBV). The variable regions of the antibodies are useful against HBV S-surface antigens, e.g. adr, adw, ayr or ayw, particularly for neutralising or removing HBV. They may also be employed to treat or prevent HBV infection. The present sequence is Escherichia coll light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New light and heavy chain variable regions of a monoclonal antibody against the S-surface antigen of the hepatitis B virus (HBV), useful for neutralizing or removing HBV, or for preventing or treating HBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390
00.00
                                                                                                                                                                                                                                                                                                                                                                                                                Ko IY, Kang HK, Song MY, Song TH, Kim
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Mismatches:
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Matches:
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29.00
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The present sequence encodes the murine anti-idiotype monoclonal antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against the antiposide 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2. As the glycosphingolipid GD2 is expressed at high density by human neuroectodermal tumours, e.g. malignant melanoma. Concertoblastoma, glioma, soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its CDN can be used in a vaccine to treat or palliate such diseases. They can also be used to reduce the anti-GD2 Ab bound to a tumour cell.

MAD 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 Ab (humoral response) and CD2-specific cells (cellular response). It can be used to purify anti-GD2, which comprises the level of cellular anti-1A7 or anti-GD2 in a sample or measure the level of cellular anti-1A7 or anti-GD2 activity.
glycosphingolipid; human; neuroectodermal; tumour; glioma; lung; malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine; treatment; palliate; detection; diagnosis; recombinant production; purification; probe; primer; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foon KA;
                                                                                                                                                                              Location/Qualifiers
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                                                                                          amplification; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                                                       95US-0372676.
96US-0591196.
95US-0372676.
96US-0591196.
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P-PSDB; AAW03199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chatterjee M,
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                                                                                                                                         Aus musculus
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                                                                                                                                                                                                                                                                                                                                                             17-JAN-1996;
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16-JAN-1996;
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    NAMES OF THE PART 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes mouse light chain variable region. This recombinant DNA is derived from PCR A which amplifies antibody light chain variable region (VL). The transforment produced using the VL gene was used transform competent E. colis. The peptide produced by transformants neutralises interleukin-18. This is useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases which are caused by excessive immunoreaction. The peptide has anti-allergic, anti-inflammatory, immunosuppressive, hematopoietic, leukocytopoletic, anti-life antipyretic and hepatic-function improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
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variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;
                                            "Mouse light chain variable region"
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 28-29; 32pp; English.
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98JP-0289044.
98JP-0365023.
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Best Local Similarity:
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                                                                                                                                                                                                                        24 - JUN-1999;
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22-DEC-1998;
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26-FEB-1997
mat_peptide
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The cDNA can be used in expression systems for 1A7 prodn., and in the prepn. of probes and primers to respectively assay for 1A7 cDNA, and amplify desired polynucleotides for use in gene therapy (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                  Sequence 447 BP; 106 A; 110 C; 108 G; 123 T; 0 other;
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29
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Mismatches:
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Matches:
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August 31, 2003, 01:16:24

Search completed: Augus Job time: 218.987 secs

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The invention provides a monoclonal antibody (MAD) designated 1A7, which elicits an anti-GD2 (tumor-associated antigen) immunological response in humans. MAD 1A7 has defined light and heavy chain variable region sequences. The MAD 1A7 and polypeptides can be used for eliciting an anti-GD2 immune response. The polypeptides can also be used for detecting or purifying anti-GD2 antibody. The products can be used for treating GD2 associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the CDNA encoding the light chain variable region of MAD 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection and treatment of cancers -
                                                                                                                                                                                      Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen; ss.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
Chatterjee SK, Chatterjee M;
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                                                                               AAZ31365 standard; cDNA; 447
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29.00
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P-PSDB; AAY49209.
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Best Local Similarity:
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Mus sp.
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DB:
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Sequence 10, Appl
Sequence 3, Appl1
Sequence 1, Appl1
Sequence 20, Appl
Sequence 7, Appl
Sequence 27, Appl
Sequence 103, Appl
Sequence 103, Appl
Sequence 103, Appl
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Sequence 20, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 95, Appl
Sequence 22, Appl
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Sequence 16, App
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Sequence 3,
Sequence 9,
Sequence 10
Sequence 9,
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Sequence 5,
Sequence 2
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                                                                                                                                        Sequence
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APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TOWARS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/09/861,294
CURRENT FILING DATE: 2001-05-17
PRIOR PILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-918-995-37859
US-10-066-543-2025
                                                                                                                   US-09-990-205-1

US-10-153-401-1

US-09-924-099-19

US-09-924-099-19

US-09-917-10-268-813-10

US-10-268-813-10

US-09-807-73-18

US-09-807-73-10

US-09-897-006-13

US-09-861-294-13

US-09-861-294-19
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US-10-006-773-14
US-09-929-665-9
US-09-929-665-9
US-09-929-665-10
US-09-929-546-10
US-09-929-546-10
US-09-929-546-10
US-09-929-546-10
US-09-967-1790-3
 US-09-007-093-1
US-09-924-099-11
US-08-779-784-16
US-08-779-784-17
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US-08-779-784-5
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Patent No. US20020098190A1
GENERAL INFORMATION:
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6255
6255
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LOCATION: (1)...(435)
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                                                                                                                                                                                         "MODEL-frame+_parameters."

"MODEL-frame+_parameters."

"OP-/cgn2_1/USPTO_spool/US08836455/runat_29082003_132954_23062/app_query.fasta_1.654-
"DB-published_Applications_NA -OFMT-fastap -SUFFIX-p2noi1,rnpb -MINNATCH-0.1

"DB-published_Applications_NA -OFMT-fastap -SUFFIX-p2noi1,rnpb -MINNATCH-0.1

"TRANS-human40.cdi -USTR-45 -DOCALIGN-200 -THR_SCORE-quality -THR_NIN-1

"ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0

"MAXIEN-200000000 -USR-ROS0883645_GCGN.1_1271_grunat_29082003_132954_23062

"MORPL6 -ICPU-3 -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100

"LONGLOG -DEV_INEOUT-120 -WARN_INEOUT-30 -THREADS-1 -SGAPOP-60 -XGAPEXT-60

"FGAPOP-6 -FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELEXT-7
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                                                                                               August 31, 2003, 01:02:06; Search time 192.198 Seconds (without alignments) 1730.853 Million cell updates/sec
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MGAPAQILGFLLLEPPGTRC.....IKRADAAPTVSIFPPSSKLG 145
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/cgn2_6/ptcdata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptcdata/2/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                  OM protein - nucleic search, using frame_plus_p2n model
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Maximum DB seq length: 200000000
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Match Length DB
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Xgapop 60.0 , X
Ygapop 60.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                             Word size:
                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                   Run on:
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41 LeuThrCysArgAlaSerGlnAspIleGlyIleAsnLeuHisTrpLeuGlnGlnGluPro
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                                                                                                                                                 435
145
0
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                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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STREET: Suite 701, 330 University Avenue
CITY: Toronto
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Sequence 1, Application US/09007093
Patent No. US20020025315A1
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Catesini, Judith E
APPLICANT: Catesini, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SerSerLysLeuGly 145
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               LOCATION: (1)...(435)
FRATURE:
NAME/KEY: sig_peptide
LOCATION: (1)...(60)
FEATURE:
                                                                               ; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
US-10-367-506-1
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Best Local Similarity:
Query Match:
DB:
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COUNTRY: Canada
                                                                                                                                      Alignment Scores:
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                                                                                                                                                 Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                           ArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIleSerSerLeuGluSer 100
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Publication No. US2003015257541
GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: Reneat A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: CHOMOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REPERENCE: 30442000620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT PILING DATE: 2003-02-13
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 1998-06-113
PRIOR FILING DATE: 1998-06-11
                                                                                             435
145
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Conservative:
Mismatches:
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                                                                                                                                                  Indels:
                                                                                              Length:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                Gaps:
                                                                                           2.36e-131
145.00
100.00%
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LOCATION: (1)...(60)
NAME/KEY: mat_peptide
LOCATION: (61)...(435)
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                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                               Alignment Scores:
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US-10-367-506-1
                                             ; LOCATION: (0
US-09-861-294-1
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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EDNESS: double
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CITY: Hackensack
STATE: New Jersey
                      Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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       Percent Similarity:
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Pred. No.:
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Fatent No. US20020128450a1
GENERAL INFORMATION:
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: NISHIDA, Yoshihiro
APPLICANT: TANIMOTO, Tadao
TITLE OF INVENTION: PEPTIDE
TITLE OF INVENTION: PEPTIDE
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1999-06-23
PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-12
PRIOR PELING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 115
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33
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**MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIble OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/007,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
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Matches:
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Matches:
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                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-765
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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29.00
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100.00%
100.00%
22.76%
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
                                                                                                                         CLASSIFICATION:
                                                                                                          FILING DATE:
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166 TCTGGTGTCCCCAAGAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATC 225
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Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWAREN STATES OF THE SOFTWAREN SO
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Mismatches:
Indels:
Mismatches:
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ER: 1199-1-001 CIPA
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~~wenter: IBM PC compatible
~~wenter: PC-DOS/MS-DOS
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232 TCTGGTGTCCCCCAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATC 291
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COUNTRY: USA
ZIP: 07601
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Best Local Similarity:
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                                                                                        SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle 95
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/08779784

Publication No. US20020164325A1

GENERAL INFORMATION:
APPLICANT: Rodriguez, Moses
APPLICANT: Miler, David J.
APPLICANT: Asakura, Kunihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
MUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TLING DATE: 07-JAN-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
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APPLICATION
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Mismatches:
Indels:
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                           US-08-836-455-2 (1-145) x US-08-779-784-16 (1-351)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1199-1-001 CIPA
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Matches:
                                                                                                                                                                                                                                                               292 ACCAGCCTTGAGTCTGAAGATTTTGTA 318
                                                                                                                                                                                                                      96 SerSerLeuGluSerGluAspPheVal 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nuclei
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; HYPOTHETICAL:
US-08-779-784-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9/
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TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV TITLE OF INVENTION: A SURFACE ANTIGEN AND A GENE ENCODING THE SAME TITLE OF INVENTION: A SURFACE ANTIGEN AND A GENE ENCODING THE SAME TITLE OF INVENTION: A SURFACE ANTIGEN AND A GENE ENCODING THE SAME CURRENT FILING DATE: 2001-05-15 CURRENT FILING DATE: 2002-05-15 PRIOR APPLICATION NUMBER: KR 10-2001-26634 PRIOR PLICATION NUMBER: KR 10-2001-05-16 SOFTWARE: KR DATE: 2001-05-16 SOFTWARE: KR OPERCENTIN 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 ThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThrValSer 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squence 5, Application US/08779784

Publication No. US20020164325A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Miller, David J.

APPLICANT: ABANURA, KUITHIAKO

TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM

TITLE OF INVENTION: REMYELLINATION USING MONOCLONAL AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390
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PAPLICATION UNDER: US/08/779,784
FILING DATE: 07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                       ; Sequence 5, Application US/10146305; Publication No. US20020173035A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
100.00%
20.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Escherichia coli
US-10-146-305-5
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MEDIUM TYPE: Floppy
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Sequence 1. Application US/09990205

Fatent No. US20020150572A1

GENERAL INFORMATION:
APPLICANT: FOOM, Kenneth A.
APPLICANT: CHATTERJEE, Malaya
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501

CURRENT APPLICATION NUMBER: US/09/990,205

CURRENT FILING DATE: 1999-11-16

PRIOR FILING DATE: 1997-11-16

PRIOR FILING DATE: 1997-11-17

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 447
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                                                                                                                                                                                                                           76 SerGlyValProLysArgPheSerGlySerArgSerGlySerAspTyrSerLeuThrIle
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Mismatches:
Indels:
                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                     Indels:
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                                                                                                                                                                                                                                                                                              137 IlePheProProSerSerLysLeuGly 145
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Publication No. US20030114398A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Foon, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.47e-19
29.00
100.00%
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20.00%
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (1)...(447)
NAME/KEY: mat_peptide
LOCATION: (58)...(447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                 Percent Similarity:
Best Local Similarity:
                                              Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
           US-09-924-099-27
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                                                                                                                                 Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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                                                                                    Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 TCTGGTGTGCCCAAAAGGTTCAGTGGCAGTAGGTCTGGGTCAGATTATTCTCTCACCATC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27, Application US/09924099

Sequence 27, Application US/09924099

Patent No. US20020120450al

SERENAL INFORMATION:

APPLICANT: NISHIDA, Yoshihiro

APPLICANT: TANIMOTO, Masashi

TITLE OF INVENTION: PEPTIDE

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/924,099

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511

PRIOR FILING DATE: BALLIER FILING DATE: 1999-06-23

PRIOR PRILING DATE: BARLIER FILING DATE: 1999-10-12

PRIOR FILING DATE: BARLIER FILING DATE: 1999-10-12

PRIOR FILING DATE: EARLIER PEPLICATION NUMBER: JP 365,023/98

PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12

PRIOR POST SAY IN NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98

PRIOR POST SAY IN NUMBER: EARLIER FILING DATE: 1998-10-12

PRIOR POST SAY IN NOW S: 33

SEQUID NOS: 33

SEQUID NOS: 33
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Mismatches:
Indels:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION UNDAER: US 08/692,084
FILING DATE: 08-AUG-1996
FILING DATE: 08-AUG-1996
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-836-455-2 (1-145) x US-08-779-784-5 (1-402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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100.00%
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20.00%
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LOCATION: (1)...(407)
NAME/KEY: sig peptide
LOCATION: (1)...(60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT APPLICATION NUMBER: 2001-08-08
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER PELLING DATE: 1999-06-23
PRIOR PILING DATE: BARLIER FILING DATE: 1999-06-3
PRIOR PILING DATE: BARLIER FILING DATE: 1999-10-12
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
RIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
NUMBER: OF SEQ ID NOS: 33
SEQ ID NO 19
               APPLICANT: NISHIDA, YOSHIHIO
APPLICANT: OKURA, Takanori
APPLICANT: TAXIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-924-099-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 ThrPheGlyGlyGlyThrLysLeuGluIleLysArgAlaAspAlaAlaProThr
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02710/153,401
FILING DATE: 27-Mq-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Catherine M. Polizzi
REGISTATION UNDRER: 40,130
REFERENCE/DCOKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-836-455-2 (1-145) x US-10-153-401-1 (1-447)
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                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSER: WORKISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 1;
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide LOCATION: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                   NUMBER OF SEQUENCES: 66
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ZIP: 94304-1018
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OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of OTHER INFORMATION: SEQ OTHER INFORMATION: ID NO:9
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FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT PILLING DATE: 2001-08-08
PRIOR PILLING DATE: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER RAPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER REPLICATION NUMBER: JP 289,044/98
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PRIOR PILLING DATE: EARLIER FILING DATE: 1998-10-12
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                        6.77e-19
29.00
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APPLICANT: OKURA, TAKANOTI
APPLICANT: TANIMOTO, TAGAO
APPLICANT: KURIMOTO, MASASHI
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LENGTH: 729
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137 IlePheProProSerSerLysLeuGly 145

US-09-924-099-19 ; Sequence 19, Application US/09924099 ; Patent No. US20020128450A1

RESULT 12

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TYPE: DNA
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                                                                                                                                                                      NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1.729
OTHER INFORMATION: /product= "520C9 sFv polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFTCATION NUMBER: US/08/133,804
FILING DATE: CUNKNOWN>
PRIOR APPLICATION NUMBER: US/08/133,804
FILING DATE: CUNKNOWN>
ATTONNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET WUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEPHONE: 617-248-7477
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 739 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                     Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
                            729
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                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09887853; Patent No. US20020168375A1; GENERAL INFORMATION: APPLICANT: Huston, James S. Oppermann, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Imaging
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TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: USA
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MOLECULE TYPE: CDNA
FEATURE:
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           Alignment Scores:
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US-09-887-853-5
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DB:
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Sequence 10, Application US/10268883

Publication No. US20030138862A1

GENERAL INFORMATION:

APPLICANT: TSO, J. Yun

APPLICANT: TSO, J. Yun

TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof

FILE REFERENCE: 05882.0062.NPUSO1

CURRENT APPLICATION NUMBER: US/10/268,883

CURRENT FILING DATE: 2003-03-26

PRIOR PRILING DATE: 2001-10-10

PRIOR PLILING DATE: 2001-11-21

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Version 3.1

SEQ ID NO 10

TANDE. DATE: AUTOR DATE: 2001-11-21

SEQ ID NO 10

TANDE. DATE: DATE:
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Job time : 193.198 secs
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Percent Similarity:
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US-10-268-883-10
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM protein - nucleic search, using frame_plus_p2n model
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Searched:	22781392 seqs, 12152238056 residues
Word size:	

Post-processing: Listing first 45 summaries

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	4 1 0	56722	3003	2747	88	S i	40	21	200	55	14	BU524124 AGENCOURT RO959057 AGENCOURT	49	53	0.4	10	0 0	0 6	40	91	96	16	90	12	18	73	080	37	64281	09045	62745	142976	00311				26-OCT-2	CDNA clone IMAGE: 3489635				Craniata; Vertebrata; Euteleostomi;	שמד דמפב' שמד דוומב' שמ
SUMMARIES	000000000000000000000000000000000000000	BQ956722	BY083003	BO922747	BF138788	BI250555	BI454240	BF583521	BQ947692	BF579422	BF785914	BU524124 BO959057	BC031349	BU523453	BO939046	BF687410	BG961850	BY 220309	BG964740	BE309991	BG904937 BM245196	BE305476	BQ175706	BO175762	BE368918	BF134573	BF579280	BM194931	BG964281	BI109045	BG962745	BF142976	BI100311	BG964192	ALIGNMENTS		594 bp	Mus mus	25		mouse)	Chordata; Cran	
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AGENCORT_8880991 NCI_CGAP_CO24 Mus musculus cDNA clone
BQ956722
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM8530 row: o column: 12
High quality sequence stop: 591.
Location/Qualifiers
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NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
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Contact: Robert Strausberg, Ph.D.
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Mus musculus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basea 1 to 374)

Sokazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomanu,Y., Hasegawa,Y., Nogami,A., Schonbbch,C., Osobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Dalake,J.A., Bradt,D., Brusico,V., Chothia,C., Corbani, L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest, A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustinicih,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., Jarvis,E.D., Kanai,A., Kawaji,H., Warasaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.B., Maltais,L., Marchis,E.D., Magnatha,T., Numata,K., Okido,T., Peeto,Y., Pertea,G., Petrovsky,N., Pillai,R., Pontius,J.U., Oi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Redb,J., Ringyand,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,M., Shimada,K., Vanga,Y., Wayner,L., Wahestedt,C., Wangisawa,M., Yang,I., Y
                                                                                                                                                                                                                                                                                                    1. .871
/ Organism="Mus musculus"
//Organism="Mus musculus"
//OL_type="mRNA"
/ Strain="FvBA"
/ Ab_xref="taxon:10090"
/ Clone="InAGE:6396481"
/ Lab_host="DH10B (T] Loba (T) Lo
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov plate: LLAM13892 row: n column: 02 Plate: LLAM13892 row: n column: 02 Location/Quality sequence stop: 630.
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Mus musculus
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Conservative: Mismatches: Matches:

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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,sex=female), (dev_stage=10 days neonate,tissue_type=brain
,sex=mix), (dev_stage=10 days neonate,tissue_type=thymus
,sex=mix), (dev_stage=10 days neonate,tissue_type=heart
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="K630040M06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshihide Hayashizaki
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Length:

2.21e-15

Alignment Scores: Pred. No.:

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/ Mod_Lype="mRNA"

/ (db_xref="miaeST:L0700H12-3"

/ (db_xref="miaeST:L0700H12-3"

/ (db_xref="miaeST:L0700H12")

/ (clone="L0700H12"

/ (issue_type="Germinal Center B Cell"

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/ (clone_lib="NIA Mouse Germinal Center B Cell cDNA Library"

/ (clone_lib="NIA Mouse Germinal Center B Cell cDNA Library"

/ (clone_lib="NIA Mouse Germinal Center B Cell cDNA Library"

/ (clone_lib="NIA Mouse Germinal Center B Cell cDNA Library"

/ (clone_lib="NIA Mouse Germinal Center B Cell contains and Center B Cells were provided by Brs. Richard Hodes, Emily Klotz (National Institute on Aging and National Center B Cells were provided by Brs. Richard Hodes, Emily Klotz (National Institute on Aging and National Center B Cells (Nas) and Garnett Kelsoe (Duke University, USA). Double-stranded cDNAs were synthesized from 0.46 ug of total RNA with an Oligo(dT)
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5'-pactractions and purified by
treated with T4 DNA polymerase, and purified by
ethanol-precipitation. The cDNAs were ligated to
lone-linker LL-Sal3 (Ref. Development 127: 1737-1749 (2000
) [PMID: 1072549]), purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, cDNAs
were amplified by long-range high fidelity PCR using Ex
Tag polymerase (Takara) and purified by phenol/chloroform,
followed by Centricon 100 purification. The cDNAs
were diffication 100 purification. The cDNAs were
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Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Klotz, E., Kelsoe, G., Hodes, R. and Ko, M.S. H.
Systematic Analyses of NIA Mouse Germinal Center B Cell CDNA
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdandlygun.grc.nia.nih.gov
Plate: L0700 row: H column: 12
Seg primer: -21M13 Forward
High quality sequence stop: 585
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM194777 585 bp mRNA linear EST 30-JF L0706H12-3 NIA Mouse Germinal Center B Cell cDNA Library Mus musculus cDNA clone L0700H12 3', mRNA sequence.
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/tissue_type="tumor, metastatic to mammary"
/lab_host="npil0B"
/clone_lib="Ncl_CGAP_Lu30"
Site_2: Sal; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
158 c 150 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

TobM Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9242 row: n column: 21

High quality sequence stop: 628.
                                                                                                                                                                                                                                                                          BF138788 630 bp mRNA linear EST 24-OCT-2000
601780387F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008404 5',
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 630)
NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/organism="Mus musculus"
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/clone="IMAGE:4008404"
                                                                                                                                                              US-08-836-455-2 (1-145) x BF138788 (1-630)
                                                       US-08-836-455-2 (1-145) x BQ922747 (1-606)
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                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                             mRNA sequence.
BF138788
BF138788.1 GI:10977828
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/organism="Mus musculus"

/organism="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone='IndAGE:6395978"

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Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.

Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.

Site_1: Site_1: Site_1: Chone unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGENCOURT_8921909 NCI_CGAP_CO24 Mus musculus cDNA clone
IMAGE:6395978 5', mRNA sequence.
BQ922747.1 GI:22337778
EST.
Sall/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is 1.2 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
Was musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 606)
MIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13891 row: i column: 03
High quality sequence stop: 605.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E (Dasses 1 to 725)
I (Dasses 1 to 725)
I (Dipublished Cranib.gov/.

Email: Gapbs.rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM10966 row: g column: 18
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Location/Qualifiers
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Site_2: Sall; cloned unidirectionally. Primer: Ollgo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
95 a 182 c 174 g 174 t
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 805)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
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                                                Mus musculus (house mouse)
Mus musculus
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    BG963055.1 GI:14350692
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SM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Lo 707)

SNIH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Gontact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Dubblished

Contact: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 707.

Location/Qualifiers
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/db_xref="taxon:10090"
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/clone="taxo=type="tumor, gross tissue"
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/clone=lb="day late lecthologies investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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BG963055
                                                                                                              BI250555 707 bp mRNA linear EST 17-JUL-2001 602993614F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:5149563 5',
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/organism="Mus musculus"
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BQ947692
AGENCOURT_8909039 NCI_CGAP_Mam2 Mus musculus cDNA clone
IMAGE:6441024 5', mRNA sequence.
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 Kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
1 215 c 183 g 177 t
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11H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13963 row: j column: 01
High quality sequence stop: 671.
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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                                                         /organism="Mus musculus"/mol_type="mRNA"
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/mol_type="mRNA"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.i column: 14
High quailty sequence stop: 627.
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://maga-llnl.gov
Hitp://maga-llnl.gov
Column: 18
High quality sequence stop: 790.
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/organism="Mus musculus"
/organism="Mus musculus"
/organism="Nus"
/db_type="mRNA"
/strain="FVBA"
/db_xref="taxon:10090"
/clone="IMAGE:4208144"
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/clone=lib="NOT_CGAP_CO34"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NOT_CGAP Library."
46 a 226 c 204 g 215 t
                                                                                                                                                                                                                                                                                                            891 bp mRNA linear EST 12-DEC-2000
602093833F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4208144 5',
BF579422
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Contact: Robert Strausberg, Ph.D.
Contact: Gapbs-rémail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9772 row: a column: 09
High quality sequence stop: 711.
Coation/Qualifiers
FCE
                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 891)
HH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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/organism="Mus musculus"
/organism="Mus musculus"
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/strain="FvB_NR"
/db_xref="taxon:10090"
/clone="taxon:10090"
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BQ940987.1 GI:22356465
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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NIH-WGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAMIGIG row: b column: 17
High quality sequence stop: 626.
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Alignment Scores:
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                                                                                                                                                                                                                                      Wiss musculus Butcheria; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E 1 (bases 1 to 906)

NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
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Tissue Procurement: Jeffrey E. Green, M.D.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Contact: NGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LLAM9955 row: p column: 11
High quality sequence stop: 718.
Location/Qualifiers
I.Coation/Qualifiers
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I.Coation/Qualifiers
I.Coation/Qualifiers
I.Coation/Qualifiers
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I.Coation/Qualifiers
I.Coation-Lib="NUS GAP-Kidley; Vector: pCMV-SpORT6; Site_I: NotI; Site_I: Salte_I: NotI; Site_I: Salte_I: Salte
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BU524124
BU524124.1 GI:22834563
                                                   906 bp mRNA linear EST 12-JAN-2001
020112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
57. mRNa series.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                               Mus musculus (house mouse)
Mus musculus
                                                                                                                                                    BF785914.1 GI:12090950
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28.00
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100.00%
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Query Match:
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BF785914
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TITLE
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
The Consortium (LLNL)
To a Galatribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Thtp://image.llnl.gov.f.E.Consortium/LLNL at:
Thtp://image.llnl.gov.f.E.Consortium/LNL at:
Thtp://image.llnl.go
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/db_xref="taxon:10090"
/clone="IMAGE:6530882"
/clone=lib="willow (Ti phage-resistant)"
/clone=lib="willow (Ti phage-resistant)"
/clone=lib="coapa": colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 ProfyrfhrPheGlyGlyGlyfhrLysLeuGlufleLysArgAlaAspAlaAlaProfhr 134
1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Best Local Similarity:
Query Match:
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anti-c-erbB

AAY44587

520C9 SEV sequence
Mouse anti-IL-18 a
P4-14 single chain
3B10xP4-14 bispeci
Murine antibody 11
Light chain of M1f
IL-2 chimeric anti
Human protein SEQ
Germine protein s
ESCFV#125-2H recom
ESCFV#125-2H recom
ESCFV#125-2H re
P5-11 single chain
IL-2 chimeric anti
PrP 37 light chain
Anti-PrP antibody
Anti-Prion protein
Anti-Prion protein

AAY44596

Filamentous phage Human anti-HBS lig Antibody variable Amino acid sequenc Antino acid sequenc Anti-human AiLIM m Anti-bovine prion

ABG77159 AAU74297 AAM50879

AAR99686 AAR98410 AAY49961

Germline protein s 520C9 hybridoma VL Murine anti-human Human IGFAM-9 immu

ABG77164 AAY90824

AAR39571

AAB35096 AAR62881

AAR42065 AAB35102

ABP51796 ABU58877

Sequence of G-FIT

Monoclonal anti-id 3H1 light chain va Anti-idiotype anti Murine MAD against

ALIGNMENTS

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note= "complementarity determining region 1"
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70..76
/label= CDR2
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11.145
Tabel Mat_protein
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/label= CDR1
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/label= FR2
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|abel= FR1
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(first entry)
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  Murine monoclonal
Mouse 11D10 antibo
Antibody 11D10 lig
Sequence of the le
Mouse light chain
Murine anti-human
Murine 44H104 mab
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                                                                                                                                                    August 30, 2003, 19:50:30 ; Search time 34.547 Seconds (without alignments) 666.204 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. SIDSI/gcgdata/geneseq/genesegp-embl/AA1980.DAT:*
2. SIDSI/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
3. SIDSI/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
4. SIDSI/gcgdata/geneseq/genesegp-embl/AA1981.DAT:*
5. SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
5. SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
6. SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
7. SIDSI/gcgdata/geneseq-embl/AA1981.DAT:*
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8. SIDSI/gcgdata/geneseq-geneseq-geneseqp-embl/AA1999.DAT:*
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1 MGAPAQILGFLLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 145
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/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:
/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2003.DAT:
                     GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                             1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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AAO16292
AAW87593
AAP30251
AAY44599
AAW22537
AAW22537
AAE20200
AAE39569
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126456789
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Result

"Mature murine 11D10 antibody light chain variable

Location/Qualifiers

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Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                      Mouse; murine; vaccine; tumour; human milk fat globules; HMFG; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                               Mouse 11D10 antibody light chain variable region.
                                                                                                                                                                                            /label= signal_peptide
21..145
/note= "Mature murine I
region"
                                                                                                                                                                                                                                                                                                                                                                 (KENT ) UNIV KENTUCKY RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Fig 1; 98pp; English
                                                                                                                                                                                                                                                                                                             17-MAY-2002; 2002WO-US15840.
                                                                                                                                                                                                                                                                                                                                       17-MAY-2001; 2001US-0861294
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast tumor) in humans
                                                                                                                                                                                                                                                                                                                                                                                         Chatterjee M, Foon
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-129216/12.
                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAL51273.
                                                                                                                                                                                                                                                             WO200292012-A2.
                                                                                                                                            Mus musculus
                                     20-MAR-2003
                                                                                                                                                                                                                                                                                     21-NOV-2002.
             AA016292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                Peptide
                                                                                                                                                                                                           Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide sequence comprises the light chain variable region (VL) of monoclonal anti-idiotype antibody ID10 produced by hybridoma cell line ArCC 12020. ID10 was obtained by immunishing malve mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human mill fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polypeptides and/or 11D10 polypeptides and/or 11D10 polynucleotides (see also AAT85149-50) are claimed. Also claimed are diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMRG-associated tumours. 11D10 is also used in a claimed method of palliating HMRG-associated disease and in claimed kits to
                                                                                                                                                                                                                                                                                                                                                                Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
'note= "complementarity determining region 2"
                                                            /label= CDR3
/note= "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 740; DB 18;
100.0%; Pred. No. 1.5e-48;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detect or quantify anti-HMFG antibody. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                /note= "framework region 4"
         77. 108
/label= FR3
/note= "framework region
                                                                                                                                                                                                                                                                                                   Foon KA;
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                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; Page 94; 130pp; English.
                                                                                                                                                                                                                                                                                                 SK,
                                                                                                                                                                                             96WO-US20757
                                                                                                                                                                                                                     95US-0575762
                                                                                                                                                                                                                                  96US-0591965
96US-0766350
                                                                                                     /label= FR1
                                                                                                                                                                                                                                                                                                Chatterjee
                                                109.117
                                                                                      118..127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                            against human milk fat g
especially breast cancer
                                                                                                                                                                                                                                                                        (KENT ) UNIV KENTUCKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT85149.
                                                                                                                                                                                                                                                                                                Chatterjee M,
                                                                                                                                           WO9722699-A2
                                                                                                                                                                                            19-DEC-1996;
                                                                                                                                                                                                                                              13-DEC-1996;
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                                                                                                                                                                  26-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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The invention comprises a method for delaying the development of, or treating a timmour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves endministering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for present antino acid sequence represents the light chain variable region of the mouse 11D10 anti-idiotype antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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                                                                                                                                                                                                                                                                         Length 145;
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                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                       100.0%; Score 740; DB 24;
100.0%; Pred. No. 1.5e-48;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW87593 standard; Protein; 145 AA.
                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 100.5
Matches 145; Conservative
                                                                                                                                                                                                                         145 AA;
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AAW87593
ID AAW8
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AA016292 standard; Protein; 145 AA.

RESULT 2 AAO16292 ID AAO1

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1 MGAPAQILGFLLLLFFGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1982;
05-DEC-1983;
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                                                                                                                                                               RESULT 4
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                                                                                 Murine; mouse; antibody; light chain; variable region; anti-idiotype;
human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the light chain variable region of the murine antibody 11D10. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delaying development of, or treating, HMFG-associated tumours -using anti-idiotype antibody 11D10 raised against antibodies to human milk fat globule protein
                                                                                                                                                                                                                                                                 'note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                          /label- CDR3
/note- "complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                       'note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 727; DB 20;
Pred. No. 1.4e-47;
0; Mismatches 1;
                                                         Antibody 11D10 light chain variable region.
                                                                                                                                                                                                  "mature protein"
                                                                                                                                                                         "signal peptide"
                                                                                                                                                                                                                                                                                                                  'note= "encoded by TGG"
                                                                                                                                                                                                                                                                            5..69
label= framework_2
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                              7..108
label= framework_3
                                                                                                                                                                                                                                                                                                                                                                                                                                118..127
/label= framework_4
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                                                                                                                                                                                                                                          14..54
/label- CDR1
                                                                                                                                                                                                                                                                                                                                70..76
/label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 98.2%;
Best Local Similarity 99.3%;
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US12250,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0096244
97US-0049540
                                 16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               ..117
                                                                                                                                                                                      666
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                                                                                                                                                                          'note=
                                                                                                                                                                                                  'note-
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N-PSDB; AAV83772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AA;
                                                                                                                                                                                                                                                                                                       Misc-difference
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13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUN-1998;
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                                                                                                                                                             Peptide
                                                                                                                                                                                      Protein
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                                                                                                                         Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                              Domain
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Gaps

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1; Indels

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                                                                                                     DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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1 MGAPAQILGFLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHTLQQEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of the leader, variable region and first 16 AAs of the constant region of the kappa-chain (light chain) of MOPC41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 1.1e-42;
5; Mismatches 7; Indels
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                                                                                                                                                                             GTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                             AAP30251 standard; peptide; 146 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosis; therapy; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23..130
/label= variable
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/label= constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..22
/label= leader
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Best Local Similarity 91.6%;
Matches 131; Conservative
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83US-0558551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moore KW, Zaffaroni A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SCHE ) SCHERING CORP. (DNAX-) DNAX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1983-772290/39.
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1 MRAPAQIFGFLLLLEFPGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSKLYWLQQEP
                                                                                                                                                                                                                                                Antibody; light chain; variable region; hybridoma cell line 44H104; immune response; enhance; stimulate; vaccine; immunodiagnosis;
                                                                                                                                                                                                                          Murine anti-human class II monoclonal antibody 44H104 VL chain.
                                                                                                                                                       AAW22537 standard; Protein; 129
                                                                                 GTKLEIKRADAAPTV 135
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                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Barber BH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-077271/07.
N-PSDB; AAT77851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AA;
                                                                                                                                                                                                                                                                           antigen delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immuno: diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen CLTB36
                                                                                                                                                                                                                                                                                                                       W09640941-A1
                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                      03-NOV-1997
                                                                                                                                                                                                                                                                                                                                              19-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Anand NN,
                                                                                                                                                                               AAW22537;
                        61
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                                                                                                                                              AAW2253
                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                       Mouse light chain variable region; VL; variable region light chain; interleukin-18; immunopathise; inflammatory disorder; autoimmune disease; mouse; anti-allergic; anti-inflammatory; immunosuppressive; hematopoletic; leukocytopoietic; antialgic; antipyretic.
                                             DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                          New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
             Length 135;
                                                                                                                                                                                                                                                  Mouse light chain variable region encoded by PCR A product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 633; DB 21;
Pred. No. 1.6e-40;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanimoto T, Kurimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 28-29; 32pp; English.
                                                                                             GTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                         (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
                                                                                                                                                                             AAY44599 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       function improving activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.5%;
92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0177580.
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                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0304977
                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 92.6'
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-118341/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ49548
                                                                                                                                                                                                                                                                                                                                 musculus
                                                                                                                                                                                                                          04-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   24 - JUN - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                    EP974600-A2
                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishida Y,
                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                    AAY44599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                  Recombinant conjugate antibody mol., modified for delivering antigen - elicits enhanced immune response without the use of adjuvant to generate antibodies which are useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 527; DB 18; Length 1:
Pred. No. 1.5e-32;
7; Mismatches 17; Indels
Klein MH;
   Caterini JE, Cates GC,
                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 1A; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.2%;
Best Local Similarity 81.1%;
Matches 103; Conservative
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MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP

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us-08-836-455-2.rag

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DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
             The invention relates to a recombinant conjugate antibody, comprising a monoclonal antibody specific for a surface structure of antigen presenting cells genetically modified to contain an antigen moiety for the purpose of delivery of the antigen moiety to antigen. Presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable light chain (VL), alternative version.

Note: This sequence SEO.ID.NO:2 is stated to be similar to the sequence shown in fig 1A (AAE20200). However these sequences differ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                                                                        Murine; mab; light chain; VL; conjugate antibody; antigen delivery; immune system; vaccine; detecting agent; antibacterial.
                                                                                                                                                                                                                                             Murine 44H104 mab variable light chain (VL), alternative version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein MH;
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80.3%; Pred. No. 7.1e-32;
tive 7; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cates GA, Caterini JE,
                                                                                                                                                                                                                                                                                                                                                                             /note= "Encoded by TAT"
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                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
93
                                                                                                                                                         AAE20204 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0007093
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                                                                                                                                                                                                                  (first entry)
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(BARB/) BARBER B H.
(CATE/) CATES G A.
(CATE/) CATERINI J E.
(KLEI/) KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anand NN, Barber BH,
                                                                      |||||:|
GTKLELK 129
                                                       GTKLEIK 127
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N-PSDB; AAD32138.
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Best Local Similarity
Matches 102; Conserv
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                                                                                                                                                                                                                  18-JUN-2002
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                         63
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61
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                        DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant conjugate antibody, comprising a monoclonal antibody specific for a surface structure of antigen presenting cells genetically modified to contain an antigen molety for the purpose of delivery of the antigen molety to antigen. Presenting cells of the immune system. The conjugate antibody is formulated as a vaccine to protect a host against a disease caused by a pathogen expressing the antigen. The antibody is useful as a detecting agent. The present sequence is murine 44H104 mab variable light chain (VL).

Note: This sequence SEQ.ID.NO:2 is stated to be similar to the sequence shown in page 11-12 of the specification (AAE20204).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel recombinant conjugate antibody, useful as a vaccine against pathogens having a specific antigen, comprises a monoclonal antibody specific for an antigen presenting cell surface structure -
                                                                                                                                                                                                                                                                                  Murine; mab; light chain; VL; conjugate antibody; antigen delivery; immune system; vaccine; detecting agent; antibacterial.
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Pred. No. 1.5e-32;
7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caterini JE,
                                                                                                                                                                                                                                                       Murine 44H104 mab variable light chain (VL).
                                                                                                                                                                   AAE20200 standard; Protein; 129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1A; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   However these sequences differ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%;
81.1%;
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                                                                                                                                                                                                                              (first entry)
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BARBER B H.
CATES G A.
CATERINI J E.
KLEIN M H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barber BH,
                                                                  GTKLEIK 127
                                                                                  ||||||:|
GTKLELK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
103; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 AA;
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BARB/) BARBER
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                                     63
            61
                                                                                           123
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Best Local S
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(CATE/)
(KLEI/)
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Matches
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N-PSDB; AAT36880
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06-FEB-1992;
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                                                                                                                                      25-MAR-2003
29-OCT-1996
                                                                                                                                                                                                                                                                                                                                                              US5534254-A.
                                                                                                              AAW02280;
              194
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                                                                                                                                                                                                                                                                                                                     Peptide
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                                         DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
3 MRVPAHVFGFLLLWFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQEISGYLTWLQQKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c-erbB-2 refers to a protein antigen expressed on the surface of tumour cells. such as breast and ovarian tumour cells, which is an approx. 200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about 5.3 (see AQ40603, AR839560). A single chain Fv (sFv) is a covalently linked VH-VL heterodimer which is expressed from a gene fusion including VH- and VL- encoding genes connected by a peptide-encoding linker. Such linker sequences are set forth in AA residues 116-135 in AAR39569, which includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084 for the 520C9 monoclonal antibody, a single chain polypeptide can be produced having a binding affinity for a c-erbB-2 related antigen. 'X' in AAR39569 refers to the location of a stop codon in AAQ46084.
                                                                                                                                                                                                                                                                                                     Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig; blosynthetic single polypeptide chain binding site; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for imaging or treating breast or ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 508; DB 14;
Pred. No. 7.6e-31;
3; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oppermann H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; pages 60-61; 87pp; English.
                                                                                                                                                                             AAR39569 standard; Protein; 246 AA.
                                                                                                                                                                                                                                                                           Sequence of 520C9 sFv protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS ONCOLOGY CORP. (CREA-) CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.6%;
90.2%;
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                                                                                                                                                                                                                                      (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houston LL, Huston JS,
                                                                                                  |||||:|
GTKLELK 129
                                                                                  GTKLEIK 127
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07-FEB-1994
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                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                          AAR39569;
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                                                       63
                                                                               121
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AAR39569
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RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRADAA 132

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A compsn. comprising a carrier and the 2 sFV protein prod. can be used for in vivo imaging, and drug targetting experiments. The case for in vivo imaging, and drug targetting experiments. The case and interest of the same antigen, therefore glving greater binding avoidity and chonger tissue retention times, compared to individual sFV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Compsns. contg. antigen-targetting antibody fragment constructs comprising dimer of single-chain Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sFv construct; polypeptide linker; C-terminal amino acid sequence; in vivo imaging; drug targetting experiment; homodimer; increased; binding avidity; tissue retention time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 507; DB 17; Length 2. Pred. No. 8.9e-31; Indels 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   520C9 anti-c-erbB-2 two single chain Fv construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ring DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
118..133
/label= linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                   AAW02280 standard; Protein; 243
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Best Local Similarity 91.8%;
Matches 101; Conservative
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92US-0831967
                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-333194/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This represents the protein sequence of a 520C9 sFV' (single chain FV) construct. This was constructed by connecting the Vh and VI genes with a DNA sequence encoding a Serine rich linker. 520C9 is a monoclonal antibody useful in targeting c-erbB-2 antigen. This dimeric construct can be used in the methods of invention of imaging a preselected antigen expressed in a mammal. The methods are used in magnetic resonance imaging of c-erbB-2 or related antigens in cancer diagnosis. The biosynthetic constructs have enhanced properties as in vivo targetting agents in comparison with intact monoclonal antibodies or their Fab fragments. The dimeric constructs permit the in vivo targetting of an epitope on an antigen with greater apparent avidity, including greater tumour specificity, tumour localisation and tumour retention properties than that of the Fab fragment having the same CDRS as the construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIOMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of antigens in vivo - using dimers of single-chain antibody
                                        RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRAD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer; c-erbB-2; tumour; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.5%; Score 507; DB 19; Length 243; 91.8%; Pred. No. 8.9e-31; 11ve 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         520C9 anti-c-erbB-2 sFv' dimeric construct protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oppermann H, Ring DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Columns 33-36; 30pp; English.
                                                                                                                                                                                                                                 AAW53170 standard; Protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP. (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0461838
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95US-0461838
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houston LL, Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-311318/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV21798
                                                                                                                                                                                                                                                                                                                                                               16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imaging of ar
Fv fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1992;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5753204-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
81
                                                             194
                                                                                                                                                                                                                                                                                              AAW53170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp.
                                                                                                                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding single-chain Fv fragment specific for antigens - and having C-terminal tail for crosslinking to form dimer with improved pharmacokinetic properties, used to deliver drugs and imaging agents, especially to tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRAD 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse anti-IL-18 antibody light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 507; DB 20;
Pred. No. 8.9e-31;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ring DB;
                                                                                                                                                                                       targeted delivery; antigen-expressing cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Columns 35-36; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oppermann H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP. (CREA-) CREATIVE BIOMOLECULES INC
                                                                                                                                                                        cell;
AAW80424 standard; Protein; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY44587 standard; Protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.5%;
ilarity 91.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            92US-0831967.
                                                                                                                                                                                                                                                                                                                                                              95US-0461386
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                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houston LL, Huston JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-023541/02.
N-PSDB; AAV63399.
                                                                                                                                                                    520C9 sFv; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                         520C9 sFv sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AA;
                                                                                                                                                                                                                                                                                                                                                            05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            06-FEB-1992;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1993;
                                                                                  28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-2000
                                                                                                                                                                                                                                                                         JS5837846-A.
                                                                                                                                                                                                                                                                                                                    17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101;
                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                          AAW80424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY44587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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(KUFE/) KUFER P.
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                                                                                              Homo sapiens
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Best Local Simi
Matches 100;
                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                  Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU72872;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU7287
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  Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present protein sequence is the mouse anti-Interleukin-18 antibody light chain variable region (VL) encoded by cDNA derived from hybridoma 1815-2H. The nucleotide sequence is used in the production of recombinant monoclonal antibody #125-2HmAb, which is capable of neutralising biological activities of interleukin-18. The antibody has antialic, antilinfammatory, Immunosuppressive, leucocytopoietic, antipyretic, antialized and hepatotropic activity and can be used for prevention and treatment of autoimmune diseases, immunopathies and inflammatory diseases, immunoreaction.
                Anti-Interleukin-18 antibody; IL-18; light chain variable region; VL; bybridoma #125-21mAb; mouse; monoclonal antibody #125-21mAb; interleukin-18; antiinflammatory; immunosuppressive; leucocytopoietic; antialgic; antipaticropic; treatment; autoimmune disease; immunopathy; inflammatory disorder; immunoreaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intraheptic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DaPlO; helminth; cytostatic; antimicrobial; immunomodulatory; 1182D10; 6H7E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQSPSSLSASLGERVSLTCRASQDIGSKLYWLQQEPDGTFKRLIYATSSLDSGVPK·60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 DIOMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New artificially produced peptide for neutralizing biological activity of interleukin-18, useful for treating and preventing immunopathies, inflammatory disorders and autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGGGTKLAIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 506; DB 21; Length 108;
Pred. No. 4.8e-31;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanimoto T, Kurimoto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ę
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 17; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.4%;
Best Local Similarity 92.6%;
Matches 100; Conservative 2
                                                                                                                                                                                                                                                                                                                                          98JP-0177580.
98JP-0289044.
                                                                                                                                                                                                                                                                                                99EP-0304977
                                                                                                                                                                                                                                                                                                                                                                                         98JP-0365023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P4-14 single chain Fv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Okura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-118341/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ49534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New artificially
                                                                                                                                                                                                                                                                                                                                          24-JUN-1998;
12-OCT-1998;
22-DEC-1998;
                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                24-JUN-1999;
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                                                                                                                                                                                                      EP974600-A2
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated pulsulated to the treatment of cancer, infections and/or autoimmune composition for the treatment of cancer, infections and/or autoimmune compositions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, the infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple clerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatisis. Sequences AMJ72875 represent the NKG2D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGS 76
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   6E5A7x4-7; P4-2; P4-3; P4-14; 5-23; 3B10xP4-3; 3B10xP4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multifunctional polypeptides comprising binding sites that specifica recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases.
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8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7;
P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B1C
p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
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Pred. No. 1.3e-30;
7; Mismatches 9;
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86.2%;
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N-PSDB; AAS97137.
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NG3D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune composition for the treatment of cancer, infections and/or autoimmune confitions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, backenia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple cuefits, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D receptor and the polypeptides of the invention.
autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7; 8G7C10; ESA7; 11B2D10447; 8G7C10, ESA7, 27; P4-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14; p53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NRG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kufer P, Riethmueller G, Lutterbuese R, Borschert K, Kischel R;
Mayer M, Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 16; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                               26-MAR-2001; 2001WO-EP03414.
                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000; 2000EP-0106467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUFE/) KUFER P.
                                                                                                                                                                                                                                                                 WO200171005-A2.
                                                                                                                                                                                                                     Homo sapiens.
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Ouery Match 68.2%; Score 505; DB 23; Length 499; Best Local Similarity 86.2%; Pred. No. 2.5e-30; Matches 100; Conservative 7; Mismatches 9; Indels 0; Gaps

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77 GVPKRESGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRADAA 132

437 GVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGGGTKLEIKRTTSS 492

Search completed: August 30, 2003, 22:04:04 Job time : 36.547 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 30, 2003, 21:57:15 ; Search time 23.3557 Seconds (without allgaments) 849.188 Million cell updates/sec Run on:

Perfect score: Sequence:

US-08-836-455-2 740 1 MGAPAQILGFLLLEFPGTRC.....IKRADAAPTVSIFPPSSKLG 145

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

510680 seqs, 136781880 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:

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/cgn2_6/ptodata/2/pubpaa/US60_NBW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 2, Appli	Sequence 2, Appli	Sequence 35, Appl	Sequence 11, Appl	Sequence 2, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 9, Appli	Sequence 10. Appl	Sequence 74, Appl	Sequence 30, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4. Appli
		ID	US-09-861-294-2	US-10-367-506-2	US-08-779-784-35	US-10-268-883-11	US-09-007-093-2	US-09-887-853-6	US-09-924-099-1	US-09-924-099-9	US-09-924-099-10	US-09-943-906-74	US-09-859-053-30	US-10-355-780-1	US-09-797-481-2	US-09-844-736-4	US-10-162-396-4
		DB	6	12	œ	12	6	10	10	10	10	10		12	6	σ	15
		Match Length DB	145	145	130	130	129	243	108	237	243	109	236	112	142	142	142
ф	Query	Match	100.0	100.0	81.2	73.1	70.0	68.5	68.4	8.79	67.8	67.0	63.8	63.6	63.6	63.6	63.6
		Score	740	740	601	541	518	507	206	502	502	496	473	471	471	471	471
	Result	NO.	-	7	e	4	2	9	7	80	6	10	11	12	13	14	15

Sequence 12, Appl Sequence 21, Appl Sequence 1, Appli Sequence 24, Appl Sequence 12, Appl	· 6 · 6	·00 ·	Sequence 25, Appl Sequence 19, Appl Sequence 2, Appl Sequence 2, Appli	4 10 4	Sequence 1, Appli Sequence 2, Appli Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
2 US-10-268-883-12 US-08-779-784-21 5 US-10-221-945-1 US-09-740-002-24 US-09-766-543-12	10 US-09-943-906-73 12 US-10-268-883-5 15 US-10-006-593-69 1 US-09-764-304-10	US-09-764-304-19 5 US-10-265-713-10 5 US-10-265-713-19 5 US-10-084-139-2	US-U9-740-U0Z-26 5 US-10-153-382-19 US-09-056-160B-100 4 US-10-011-125-2 5 US-10-070-786-8	b 1	S US-10-227-694-1 US-09-940-166A-2 US-09-811-384-11 US-10-356-974-1 5 US-10-253-366-1 5 US-10-253-364-1 5 US-10-056-794-17
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ALIGNMENTS

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Sequence 2, Application US/09861294

Patent No. US20020099190A1

GENERAL INDORMATION:

APPLICANT: Malaya CHATTERJEE

APPLICANT: Kenneth A. FOON

TITLE OF INVEWTION: TUMORS BEARING HMFG AND CEA ANTIGENS

FILE REFERENCE: 30414200620

CURRENT APPLICATION NUMBER: US/09/861,294

CURRENT FILING DATE: 1997-06-13

PRIOR PILING DATE: 1997-06-13

PRIOR PILING DATE: 1998-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-09-861-294-2
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 145
TYPE: PRT
-09-861-294-2
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Gaps ö Length 145; Indels Query Match 100.0%; Score 740; DB 9; Best Local Similarity 100.0%; Pred. No. 8.9e-59; Matches 145; Conservative 0; Mismatches 0; 1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP

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61 DCTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120 61 q q δ

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SEQ ID NO 11
LENGTH: 130
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Publication No. US20020164325A1
GENERAL INFORMATION:
APPLICANT: Rollier, David J.
APPLICANT: ASARVIA, KUNIMIKO
TITLE OF INVENTION: REMYELINATION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                    SCHERAL INCOCRATION:
SCHERAL INCOCRATION:
SCHERAL INCOCRATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: Renneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 05/09/861,294
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOSS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 740; DB 12; Best Local Similarity 100.0%; Pred. No. 8.9e-59; Matches 145; Conservative 0; Mismatches 0;
                    121 GTKLEIKRADAAPTVSIFPPSSKLG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTKLEIKRADAAPTVSIFPPSSKLG 145
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Publication No. US20030152575A1
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
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: USA
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STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: SIGNAL
; LOCATION: (1) ...(20)
US-10-367-506-2
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121
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APPLICANT: TSO, J. Yun
APPLICANT: TSO, J. Yun
APPLICANT: TSO, J. Yun
APPLICANT: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REPERENCE: 05882.0062.NPUSA
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
NUMBER OF SEC ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 130;
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                                     Patentin Release #1.0, Version #1.30
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Pred. No. 2e-46;
3; Mismatches 6
                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISCOPOCKET NUMBER: 1199-1-001 CIPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                   SOFTWARE STATES.
SOFTWARE PATENT RELEASE #1.0, VET CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION NUMBER: US 08/236,520
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-268-883-11

'Sequence 11, Application US/10268883

; Publication No. US20030138862A1

; GENERAL INFORMATION:
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ilarity 93.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO FRACHENTYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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123 GTKLEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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63 DGTIKRLVYAASTLDSGVPKRFSGSRSGSDTSLTISSLESEDFADYYCLQYTNYPLTFGA 122
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                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
STREET: Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRAD 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                            Upperment. L. L.
Houston, L. L.
Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.5%; Score 507; DB 10;
91.8%; Pred. No. 9.6e-38;
tive 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
CLASSIFICATION: <u >cunknown></u>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/133,804
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kelley, Robin D. REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            Sequence 6, Application US/09887853 Patent No. US20020168375A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09924099; Patent No. US20020128450A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 243 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                            APPLICANT: Huston, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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Best Local Similarity 91.88
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                    |||||:|
123 GTKLELK 129
                                                           121 GTKLEIK 127
                                                                                                                                                                              us-09-887-853-6
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US-09-924-099-1
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                                                                                                                                                     61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                  3 MRVPAHVFGFLLLWFFGTRCDIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Anado, Naveen N
APPLICANT: Anado, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMBRIC ANTIBODIES FOR DELIVERY OF
TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
CORRESPONDENCE ADDRESS:
                                           Gaps
  Length 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 129;
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Pred. No. 5e-39;
7; Mismatches 18; Indels
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/007,093
Score 541; DB 12;
Pred. No. 4.5e-41;
5; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09007093
Patent No. US20020025315A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.0%;
80.3%;
73.1%;
83.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 129 amino acids
                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                       GTKLEIKR 128
                                                                                                                                                                                                                                                            |||||||||
|123 GTKLEIKR 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 102; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
              al Similarity
107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Query Match
Best Local Si
Matches 107,
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Best Local (
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us-08-836-455-2.rapb

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100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                            US-09-924-099-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-943-906-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 GGSDIQMTQSPSSLSASLGERVSLTCRASQDIGSKLYWLQQEPDGTFKRLIYATSSLDS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DIQMIQSPSSLSASLGERVSLICRASQDIGSKLYWLQQEPDGTFKRLIYATSSLDSGVPK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT APPLICATION NUMBER: US/08/08
CURRENT FILING DATE: 2001-08/08
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
SEQ ID NOS: 33
APPLICANT: TANIMOTO, Taddo
APPLICANT: TANIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR APPLICATION NUMBER: EARLIER PRIOR APPLICATION NUMBER: J998-06-23
PRIOR PILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR PLILNG DATE: EARLIER FILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: J9 365,023/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 506; DB 10; Length 108;
Pred. No. 4.8e-38;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 237;
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Pred. No. 2.6e-37;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09924099
Patent No. US20020128450Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          68.4%;
92.6%;
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NISHIDA, YOSHIHLIO
APPLICANT: OKURA, TAKANOTI
APPLICANT: TANIMOTO, TAGAO
APPLICANT: KURIMOTO, MASASHI
TITLE OF INVENTION: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus
US-09-924-099-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 100;
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Best Local 9
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Best Local
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                                                                                                                                                                                                                                                                                                                               LENGTH:
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OTHER INFORMATION: Artificially produced peptide in the form of a single OTHER INFORMATION: chain OTHER INFORMATION: variable region fragment (scfv) which neutralizes IL-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 GTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGS
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/924,099
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-23
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
187 GVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPYTFGGGTKLAIK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 GVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIK 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Prusiner, Stanley B.
Williamson, R. Anthony
Burton, Dennis R.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 74, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
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                                                                                                                                                                       ; Sequence 10, Application US/09924099
; Patent No. US20020128450A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: NISHIDA, YOShihiro
                                                                                                                                                                                                                                                                                 APPLICANT: OKURA, Takanori
APPLICANT: TANIMOTO, Tadao
APPLICANT: KURIMOTO, Masashi
TITLE OF INVENTION: PEPTIDE
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
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LENGTH: 112
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                                                                                      US-10-355-780-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 GKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFPWTFGQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGAPAQILGFLLLEPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 236;
                                                                                                                                                                                                                                                                                                                                                               Length 109;
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                                                                                                                                                                                                                                                                                                                                                            Score 496; DB 10;
Pred. No. 3.8e-37;
7; Mismatches 5;
                                                                               REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEPRAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTLE REPERBNCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/659,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NOS: 82
LENGTH: 236
                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-943-906-74
              APPLICATION NUMBER: 09/550,374 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                      LENGTH: 109 amino acids TYPE: amino acid
                                             ATTORNEY/AGENT INFORMATION:
NAME: Bozicevic, Karl
                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 74: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%;
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ilarity 89.0%;
Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                     <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.99
Best Local Similarity 66.49
Matches 95; Conservative
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ORGANISM: Homo sapiens
US-09-859-053-30
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Best Local Similarity
watches 97; Conserva
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21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
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TITLE OF INVENTION: MURINE ANTI-IDIOTYPE ANTIBODY 3H1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  APPLICANT: Prusiner, Stanley
APPLICANT: Safar, Jiri
APPLICANT: Safar, Jiri
APPLICANT: Williamson, Anthony
APPLICANT: Williamson, Anthony
APPLICANT: Williamson, Anthony
TITLE OF INVENTION: Antibodies Specific for Ungulate PrP
FILE REFERENCE: UCAL-194
CURRENT APPLICATION NUMBER: US/10/355,780
PRIOR APPLICATION NUMBER: US/03-01-30
PRIOR PLING DATE: 2000-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 471; DB 12;
Pred. No. 6.6e-35;
9; Mismatches 10;
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FILING DATE: 28-Feb-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/579,940
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: synthesized peptide US-10-355-780-1
APPLICANT: Chatterjee, Malaya
Kohler, Heinz
Foon, Kenneth A.
                                                                                                                                   Sequence 1, Application US/10355780 Publication No. US20030143224A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09797481 Patent No. US20010047083A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.6%;
ilarity 83.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304-1018
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Best Local Similarity
Matches 93; Conserv
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Length 142;

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Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Indels
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
63.6%; Score 471; DB 9;
Best Local Similarity 67.6%; Pred. No. 8.6e-35;
Matches 96; Conservative 13; Mismatches 33.
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REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/844,736
FILING DATE: April 27, 2001
APPLICATION NUMBER: US 08/838,692
FILING DATE: April 9, 1997
APPLICATION NUMBER: US 60/044,455
FILING DATE: April 12, 1996
APPLICATION NUMBER: US 08/631,085
FILING DATE: April 12, 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GTKLEIKRADAAPTVSIFPPSS 142
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10162396 Publication No. US20030077274A1 GENERAL INFORMATION:
       TELEFAX: (415) 494-0792
                                                                                                                                             LENGTH: 142 amino acids
                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEC ID NO: 4:
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                                                                                                                                                                                                                                                                                                                US-09-844-736-4
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Chatterjee, Sunil K.
CHILE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
CEA-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 3H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GKSPKTLIYRANRLIDGVPSRFSGSGGQYYSLTISSLEYEDMGTYYCLQFDEFPWMFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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67.6%; Pred. No. 8.6e-35;
ive 13; Mismatches 33; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/844,736
FILING DATE: 09-Apr-1997
CLASSIFICATION: <unimage color of the color o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: POlizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20004.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000102
TELECOMMUNICATION INFORMATION:
                                   08/365,484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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STREET: 755 PAGE MILL ROAD
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
APPLICATION NUMBER: US 08 FILING DATE: 28-DEC-1995 FILING DATE: 28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09844736
Patent.No. US20020041872Al
GENERAL INFORMATION:
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Best Local Similarity 67.6%
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                            TELEX: 706141
                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-844-736-4
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| SEQUENCE CHARACTERISTICS:
| ILBNGTH: 142 amino acids | TYPE: amino acids | TYPE: amino acid | STRANDEDNESS: single | STRANDEDNESS: single | STRANDEDNESS: single | TOPOLOGY: linear |
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Search completed: August 30, 2003, 22:06:56 Job time: 25.3557 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                           OM protein - protein search, using sw model
                                                                                                                                           Run on:
```

August 30, 2003, 22:02:45; Search time 17.5168 Seconds (without alignments) 796.063 Million cell updates/sec US-08-836-455-2 740 1 MGAPAQILGFLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 145 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir_76:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Iq kappa chain pre	kappa chain	6	ь	g kappa chain	g kappa chain	5	g kappa chain	itrophenyl pho	g kappa cha	ь	g kappa chain	Б	g kappa chain	5	g kappa	5	g kappa chain	6	б	Б	б	g kappa chain -	σ	q kappa chain	ь ь	g kappa	g kappa	g kappa chain V-
		KVMSM4	PL0260	PL0259	S14237	D32513	PL0262	KVMS3B	S01320	B47271	A26406	PH1224	S40369	PH1062	A34904	S40353	S40368	B23986	A29380	A49134	S33161	S40317	S52447	m	JL0080	S40313	9	S52789	S40352	S40349
	DB	: -	~	7	~	N	~	Н	N	4	~	~	7	~	N	~	7	~	7	7	7	7	~	~	7	~	7	~	7	7
	Length	130	106	106	234	129	106	117	234	108	128	127	129	86	126	125	130	129	122	141	230	129	127	132	115	123	88	129	131	125
æ (Query		67.7			64.6		61.1									28.6							•						
	Score	596	501	497	496	478	459	452	447	445	443	439	438	435	435	434	434	433	431	429	428.5	428	426	425	424	422	419	419	419	418
1000		-	7	m	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	25	56	27	28	53

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	kappa														
Ιđ	Ig	IG	Ιg	19	Ιď	Ig	Ιġ	БI	Ιđ	Ιď	5I	Ιđ	Ιg	Ig	, 5
67															
ñ	793	372	333	ST1	331	646	101	840	840	316	335	320	106	315	702
S403	S52793	S46372	840333	KVMST1	S40331	538646	PL0101	C28840	B28840	S40316	S40335	524320	PL0106	S40315	552702
2 \$403	2 \$52793	2 \$46372	2 \$40333	1 KVMST1	2 S40331	2 \$38646	2 PL0101	2 C28840	2 B28840	2 S40316	2 \$40335	2 \$24320	2 PL0106	2 \$40315	2 652702
ď	129 2 S52793	N	ď		N	7	7	7	~	~	7	~	7	7	c
127 2	129 2	128 2	125 2	128 1	123 2	132 2	128 2	101 2	101 2	125 2	126 2	135 2	144 2	125 2	120
127 2	ď	128 2	125 2	128 1	123 2	132 2	128 2	101 2	101 2	125 2	126 2	135 2	144 2	125 2	120
56.5 127 2	129 2	56.1 128 2	55.8 125 2	55.7 128 1	55.4 123 2	55.4 132 2	55.3 128 2	55.0 101 2	55.0 101 2	54.7 125 2	54.7 126 2	54.5 135 2	54.3 144 2	54.1 125 2	54 1 129 2

ALIGNMENTS

KESULT 1 KVMSM4 Ig kappa chain precursor V region (MOPC 41) - mouse N.Contains: Ig kappa chain precursor V region VK41
C.Species: Mus musculus (nouse mouse) C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 28-May-1999 C;Accession: A93211; B93211; A93815; A94239; A01922; A01923 R:Seidman, J.G.; Max, E.E.; Leder, P.
A.Title: A kappa-immunoglobulin gene is formed by site-specific recombination without A.Reference number: A93211; MUID:79221900; PMID:111146 A.Rocession: A93211 A.Rocession: A93211 A.Rocession: A93211
A; Residues: 1-130 < PC41> A; Accession: B9321 A; Molecule type: DNA A; Doctoring the control of
A; Residuces: 1.11/ CVN412 A;Cross-references: GB:V00804; GB:J00566; NID:g52127; PIDN:CAA24186.1; PID:g575660 A;Note: the sequences were determined from the differentiated gene MOPC 41 and the generators of Schoots.
A; Discourant, 1.7, Denough, 74, 716-720, 1977 A; Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precurs A; Reference number: A93815; MUID:77148916; PMID:403522 A; Accession: A93815
A.Wolecule type: protein A.Residues: 1-33 <bur> A.Note: Met-3 is apparently used as an alternative initiator in 25% of the chains R.Gray, W.R.; Dreyer, W.J.; Hood, L.</bur>
Science 155, 465-467, 196/ A;Title: Mechanism of antibody synthesis: size differences between mouse kappa chains A;Reference number: A94239; MUID:67056897; PMID:4162931 A;Accession: A94239
A; Molecule type: protein A; Residues: 23-49, B',51-53, LSB',57-58, 'ZZ',61-62, 'BZ',65-76,'B',78-108,110-130 <gra A; Experimental source: Bence Jones protein MOPC 41 C; Genetics:</gra
F:1-22/Domain: signal sequence #status experimental <sig1> F:3-22/Domain: signal sequence #status experimental <sig2> F:33-2130/Product: Ig kappa chain V region (MoDC 41) #status experimental <m41> F:38-112/Domain: immunoglobulin homology <imm> F:45-110/Disulfide bonds: #status predicted</imm></m41></sig2></sig1>
Query Match 80.5%; Score 596; DB 1; Length 130; Best Local Similarity 92.2%; Pred. No. 3.7e-42; Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60

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Ig kappa chain precursor (15C5) - mouse

G Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Species: Mus musculus (house mouse)

C; Date: 134237

R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Bur. J. Blochem. 192, 767-775, 1990

A; Title: Construction and characterization of a recombinant murine monoclonal antibod A; Reference number: S14236; MUID: 91006173; PMID: 2209622

A; Accession: S14237

A; Molecule type: mRNA

A; Residues: 1-234 < VANA

A; Collence of type: MRNA

C; Cyperfamily: immunoglobulin V region; immunoglobulin homology

C; Superfamily: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain precursor V region (BXW16) - mouse (Species: Mus musculus (house mouse) (CjSpecies: Mus musculus (house mouse) (CjSpecies: J1-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000 (CjAccession: D32513 R;Cofler, R:; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A. J. Clin. Invest. 82, 852-860, 1988 A;Title: Immunoglobulin kappa light chain variable region gene complex organization, a A;Reference number: A94689; MUID:88331394; PMID:3138286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPSSLSASLGERVSLTCRASQDIGRSLNWLQQEPDGTIKRLIYATSSLDSGVPK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK
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                                                      Gaps
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                                                                                                                                                                                                        81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 234;
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     Length 106;
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Pred. No. 1.8e-32;
6; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 496; DB 2; Lv; Pred. No. 1.1e-33; 15; Mismatches 30;
  Score 497; DB 2;
Pred. No. 4.1e-34;
                                                   5; Mismatches
67.2%; Score 497; 92.5%; Pred. No. 4.
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Best Local Similarity 76.8%;
Matches 96; Conservative
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Best Local Similarity 68.5%
                                                   98; Conservative
                            Similarity
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A; Residues: 1-129 <KOF>
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  Query Match
Best Local S:
Matches 98
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(Species: Mus musculus (house mouse)
(Species: Nus musculus (house mouse)
(Spate: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
(SAccession: PLO259
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, P. Exp. Med: 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: PL0260
R; Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. B. Exp. Med. 171, 265-297, 1990
A; Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A; Reference number: PL0231; MUID:90111618; PMID:2104919
A; Accession: PL0260
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                                                                                                     DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Mus musculus (house mouse)
Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-106 <SHL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: i--
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C; Keywords: heterotetramer; immunoglobulin
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Pred. No. 1.9e-34;
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F:50-56/Region: complementarity-determining
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining
F:99-106/Region: framework 4
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93.48;
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Best Local Similarity
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A; Residues: 1-106 <SHL>
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F;50-56/Region:
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A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
C;Accession: B47271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.5A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic A;Reference number: A47271; MUID:93165660; PMID:8094556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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                                                                                                                                            1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
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                                                                                                                                                                                                                                                                                  61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115
                                                                                                                                                                                                                                                                                                                          GETIKHLIYETSNLDSGVPKRFSGSRSGSDYSLIIGSLESEDFADYYCLQYASSP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-234 <DE1>
A; Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785
A; Note: this sequence was determined from the differentiated gene
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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                                                                           18;
Score 452; DB 1;
Pred. No. 2.2e-30;
5; Mismatches 18
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; Pred. No. 1.1e-29;
22; Mismatches 35
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80.0%;
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Best Local Similarity 60.1%
Matches 86; Conservative
                                                                           Conservative
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Best Local Similarity
Matches 89; Conserv
                                    Similarity
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Query Match
Best Local S:
Matches 92
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain precursor V region (VKM173B) - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 21-Jan-2000 C.Accession: A01924 R.Max, E.E.; Seidman, J.G.; Miller, H.; Leder, P. A. Max, E.E.; Seidman, J.G.; Miller, H.; Leder, P. A. Miller, H.; Leder, P. A. Miller, H.; Leder, P. A. Miller, M. Miller,
                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain V region (anti-DNA, 60VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0262
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PL0231; MUID:90111618; PMID:2104919
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                                TIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGT 122
                                                                    21 DIOMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
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5; Mismatches 10
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A; Residues: 1-117 <MAX>
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|| KLEIK 129
                                                                                                                                                                      KLEIK 127
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Matches
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QY 21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80 :::	OY 61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120 :
QY 81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIK 127 .	Qy 121 GTKLEIK 127 Db 121 GTKLEIK 127
RESULT 10 A26406 Ig kappa chain V region (Ars-A) - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Saccession: A6406 R;Sanz, I.; Capra, J.D. Proc. Natl. Acad. Sci. U.S.A. 84, 1085-1089, 1987 A;Title: V-K and J-K gene segments of A/J Ars-A antibodies: somatic recombination general A;Reference number: A26406, MUID:87147197; PMID:3103124 A;Recession: A26406 A;Residues: 1-128 <an> A;Residues: 1-128 <an> A;Cross.references: GB:M15519 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <imm></imm></an></an>	RESULT 12 \$40369 Ig kappa chain - human C;Species: Home sapiens (man) C;Species: Home sapiens (man) C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession: \$40369 R;Klein, R.; Jaenichen, R.; Zachau, H.G. Bur. J. Immunol. 23, 3248-3271, 1993 A;Title: Expressed human immunoglobulin chi genes and their hypermutation. A;Reference number: \$40312; MUID:94080891; PMID:8258341 A;Accession: \$40369 A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-129 KKLE> A;Cross-references: EMBL:X72479; NID:9441426; PIDN:CAA51147.1; PID:9441427 C;Superfamily: Immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology
Query Match . 59.9%; Score 443; DB 2; Length 128; Best Local Similarity 70.3%; Pred. No. 1.38-29; Matches 90; Conservative 11; Mismatches 27; Indels 0; Gaps 0; Qy 1 MCAPAQLIGELLIFPGTRCDIQMTQSPSSLSASIGQRVSLTCRASQDIGINLHWLQQEP 60	F;37-111/Domain: immunoglobulin homology <imm> Query Match 59.2%; Score 438; DB 2; Length 129; Best Local Similarity 70.2%; Pred. No. 3.4e-29; Matches 87; Conservative 11; Mismatches 26; Indels 0; Gaps 0; Qy 5 AQLIGFULLFPGTRCDIOMTOSSISSASLGONVSITCRASQDIGINLHWLQQEPDGTI 64</imm>
61 DGTIKKLIYATSSLGSGVPKRFSGSRSGSDVSLTISSLGSEDFVAYCLQYASSPYTFGG 11:1 1 1 1 1 1 1 1 1	Db 6 AGLIGILLICFPGARCDIQMTGSPSSLSASVGBRVITCRASHVISHLVWFQGRFRAP 65 QY 65 KRLIYANSSLGSGVPKRPSGSRGSDYSLTISSLESEDPVAYYCLQYASSPYTFGGGTKL 124 Db 66 KSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYPYTFGGGTKL 125 QY 125 EIKR 128 Db 126 EIKR 129
RESULT 11 PH1224 Ig kappa chain precursor V region (M-T151) - mouse (fragment) C;Specides: Mus musculus (house mouse) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000 C;Accession: PH1224 R;Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; Lenz (Gene 121, 271-278, 1992 A;Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and or A;Reference number: PH1224 A;Accession: PH1224 A;Molecule type: mRNA A;Residues: 1-127 VWEL A;Molecule type: mRNA A;Molecule ty	SULT 13 1062 11 Light chain V ref Inght chain V ref Species: Mus musc bate: 30-Sep-1993 Accession: PH1065 Exp. Med. 176, 7 Exp. Med. 176, 7 Exp. Med. 176, 7 Exp. Med. 176, 7 Exp. med. 179, 8 Reference number: nucleic a Reference number: nucleic a Reference number: Status: nucleic a Residues: 1-98 (1 Experimental souz Superfamily: immunog
Query Match 59.3%; Score 439; DB 2; Length 127; Best Local Similarity 69.3%; Pred. No. 2.8e-29; Matches 88; Conservative 12; Mismatches 27; Indels 0; Gaps 0;	
OMTOSPSSLSASLGORVSLTCRASQDIGINLHW :	Qy 21 DIQMTQSPSSLSASLGGRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPR 80

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Search completed: August 30, 2003, 22:08:53 Job time : 18.5168 secs
                                                                                                                                                          C; Species: Mus musculus (house mouse)
C; Abate: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C; Accession: A34904
R; Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J; Blol. Chem. 265, 133-138, 1990
A; Title: Active site structure and antigen binding properties of idiotypically cross-rea
A; Reference number: A34903; MUID:90094387; PMID:2104617
A; Accession: A34904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LIYAASSFQSGVPSRFSGSGSGTEFTLTISGLQPEDFATYYCLQHNSYPLTFGGGTRVEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V-J-C region - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Bate: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40353
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
A;Klein, R.; Jaenichen, R.; Sachau, H.G.
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 126;
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                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-126 <BED>
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58.8%; Score 435; DB 2; 70.5%; Pred. No. 5.9e-29; tive 12; Mismatches 24,
                                                                                                                                       Ig kappa chain precursor V region (5-27) - mouse
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68.0%;
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Best Local Similarity 70.55
Matches 86; Conservative
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A; Residues: 1-125 <KLE>
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us-08-836-455-2.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 30, 2003, 19:57:10; Search time 10.2181 Seconds (without alignments) 667.331 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-08-836-455-2 740 1 MGAPAQILGFLLLEFPGTRC.....IKRADAAPTVSIFPPSSKLG 145

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01639 mus musculu	P01641 mus musculu	P01637 mus musculu	PO4431 homo sapien	6	mns	P01648 mus musculu	P01646 mus musculu	P01647 mus musculu	P01601 homo sapien	P01645 mus musculu	P01610 homo sapien	mus m	P04432 homo sapien	P01652 mus musculu	P04946 mus musculu	P01650 mus musculu	P01653 mus musculu	P01602 homo sapien	homo	homod	homod	mus n	P18135 homo sapien	homo	homo	P01599 homo sapien	homo	homo	homo	homo	594 homo	P01595 homo sapien
SUMMARIES	QI	KV5G_MOUSE	KV5H_MOUSE	KV5E_MOUSE	KV1W_HUMAN	KV5J_MOUSE	KV5K_MOUSE	KV50_MOUSE	KV5M_MOUSE	KV5N_MOUSE	KV1I_HUMAN	KV5L_MOUSE	KV1R_HUMAN	KV5F_MOUSE	KV1X_HUMAN	KV5S_MOUSE	KV5U_MOUSE	KV5Q_MOUSE	KV5T_MOUSE	KV1J_HUMAN	KV10_HUMAN	KV3H_HUMAN	KV3M_HUMAN	KV5R_MOUSE	KV3L_HUMAN	KV1Y_HUMAN	KV3K_HUMAN	KV1G_HUMAN	KV1L_HUMAN	KV1P_HUMAN	KV1H_HUMAN	KV1V_HUMAN	KV1B_HUMAN	KV1C_HUMAN
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KV1E_HUMAN KV1D_HUMAN KV1S_HUMAN KV1Z_HUMAN KV1Z_HUMAN KV5P_MOUSE KV1T_HUMAN KV2F_HUMAN KV2F_HUMAN KV2F_HUMAN KV1F_HUMAN
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ALIGNMENTS

RESULT 1 KV5G_MOUSE AC 2015G DT 21-JU DT 21-JU DD 121-JU DD 121-JU DD 121-JU DD 131-JU DD 131-JU DD 131-JU DD 131-JU DD 131-JU RRA MEDLI RRA GRAY RRA GRAY RRA GRAY RRI MAMINA RRI SCIENA RRI SCIE
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                                                                                           1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                             Gaps
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Max E.E., Seldman J.G., Miller H., Leder P.;
Wayriation in the crossover point of kappa immunoglobulin gene V-J
recombination: evidence from a cryptic gene.";
Cell 21:793-799(1980).
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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 MISSING (IN 25% OF THE MOLECULES).
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Pred. No. 5e-38;
5; Mismatches 18; Indels
                                        Length 130;
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COMPLEMENTARITY-DETERMINING-1.
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                                      Score 596; DB 1; Length 13 Pred. No. 2.9e-52; 4; Mismatches 6; Indels
                    130 AA; 14311 MW; SEFE0FE71D5F1BEC CRC64;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-V region MOPC 173B precursor.
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HSSP; POLGO7; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; 19; 1.
SMART; SMO0405; IGv; 1.
Immunoglobulin V region; Signal.
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                                       80.5%;
92.2%;
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                                                 Best Local Similarity 92.2
Matches 118; Conservative
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130
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SEQUENCE FROM N.A.
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                          1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
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                                                                                                 61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Altenburger W., Steinmetz M., Zachau H.G.; "Functional and non-functional joining in immunoglobulin light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                            COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAPPA CHAIN V-V REGION T1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14385 MW; AFA5563D31BB7E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.7%; Score 412; DB 1;
Best Local Similarity 63.3%; Pred. No. 5.2e-34;
Matches 81; Conservative 14; Mismatches 33.
                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                             128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-V region T1 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P60362; IWTL.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SMO0406; IGV: 1.
IMMRT; SMO0406; IGV: 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-81052342; PubMed-6776411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes of a mouse myeloma.";
Nature 287:603-607(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V00772; CAA24150.1; -.
                                                                                                                                                                                                                                                                                STANDARD;
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69
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128
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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121 GTKLEIKR 128

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NCBI_TaxID=10090;
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P01644;
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                                                             KV5J_MOUSE
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SEQUENCE
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                                                                             P01643;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-85014148; Pubmed=6091049;
KIODECK H.G., Combriato G., Zachau H.G.;
Immunoqlobulin, genes of the Rappa light chain type from two human lymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-AUG-1999 (Rel. 38, Last annotation update)
15-AUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-I region Walker precursor.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR003596; Ig_W.
                                                                                        129 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X00965; CAA25477.1; ALT_TERM.
PIR; A01883; K1HUWK.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
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nes 82; Conservative
                                                                                        STANDARD;
||||||:||
GTKLELKR 128
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|123 GTRLEIK 129
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120
45
129
129 AA;
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                                                                                      KV1W_HUMAN
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DISULFID
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                                                                        KV1W_HUMAN
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1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIXYTSSLHSGVPS 60
                                                                                                                                                                                                                                                                                                                                                    A SCHIFF C., Fougereau M.;

A SCHIFF C., Fougereau M.;

Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

Schiff C., Fougereau M.;

T "Determination of the primary structure of a mouse IgG2a
T "mannoglobulin. Amino-acid sequence of the light chain.";

Eur. J. Blochem. 59:525-337(1975).

C -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN.

R PIR; A01926; KWS73.

R PRIST: PO19607: 1REI.

R InterPro; IPR003106; Ig_MC.

R InterPro; IPR003506; Ig_WC.

R InterPro; IPR003506; Ig_W.

R PROSTIF; SSMO0407; Ig. 1.

SMART; SMO0406; IGV; 1.

R PROSTIF: PSSMO35; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%; Score 389; DB 1; Length 108; 69:4%; Pred. No. 8e-32; Indels 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORN - Z.
COMPLEMENTARITY - DETERMINING - 2.
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                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-V region MOPC 173.
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21-JUL-1986 (Rel. 01, Last sequence update)
21-EBB-21003 (Rel. 41, Last annotation update)
Ig kappa chain V-V region HP R16.7.
108 AA.
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PRT;
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STANDARD;
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                                                                                                                                                                                  Mus musculus (Mouse).
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STANDARD;
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108
108 AA;
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                                                      NON_TER
SEQUENCE
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     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIQMIQITSSLSASLGDRVIISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Siegelman M., Capra J.D.;

"Complete amino acid sequence of light chain variable regions derived from flve monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idlotype.";

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

"INSTELLANDOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

HSSP; PO1607; IREI.

InterPro: IPR007100; Ig-like.

InterPro: IPR007100; Ig-like.

InterPro: IPR0073006; Ig_WHC.

InterPro: IPR0073006; Ig_W.

Ffam; PR00407; ig: I.

SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  from five monoclonal anti-p-azophenylarsonate antibodies differing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 384; DB 1; Length 108;
; Pred. No. 2.5e-31;
10; Mismatches 21; Indels
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
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FRAMEWORK-3.
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                      11910 MW; A554642C63EFF597 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ig kappa chain V-V region HP 91A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
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MEDLINE-82150934; PubMed=6801658;
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71.3%;
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P01648;
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SEQUENCE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                        81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKR 128
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                                                                                             Length 108;
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Pred. No. 4e-31;
9; Mismatches 22; Indels
                                                                                           ); Score 383; DB 1; Length 10
s; Pred. No. 3.2e-31;
12; Mismatches 20; Indels
                                                         D52EDA5E9A45291C CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rappa chain V-V region HP 123E6.
Mus musculus (Mouse).
                    BY SIMILARITY.
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  FRAMEWORK-4
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MEDLINE-82150934; PubMed-6801658;
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108 FF
88 B1
108
11961 MW;
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                                                                                             51.8%;
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Best Local Similarity 71.3%;
Matches 77; Conservative
                                                                                       Query Match
Best Local Similarity 70.49
Matches 76; Conservative
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Siegelman M., Capra J.D.;
                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                          conversion.";
Cell 32:181-189(1983).
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Best Local Similarity
76; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
             MEDLINE-83129397;
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KV5L_MOUSE
ID KV5L_MOUSE
AC P01645;
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SEQUENCE
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                                                                                                                                                                  Siegelman M., Capra J.D.;

Tomplete amino acid sequence of light chain variable regions derived a complete amino acid sequence of light chain variable regions derived a croplete amino acid sequence of light chain variable regions derived a rossreactive idiotype.";

Trom five monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";

Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).

H. MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.

R. INTERPRO: IPRO0710; Ig.-like.

R. InterPro: IPR003106; Ig.-M.C.

R. InterPro: IPR003106; Ig.-W.

R. MIRCHART; SM00406; IG.V.

R. RAMART; SM00406; IG.V:

R. MIRMINGALOMAT; VEGION.

R. MIRMINGALOMATI, V. region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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MEDLINE-81098966; PubMed-6779204;
Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two
Kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Appa chian V-I region HK101 precursor (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.6%; Score 382; DB 1; Length 108; 70.4%; Pred. No. 4e-31; Live 11; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                    11965 MW; 39971BC653EFEFA2 CRC64;
                                          21.JUL-1986 (Rel. 01, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
19. Kappa chain V-V region HP 124E1.
Mus musculus (Mouse).
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MEDLINE-82150934; PubMed-6801658;
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                                 21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA;
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P01601;
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DISULFID
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KV5N MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTI
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by gene
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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COMPLEMENTARITY-DETERMINING-1.
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                      Bentley D.L., Rabbitts T.H.; "Evolution of immunoglobulin V genes: evidence indicating recently duplicated human V kappa sequences have diverged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.5%; Score 381; DB 1;
68.5%; Pred. No. 5.5e-31;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ilg kappa chain V-V region HP 93G7.
Mus musculus (Mouse).
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MEDLINE-82150934; Pubmed=6801658;
PubMed=6402305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; K01322; AAA58930.1; -. EMBL; K01324; AAA58932.1; -. EMBL; V00558; CAA23824.1; -. PIR; A01881; K1HU11.
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                                                                                                                                                                                                                                                                                                                                                                  1 DIQMIQITSSLSASLGDRVIISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60
                                                                                                                                                                                                                                                                                                                                                     21 DIOMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goni F., Frangione B.;
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein WEA) with antibody activity against 3.4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUYYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
"Complete amino acid sequence of light chain variable regions derived from flve monoclonal anti-p-azophenylarsonate antibodies differing with respect to a crossreactive idiotype.";
Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
-I- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVIR_HOWAN STANDARD; PRT; 108 AA.
P01610;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 Appa chain V-I region WEA.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                 61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNMLPRTFGGGTKLEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                      81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKR 128
                                                                                                                                                                              COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                       Length 108;
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                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                              11954 MW; 22F4642C63EFF58E CRC64;
                                                                                                                                                                                                                                                                                                    51.2%; Score 379; DB 1; L
70.4%; Pred. No. 7.9e-31;
ive 10; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSEP, PR0362; 1WTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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DOMAIN 1 23 FRAMEWORK-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-83273707; PubMed-6410398;
                                                                                                 InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
                                                                       InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.4%
Matches 76; Conservative
                                                                                                                                                     ſmmunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1
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                                                                                                                                                                                                                                                                             108 AA;
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                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                             SEQUENCE
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ö ó 21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80 9 9 1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP Gaps Gaps 61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115 Pech M., Hochtl J., Schnell H., Zachau H.G.; "Differences between germ-line and rearranged immunoglobulin V kappa coding sequences suggest a localized mutation mechanism."; Nature 291:668-670(1981) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090; ö 81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKR 128 = = = Length 108; Length 115; COMPLEMENTARITY-DETERMINING-1. COMPLEMENTARITY - DETERMINING - 2. COMPLEMENTARITY - DETERMINING - 3. COMPLEMENTARITY - DETERMINING - 1. COMPLEMENTARITY - DETERMINING - 2. FRAMEWORK - 3 . COMPLEMENTARITY - DETERMINING - 3 . IG KAPPA CHAIN V-V REGION L6 20; Indels 31; Indels 11840 MW; 9249B61F0945618C CRC64; 12986 MW; BA852C58F328E1C3 CRC64; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 kappa chain V-V region L6 precursor (Fragment). ; Score 373; DB 1; ; Pred. No. 3.1e-30; 16; Mismatches 20 50.0%; Score 370; DB 1; llarity 64.3%; Pred. No. 6.7e-30; Conservative 10; Mismatches 31. 115 AA BY SIMILARITY BY SIMILARITY FRAMEWORK-2. FRAMEWORK-3 FRAMEWORK-1 PRT; SEQUENCE FROM N.A. MEDLINE-81220975; PubMed-6264318; PROSITE; PS50835; IG_LIKE; 1. Immunoglobulin V region; Signal. HSSP, A01921, KVMSL6.
HSSP, P01607, 1REI.
InterPro, IPR007110, Ig-like.
InterPro, IPR003596; Ig_MHC.
InterPro, IPR003596; Ig_WHC. 50.4%; 72; Conservative STANDARD; 34 49 56 88 97 107 108 Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. >115 Mus musculus (Mouse) 115 AA; Similarity 108 AA; Similarity Query Match Best Local Simi Matches 74; KV5F_MOUSE DOMAIN DISULFID NON_TER SEQUENCE DISULFID NON_TER Query Match SEQUENCE Local DOMAIN SIGNAL DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN P01638 DOMAIN DOMAIN KV5F_MOUSE Matches

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Search completed: August 30, 2003, 22:04:34 Job time : 10.2181 secs
                   RESULT 15
KV5S_MOUSE
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61 GKSPKTLIYRANRLVDGVPSRFSGSGGGDYSLTISSLEYEDMGIYYCLQYDEFP 115
                                                                                                                                                                                                                                                                        Klobeck H.G., Combriato G., Zachau H.G.;
Immunoglobulin genes of the kappa light chain type from two human
Iymphoid cell lines are closely related.";
Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                               Homo Sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_MHC.
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Pred. No. 1.2e-29;
                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                    13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update, 15-JUL-1999 (Rel. 38, Last annotation update) kappa chain V-I region Daudi precursor.
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lobulin V region; Signal.
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. IMMUND1, 128:302-307(1982).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                             MEDLINE-82099361; PubMed-6798111;
Johnson N., Slankard J., Paul L., Hood L.;
"The complete V domain amino acid sequences of two myeloma inulin-
                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
  108 AA
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BY SIMILARITY.
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  PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Fram; PF00047; ig; 1.
SMART; SM00406; Igv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
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  STANDARD;
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Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                               binding proteins."
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KV5S_MOUSE
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1 MGAPAQILGFLLLFPGTRC.....IKRADAAPTVSIFPPSSKLG 149
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*

sp_bacteriap:*

sp_archeap:*

sp_human:*
sp_invertebrate:*
sp_mammal:*

sp_fung1:*

sp_organelle:* sp_phage:*

sp_rodent:* sp_virus:*

	Description	Q925s9 mus musculu	Snm	Q91wf8 mus musculu	Q91ws9 mus musculu	Q8vcp0 mus musculu	Q9rla5 mus culu	Q8nek1 homo sapien	Q8k0f8 mus musculu	Q91w12 mus musculu	Q9j184 mus musculu	Q99m37 mus musculu	Q8tcd0 homo sapien	Q8vci6 mus musculu	Ogvdd0 mus musculu	Q8k1f1 mus musculu	Ogul70 homo sapien
SUMMARIES	Ð	092589	Q8R062	Q91WF8	091WS9	Q8VCP0	Q9R1A5	Q8NEK1	Q8K0F8	Q91W12	Q9JL84	Q99M37	Q8TCD0	Q8VC16	QBVDD0	QBK1F1	09UL70
	DB	11	11	11	11	11	11	4	11	11	11	11	4	11	11	11	4
	Query Match Length DB	127	234	234	233	234	214	234	239	235	107	238	239	238	134	114	108
dP	Query Match	86.8	69.3	68.4	66.5	8.09	58.5	56.2	52.9	51.7	51.4	50.5	50.2	20.0	49.1	48.7	48.6
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7 4 0965A9 2 11 08KLF3 9 4 09WC55 9 4 08N2WC 4 11 08RC28 10 08KLF2 2 11 08KLF2 2 11 08KLF2 11 08KLF9 11 08KLF9 11 08KLF9 12 11 08KLF9 13 1 09UL81 14 09UL81 14 09UL83 15 09UL86 16 4 09UL83 17 09UL86 18 4 09UL83 19 4 09UL83 10 092LF6 11 092UL83 11 092UL86 12 09UL86 13 09UL86 14 09UL86 16 1 092UL86 17 11 092UL96 18 1 092UL86 19 1 092UL86 10 1 1 1 092UL96 11 1 1 092UL96	1444141
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17 359.5 18 357.5 19 357.5 21 357.5 22 34.6 22 34.6 24 34.5 25 34.6 26 338 27 34.5 28 33.6 30 32.8 31.6 31.6 31.6 31.6 31.6 31.6 31.6 31.6	39 293 40 275 41 273 42 270.5 43 269 44 268.5 45 267

ALIGNMENTS

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1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60

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PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
InterPro; IPR003006; Ig_MHC.
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Best Local Similarity
Matches 97; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
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Q91WS9
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                     DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.9 kba protein.
Wus musculus (Mouse).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthazoa; Chordata; Sciurognathi; Muridae; Musinae; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25-9 kDa protein.
Mus musculus (Wouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 69.3%; Score 513; DB 11; Length 234; Best Local Similarity 71.3%; Pred. No. 7.3e-46; Matches 102; Conservative 13; Mismatches 28; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC027418; AAH27418.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC015292; AAH15292.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 protein.
234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; 13', 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                          GTKLEIK 127
                                                                                                GTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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                                                                                              121
                                                                                                                                                                                                                                       Q8R062
Q8R062;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LILCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYY 69
                                                                                                                                                                                                                                                                                                                                                       1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYA 70
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                               Length 234;
                                                                                                                                                                                                                              Score 506; DB 11; LL...
Pred. No. 4e-45;
Tropies 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013496; AAH13496.1; -.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007006; Ig_MHC.
InterPro; IPR003396; Ig_V.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
InterPro; IPR003596; 1g_v.
InterPro; IPR003596; 1g_v.
InterPro; IPR001865; Ribosomal_S2.
Pram; PF00047; 1g; 2.
SMART; SMO406; 1Gv; 1.
PROSITE; PS00250; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1 SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q91WS9 PRELIMINARY; PRT; 233 AA.
Q91WS9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.8 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.5%; Score 492; DB 11;
1larity 72.9%; Pred. No. 1.2e-43;
Conservative 12; Mismatches 24;
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.9%; Pred. No. 4e-4
Matches 100; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GTKLEIKRADAAPTVSIFPPSSK 143
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Gaps

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61 DGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGDYSLTISSLEYEDMGIYYCLQYDEFFTFGSGTKLEIKRADAAPTVSIFPP 120
                                                                                                                                                                                                                 81 RFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTFGGGTKLEIKRADAAPTVSIFPP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK 80
                                                                                                                                                     1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hymosapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.
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                                            Length 214;
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                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC030813; AAH30813.1; -
InterPro; IPR07110; Ig-11ke.
InterPro; IPR003997; Ig_c1.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 2. 578 MARY; SM00477; 1g; 2. 58ARY; SM004077; 1gcd; 1. PROSITE; PS50835; 1G_LIKE; 2. PROSITE; PS050835; 1G_LIKE; 1. PROCHE; PS050836; 1G_MHC; 1. SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
23922 MW; 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                        234 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 84; Conserv
  214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    141 SSK 143
                                                                                                                                                                                                                                                                                                                                            121 SSE 123
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01-OCT-2002 (
01-MAR-2003 (
  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEP
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 60.8%; Score 450; DB 11; Length 234; I Similarity 60.1%; Pred. No. 3.1e-39; 86; Conservative 23; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC019474; AAH19474.1; InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO0406; ĬĠv; 1.
PROSTIE; PSO0290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kba protein.
Mus musculus (Mouse)
                                          234 AA
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Best Local Similarity
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                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                    rissum-colon;
                                     Q8VCP0
Q8VCP0;
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RESULT 5
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                    Q8VCP0
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9

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PROSITE; PS50835; IG_LIKE; 1.
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es 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                  29
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Matches
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                                                                                                                                                                                                                                                                              RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 LQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LLQRPGQSPKRLISLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643, AAH06643.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                      Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC031498; AAH31498.1; ... InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSTIE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D7BE84398AA341F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown (Protein for MGC:6582).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.9%; Score 391.5; DB 1 Best Local Similarity 55.4%; Pred. No. 4.7e-33; Matches 82; Conservative 20; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 YTFGGGTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00061; ADH_SHORT; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26366 MW;
                                                                                                                                                                                                                                                    InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003596; IG_C1.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_V.
Pfam; PF00047; IG; 2.
SWART; SM00409; IGC1: 1.
SWART; SM00406; IGC1: 1.
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Breast tumor;
                                                                                                                                                  TISSUE-Breast tumor;
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                                                                                                                              SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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EPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTF 118
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"T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
Infect. Immun. 68:8803-5808(2000).
EMBL; AF206022; AAF69320.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003006; Ig_WHC.
SMART; SM00406; IGv: 1.
                            21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQEPDGTIKRLIYATSSLGSGVPK
1 MGAPAQILGFLLLFPG--TRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 13, Last sentettion update)
Anti-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 107
107 Aa; 11648 MW; ACF9B1253ACA1E5D CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.3 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.4%; Score 380; DB 11;
11arity 71.0%; Pred. No. 2.6e-32;
Conservative 5; Mismatches 26;
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                                                                                                                                                                                                                            119 GGGTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                                                           120 GVGTKLELKRADAAPTVSIFPPSSE 144
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                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQOEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDI-----GINLHW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |||:|| |:| ||: ||: ||-||| || || ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.,
Strausberg R.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BCC023862, AAM122382.1;
InterPro; IPR007110; 1g-1ike.
InterPro; IPR003006; 1g_MHC.
InterPro; IPR003596; 1g_V.
Pfam: PF00047; 1g; 2.
SWART: SW00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002035; AAH02035.1;
                                                                                                                                                                                                                                                                                                                                       FB2B06A0B801330A CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        ; Score 374; DB 11;
; Pred. No. 3.2e-31;
20; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 YTFGSGTKLEIKRADAAPTVSIFPPSSE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTFGGGTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 YTFGGGTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                          HSSP; P01679; 2FBJ.
InterPro; IRR007110; Ig-like.
InterPro; IRR003006; Ig_MHC.
InterPro; IRR003596; Ig_V.
Pfam; PP00047; 19; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26344 MW; FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26234 MW;
                                                                                                                                                                                                                                                                                                                                                                                           50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 52.00
Local Similarity 52.00
Local Similarity 52.00
Local Similarity 52.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SEQUENCE 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
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56 LQQEPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MGAPAQILGFLLLLFPGTRCDIQMTQSPSSLSASLGQRVSLTCRASQDI-----GINLHW 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAH19760.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416331; CAC94866.1; -
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chernajovsky Y.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 370; DB 11;
52.7%; Pred. No. 8.5e-31;
tive 21; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence upd
01-WAR-2003 (TrEMBLrel. 23, Last annotation u
ALT-MOG 212 variable light chain (Fragment).
ANTI-MOG KAPPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 YTFGGGTKLEIKRADAAPTVSIFPPSSK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                              TISSUE-Colon;
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59 EPDGTIKRLIYATSSLGSGVPKRFSGSRSGSDYSLTISSLESEDFVAYYCLQYASSPYTF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDFQVQIFSFLLISASVILSRGQIVLTQSPAIMSASPGEKVTWTCSASSSISY-MHWYQQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIQMTQSPSSLSASLGQRVSLTCRASQDIGIN-LHWLQQEPDGTIKRLIYATSSLGSGVP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGAPAQILGFLLLLFPG--TRCDIQMTQSPSSLSASLGQRVSLTCRASQDIGINLHWLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
Anti-VIPase light chain variable region (Fragment).
Mus musculus (Mouse).
Mus musculus (Mouse).
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Murinae; Murinae; Murinae; MusinaxiD=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                       ;; Score 363.5; DB 11; Length 134;
;; Pred. No. 1.9e-30;
17; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.7%; Score 360.5; DB 11; Length 114; 63.2%; Pred. No. 3.2e-30; ative 16; Mismatches 25; Indels 1;
                                                                                                                                                          NON_TER 134 134
SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2DOCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AA; 12162 MW; 8BD9833DBF3EEFD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; EF00047; 19; 1.
SMART; SM00409; 1G; 1.
SMART; SM00406; 1G; 1.
PROSITE; PS50835; 1G_LIKE; 1.
NON_TER 1
                            InterPro; IPR003596; 19_v.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.8%;
Matches 78; Conservative 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 GGGTKLEIKRADAAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GGGTKLEIKRADAAP 133
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 63.2.

T2; Conservative
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QBK1F1
      SO FIRE DR.
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Search completed: August 30, 2003, 22:05:59
Job time : 37.547 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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August 30, 2003, 18:46:00; Search time 2089.42 Seconds (without alignments) 9026.108 Million cell updates/sec
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461
1 ATGGAATGCAGCTGGGTCTT......CTGGTCCCTGGAAGCTTGGG 461
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                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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GenEmbl:*

1: 90-ba:*
2: 90-htg:*
3: 90-bi:*
4: 90-om:*
5: 90-om:*
6: 90-om:*
7: 90-ph:*
8: 90-pi:*
9: 90-pi:*
10: 90-pi:*
11: 90-pi:*
11: 90-pi:*
12: 90-pi:*
13: 90-ui:*
13: 90-ui:*
14: 90-vi:*
15: em_bi:*
16: em_fun:*
17: em_him:*
18: em_him:*
19: em_oi:*
22: em_oi:*
23: em_pi:*
24: em_pi:*
25: em_oi:*
25: em_oi:*
26: em_co:*
27: em_pi:*
28: em_li:*
29: em_vi:*
29: em_vi:*
31: em_htg_nus:*
31: em_htg_nus:*
33: em_htg_nus:*
34: em_htg_nus:*
35: em_htg_nus:*
36: em_htg_nus:*
37: em_htg_nus:*
38: em_htg_nus:*
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38: em_htg_nus:*
39: em_htg_nus:*
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34: em_htg_nus:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	equence ethods o	AF124/20 Mus muscu AF303872 Mus muscu	Mus	AJ250/60 Mus muscu U49832 Svothetic s	-	AR198720 Sequence AR275320 Sequence	s musc	use an	musculus	Z25443 M.musculus	ZZ5443 M.musculus ZZ5451 M.musculus	AF303873 Mus muscu	225457 M.musculus	Z25449 M.musculus	Mus	AII/I952 Mus muscu Z73339 M.musculus	Z73342 M.musculus	AY247151 Mus muscu	2/333/ M.musculus 273338 M.musculus	AY229957 Mus muscu	AF277091 Synthetic	AY178830 Mus muscu AY178830 Mus muscu	edne	AX057985 Sequence	Aroza443 mus muscu AX057945 Sequence	AX057947 Sequence	AB090857 Mus muscu	ABOS8183 Mus muscu	AB058198 Mus muscu	AB057826 Mus muscu	ABO5/82/ Mus muscu ABO90858 Mus muscu	X97535 M.musculus			linear PAT 17-OCT-2001						associated tumors using	
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SOMMANIES	ID	AR164506 BD085738	AF124/20 AF303872	AB050080	XXU49832	AR083801	AR198720 AR275320	MUSIGH4C11	MUSIG4C11A	MMIGGCVRG	MMIGGCVRB	MMIGGCVRF	AF303873	MMIGGCVRI	MMIGGCVRE	AY171955	AY1/1952 MMMD50C	MMMD47C	AY247151	MMMD52C	AY229957	AF277091	AY178830	AX057984	AX057985	AX057945	AX057947	AB090857	AB05818	-	~ .	AB05/82/ AB090858	AD24	ALIGNMENTS		461 bp	F1 F / 30 CO	556			4 H . U	. >	3 14-AUG-2001;
	DB	ပ ပ	2 5	0	77	9		10	010	10	10	20	10	25	10	10	201	10	10	20	10	17	25	9	9	9	9	10	9 -	10	10	10	10			4		62375			, 461) and Foon.K	ing c	3-A
	Length	461	294	471	902	458	4 58 58	484	490	279	282	290	294	302	305	306	352	355	356	358	360	360	457	765	765	א ע	1280	336	360	360	363	363 363	368			from		GI:16		· · ·	1 to 46	delaying	627414
a	Match	000	20.3		 	16.5	 	4	÷.~						. m	٠. د	. n	М	ė,		س	ლ.	13.0	. e	•	. n		٠i د		, d	4	12.8				AR164506	AR164506	54506.1	Unknown.	Unknown. Unclassified	1 (bases 1 to	Methods of	Ratent: US 6274143-A 3
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AF124720 411 bp mRNA linear ROD 22-MAY-2001
Mus musculus immunoglobulin heavy chain mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (129-7AN-1999) Internal Medicine, University of Kentucky, 800 Rose Street, Lexington, KY 40536, USA Location/Qualifiers
                                                                                                                                                                              09
                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tripath, P.K., Oli, H., Bhattacharya-Chatterjee, M., Ceriani, R.L., Fron, K.A. and Chatterjee, S.K.
Construction and characterization of a chimeric fusion protein consisting of an anti-idiotype antibody mimicking a breast encer-associated antigen and the cytokine GM-CSF Hybridoma 18 (2), 193-202 (1999)
                                                                                                                                                                                                                                                                                 CAGAAGITITAAGGGCAAGGCCTCATIGACIGCAGACACATCCTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                  CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGAATGCAGCTGGGTCTTTCTTCTTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                     GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG
                                                                                                                                                       Gaps
                                                                                                                                                       ö
                                                                                                                             Length 461;
                                                                                                                                                       Indels
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                                                                                                                             DB 6;
                                                                                                                             Score 461; DB 6;
Pred. No. 3e-256;
                                                                                                                                                     0; Mismatches
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                     Location/Qualifiers
1. 461
/organism="unidentified"
/organism="unidentified"
/do_type="genomic DNA"
/db_xxef="taxon:32644"
a 121 c 119 g 109
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Chatterjee, S.K. and Tripathi, P.K.
Direct Submission
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Mus musculus
                                                                                                                             100.0%;
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                                                                                                                                         al Similarity 100.
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Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11010
Patent: JP 2001523269-A 2 20-NOV-2001;
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PN JP 2001523269-A/2
PP 12-JUN-1998 JP 1999503252
PR 13-JUN-1998 US 60/049540,11-JUN-1998 US 09/096244 PI
                                                                                                                                                                                                                              Topology: Linear;
Methods of delaying development of HMFG-associated tumors
                                                                                                                             1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                          CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
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RA CHATTERJEE, KENNETH A FOON
A61K39/395,A61K39/39//C07K16/42
Strandedness: Single;
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Pred. No. 3e-256;
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Location/Qualifiers
                      /organism="unknown"
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JP 2001523269-A/2.
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1 (bases 1 to 461)
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Mus musculus
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Mus musculus clone J558.41 immunoglobulin heavy chain variable
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 294)
Haines, B.B., Angeles, C.V., Parmelee, A.P., McLean, P.A. and
Brodeur, P.H.
                                                                                                                                                                                                                                                                                            5 AATGCAGCTGGGTCTTTCTCTTTCTTCTTCTTCAATAACTACAGGTGTCCACTCCCAGGCTT
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    >>411
/note="anti-idiotype antibody 11D10; mimics a breast
cancer-associated antigen, human fat globule (HMFG)"

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21376477
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Haines, B.B., Angeles, C.V., Parmelee, A.P., McLean, P.A. and
Brodeur, P.H.
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100.0%; Pred. No. 7.9e-225;
ive 0; Mismatches 0;
1. .411
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                  /db_xref="taxon:10090"
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AF303872
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/product-"immunoglobulin heavy chain variable region"
/protein_id="AAG39153.1"
/brotein_id="AAG39153.1"
/dxxed="G1:11612051"
/translation="GAYLQQSGAELVRSGASVKMSCKASGYFFTSYNMHWYKQTPGQG
LEWIGYIYPGNGGTNYNQKFKGKATLTADTSSSTAYMQISSLTSEDSAVYFCAR"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 CAGGCTTATCTACACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAGGCTTATCTACAGCAGTCTGGGGCTGAGCTGGGGTCTGGGGCCTCAGTGAAGATG
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Direct Submission
Submitted (08-SEP-2000) Pathology, Tufts University S
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
Location/Qualifiers
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                                                                                                                  /organism="Mus musculus"
/mol_type="mRNA"
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/strain="BALB/CByJ"
/db_xref="taxon:10090"
/chromosome="12"
/clone="1558.41"
/tissue_type="spleen"
/note="isolated from IgM mRNA fr
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Published Only in Database (2002)
3 (bases 1 to 471)
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/note="VhJ558 family"
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LEWIGYIYPRDGDTNYNQKFKGKATLTADTSSSTAYMQISSLTSEDSAVYFCTRSRDA
XYVGAMDFWGGGTSYTYSSGGGGGGGGGGGGGGDDIVMTQSQKFMSTSVGDRVSVTC
XXSONVGTRVYAMYQQKFGQSFKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSE
DLABYFCQQVNSYPYTFGGGTNLELKR"
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SCR 40"
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                                                                                                                           /translation-"EVQLQQSGAELVRSGASVKMSCKASGYTFARYNVHWVKQTPGQG
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artificial sequences.
1 (bases 1 to 902)
Chen, Z.C., Cockburn, W., Torrance, L., Barker, H. and Whitelam, G.C.
Cytoplasmic accumulation of a soluble functional scry protein to a plant virus expressed as a thioredoxin fusion in Escherichia coli
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sn.z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                              263 CATTGACTGCAGACACATCCTCCAGCACAGCCTACATGCAGATCAGCAGCCTGACATCTG

    .366
/product="immunoglobulin heavy chain variable region"

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170 c 206 g 165 t
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                                  /codon_start=1
/transl_table=11
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/protein_id="CAB60133.1"
/db_xref="G1:6272273"
                                                                                                                                                                                                                                                                                                                                                                       Length 735;
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                                                                                                                                                                                                                                                                 /note="(Gly4Ser)3 linker sequence"
412. .735
                                                                                                                                                                                                                                                                                                                                                                       18.0%; Score 83; DB 12; I 100.0%; Pred. No. 2.4e-36; tive 0; Mismatches 0;
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/mol_type="mRNA"
/db_xref="taxon:32630"
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Submitted (23-FEB-1996) Z C. Chen, Bu
University Road, Leicester LE1 7RH, Location/Qualifiers
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Synthetic single chain Fv ar
protein, mRNA, partial cds.
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AJ250760 1 G1:6272272 antibody; heavy chain; immunoglobulin superfamily; light chain; SCFV, variable region.
Synthetic construct synthetic construct artificial construct artificial construct
                                                                                                                                                                                                            /product="anti-A/U antibody"
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/d_xref="G1:19909936"
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SLISEDSAVYFCARGEYGNPWFAYWGGGTLVTVSAAKTTAQPVYPLAPGSL"
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and Koehl,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 GCAGACACATCCTCCAGCACCACAACATCAGAACAGCAGCCTGACATCTGAAGACTCT 337
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MOL. Immunol. 38, 1235-1247 (1999)
2 (bases 1 to 735)
                                                                                                                                                                                                                                                                                                                                                                                                                                              271 GCAGACACTCCTCCAGCACAGCCTACATGCAGATCAGCAGCCTGACATCTGAAGACTCT
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/organism="synthetic construct"
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/clone="E10"
                                                                                 /db_xref-"taxon:10090"
/cell_line-"hybridoma 9H8"
1. 471
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/organism="Mus musculus"
/mol_type="makna"
/db_xref="taxon:10090"
412. .735
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/mol_type="mRNA"
/db_xref="taxon:10090"
                                    /organism-"Mus musculus"
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   Location/Qualifiers
                                                                     /strain="BALB/c"
                                                   /mol_type="mRNA"
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                                                                                                                                           /gene="VH9H8"
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Best Local Similarity
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Foon, K.A. and Chatterjee, M.
Methods and compositions for the treatment of psoriasis
Patent: US 6355244-A 3 12-MAR-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Length 902;
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                                       Score 77; DB 12;
Pred. No. 7.2e-33;
0; Mismatches 1
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Sequence 3 from patent US 6355244.
AR198720
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Sequence 3 from patent US 5977316.
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131 c 114 g
LEGAGSGQPELAPEDPED"
         234 g
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AR083801.1 GI:10010572
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                                       Query Match 16.7%;
Best Local Similarity 99.2%;
Matches 127; Conservative
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AR198720
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AR083801
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                                                                    Unclassified.

1 (bases 1 to 458)
Chatterjee, M., Foon, K.A. and Chatterjee, S.K.
Monoclonal antibody 1A7 and use for the treatment of melanoma and small cell carcinoma small cell carcinoma Fatent: US 6509016-A 3 21-JAN-2003;
Patent: US 6509016-A 3 21-JAN-2003;
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             Length 458;
                                                                                                                                                                                                                                linear
DB 6; Leus.
          Ouery Match 16.5%; Score 76; DB Best Local Similarity 100.0%; Pred. No. 2.9 Matches 76; Conservative 0; Mismatches
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AR275320
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/db_xref="taxon:10090"
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Location/Qualifiers
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131 c 114 g
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мм024114
Mus musculus immunoglobulin F9.13.7 heavy chain mRNA, partial cds.
U24114
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PSDSypnynekfkckatlydkssstaimolssltsedsavyycaslyygtsygvld
YWGQGTSYTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-APR-1995) Norman C. Peterson, Pathology and Laboratory Medicine, University of Pennsylvania School of Medicine, 252 John Morgan Bldg., 36th St. and Hamilton Walk, Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                   364 GGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCCAGCCAAAACGACA 423
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 453)
Lescar, J., Pellegrini, M., Souchon, H., Tello, D., Poljak, R.J., Peterson, N.C., Greene, M.I. and Alzari, P.M.
Crystal structure of a cross-reaction complex between Fab F9.13.7 and Guinea-fowl lysoxyme
J. Biol. Chem. (1995) In press
2 (bases 1 to 433)
Peterson, N.C.
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/protein_id="AAAA5180.1"
/db_xref="G1:777411"
                                                                                                                                                                                                                                                                                            Length 490;
                                                     /note="complementarity determining region" 388. .411 /gene="CDR3" 388. .411
 /note="complementarity determining region"
                                                                                                                                                                                   /note="complementarity determining region'
                                                                                                                                                                                                                                                                                          14.3%; Score 66; DB 10; Length 49 larity 100.0%; Pred. No. 1.9e-26; Conservative 0; Mismatches 0; Indels
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<1. .>453
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                                                                                                                                                                                                                                         116
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/codon_start=1
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/gene="4C11"
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/label=CDR2
268. .309
                 241. .291
/gene="CDR2"
                                                                                                                                               388. .411
/gene="CDR3"
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                                                                                                                                                                                               /translation-"WGWSWIFLFLLSGTAGVLSEVOLOQSGPELLKPCASVKISCKAS
GYTFTDYTMHWVKQSHGKSLEWIGGFDPNYDNTFYNEKFKDKATLTVDKSSTTAYMEL
RSLTSEDSAVYXCASYDYGALDYWGQGTSVTVSSAKTTPPSVYPLAP"
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Cheng, H. L., Sood, A. K., Ward, R. E., Kieber-Emmons, T. and Kohler, H. Structural basis of stimulatory anti-idiotypic antibodies Mol. Immunol. 25 (1), 33-40 (1988)
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                                                                                                                                           /product="immunoglobulin heavy chain precursor"/
/protein_id="AAA51051.1"
/db_xref="GI:553945"
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                                'tissue_type="anti-idiotypic hybridoma"
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/gene="IgH"
94...4984
/gene="igH"
/product="immunoglobulin heavy chain"
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Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 66; Conservative 0; Mismatches 0;
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/db_xref="taxon:10090"
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/organism="Mus musculus"
/map="chromosome 12"
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/strain="BALB/c"
                 /cell_line="4C11
                                                                    /gene="1gH"
37. .>484
/gene="1gH"
/codon_start=1
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/gene="4C11"
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/gene="CDR1"
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/gene="CDR1"
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/gene="IgH"
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/gene="4C11"
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YPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARRE"
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M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
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Mo.J.A., Bona,C.A. and Holmdahl,R.
Mo.J.A., Bona,C.A. and Holmdahl,R.
Variable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. (1993)
Mo.J.A., Bona,C.A. and Holmdahl,R.
Variable region gene selection of immunoglobulin G-expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. 23 (10), 2503-2510 (1993)
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Mus musculus (house mouse)
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/protein_id="CAA80940.1"
/db_xref="GI:407823"
                                                                                            Length 453;
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/chromosome="12"
/cell_line="CIICB340 hybridoma"
/cell_type="B cell hybridoma"
/tissue_type="lymph node"
/dw_xtage="adult"
                                                                                         13.2%; Score 61; DB 10; I
100.0%; Pred. No. 1.5e-23;
ive 0; Mismatches 0;
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="DBA/1"
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<1. .>279
/label=CDR3
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MMIGGCVRB 282 bp mRNA linear ROD 13-OCT-1993
M.musculus immunoglobulin gamma heavy chain (DBA/1) gene, v region.
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YPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYYCARGEA"
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Mo.J.A., Bona,C.A. and Holmdahl,R.
Worlable region gene selection of immunoglobulin G expressing B cells with specificity for a defined epitope on type II collagen Eur. J. Immunol. (1993) In press
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Mo.J.A., Bona.C.A. and Holmdahl,R.
Wariable region gene selection of immunoglobulin G-expressing B
cells with specificity for a defined epitope on type II collagen
Eur. J. Immunol. 23 (10), 2503-2510 (1993)
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Mus musculus (house mouse)
Mus musculus
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/protein_id="CAA80930.1"
/db_xref="GI:407813"
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Pred. No. 6.1e-23;
0; Mismatches 0;
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/cell_type="B cell hybridoma"
/tissuc_type="lymph node"
/dev_stage="adult"
13.0%; Score 60; DB 100.0%; Pred. No. 6.1 ive 0; Mismatches
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/strain="DBA/1"
/db_xref="taxon:10090"
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Search completed: August 30, 2003, 21:04:56 Job time: 2091.42 secs

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Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
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AAN91146
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Monoclonal antibod
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Result 2

Anti-bGH monoclona Combined CDNA inse mRNA encoding gamm Anti-tobacco mosai 3B1 single chain a Chimeric gene cont Plasmid pi0169 enc DNA encoding anti-

TSH receptor antib TSH receptor antib Mouse DNA encoding H-chain V-region o

Sequence encoding Murine anti-BGH MA Heavy chain of ant

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human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the coding sequence for the murine antibody 11D10 heavy chain variable region. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma,
                                                                                                                                                                                                                          /product= "antibody 11D10 heavy chain variable region"
/note= "no stop codon is given at the 3' end of the
sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Delaying development of, or treating, HWFG-associated tumours using anti-idiotype antibody 11D10 raised against antibodies thuman milk fat globule protein
                                                Antibody 11D10 heavy chain variable region coding sequence.
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100.0%; Pred. No. 8.2e-203;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                     This cDNA sequence encodes the heavy chain variable region VH (AAWB5150) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line Arcc 12020. 11D10 was obtained by immunising naive mice with Mc-10 anti-HWFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol. Wt. mucin of human milk fait globule (HWFG). It induces an immunological response to HWFG in mice, rabbits, monkeys and patients with advanced HWFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polypurclectides are claimed. Also claimed are diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polypurclectides, including methods of treating HWFG-
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                                                                                                                               Monoclonal anti-idlotype antibody 11D10 - elicits against human milk fat globule disease associated especially breast cancer
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                                              Chatterjee M, Chatterjee SK,
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                                                                          /product= "Mouse 11D10 anti-idiotype antibody heavy chain
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CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                                                                                                                    HMFG;
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         CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                               Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                                                                                                                                                                                                Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA; 11D10; 3H1; HWFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                              Mouse 11D10 antibody heavy chain variable region coding sequence.
                                                                                                                 ACACCCCCACCGTCTATCCACTGGTCCCTGGAAGCTTGGG 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KENT ) UNIV KENTUCKY RES FOUND
                                                                                                                                                                                     AAL51274 standard; cDNA; 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2001; 2001US-0861294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002WO-US15840.
                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               breast tumor) in humans
                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                      ..459
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P-PSDB; AAO16293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2002;
                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                           20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2002
                                                                                                                                                                                                      AAL51274;
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                                                                           361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCTTATCTACACAGTCTGGGGCTGAGCTGGTGAGCTCTGGGGCCCTCAGTGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                       CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                         1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                              1 ATGGAATGCAGCTGGGTCTTTCTCTTCTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                            241 CAGAAGTTTAAGGGCCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                                                                                                       GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                  TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-idiotype monoclonal antibody 1A7 variable heavy chain, cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine; mouse; anti-idiotype; monoclonal antibody; MAD; 1A7; variable heavy chain; ganglioside 2; GD2; 14G2a; neuroblastoma; glycosphingolipid; human; neuroectodermal; tumour; glioma; lung; malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine; treatment; palliate; detection; diagnosis; recombinant production; purification; probe; primer; assay; amplification; gene therapy; ss.
                                                                                                                                    ó
                                                                                                  Length
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACCCCCACCGTCTATCCACTGGTCCCTGGAAGCTTGGG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pos:373..375, aa:Trp
                                                                                                                  8.2e-203
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                                                                                                DB
                                                                                             Score 461; D
Pred. No. 8.2
0; Mismatches
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                                                         Sequence 461 BP; 112 A; 121 C; 119
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Chatterjee M;

96US-0591196 95US-0372676

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Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection and treatment of cancers -
                                                                                                                                                                                                                                                                                                             Disclosure, Fig 2; 74pp; English.
                                                                                                                                                          Chatterjee SK,
                                                                                                                      (KENT ) UNIV KENTUCKY
                                                                                                                                                                                          WPI; 1999-619711/53.
                                                                                                                                                                                                            P-PSDB; AAY49210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                    16-JAN-1996;
                                                                                      17-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-1999
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                   02-NOV-1999
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                                                                                                                                                            Foon KA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes the murine anti-idiotype monoclonal antibody (MAb) 1A7 variable heavy chain. MAb 1A7 was raised against the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2. As the glycosphingolipid GD2 is expressed at high density by human neuroectodermal tumours, e.g. malignant melanoma, controlled to a clina, soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its cDNA can be used in a vaccine to treat or palliate such disease. They can also be used to reduce the risk of recurrence of a clinically detectable tumour, and detect an atti-GD2 Ab bound to a tumour cell.

MAb 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 Ab (humoral response) and CD2-specific cells (cellular response). It can be used to purify anti-GD2 (Ab1') or 14G2a (Ab1') detect anti-1A7 or anti-GD2 in a sample or measure the level of cellular anti-1A7 or anti-GD2 activity.

The CDNA can be used in expression systems for 1A7 produ., and in the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the prepn. of probes and primers to respectively assay for 1A7 cDNA, and amplify desired polynucleotides for use in gene therapy. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                           Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) – useful to treat or palliate a GD2-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAb 1A7 heavy chain variable region encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76; DB 17; I
Pred. No. 3.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.5%; Scor.
v 100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                        Chatterjee M, Chatterjee SK, Foon KA;
                                                                                                                                                                                                                                             polypeptide(s) – useful to treat odisease, e.g. melanoma and glioma
                                                                                                                                                                                                                                                                                               Claim 11; Fig 2; 141pp; English.
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                              960S-0591196.
950S-0372676.
960S-0591196.
                 95US-0372676
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                                                                                                    (KENT ) UNIV KENTUCKY
                                                                                                                                                                          WPI; 1996-354530/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                          P-PSDB; AAW03200
                              16-JAN-1996;
17-JAN-1995;
16-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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elicits an anti-GDZ (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti-GDZ immune response. The polypeptides can also be used for detecting or purifying anti-GDZ antibody. The products can be used for treating GDZ associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the CDNA encoding the heavy chain variable region of MAb 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACGACACC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a monoclonal antibody (MAb) designated 1A7, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy chain variable region; antibody 1A7; T cell response; melanoma; ganglioside GD2; CDR; complementarity determining region; carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                          Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                        Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 76; DB 20; 100.0%; Pred. No. 3.2e-25; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "No stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heavy chain variable region of MAb 1A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/product=
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/*tag=
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/*tag=
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The invention provides a method of treating of psoriasis by administering an antigen which has similar immunogenic properties to an antigen expressed on cells of psoriatic tissue so that an immunological response is elicited in the individual. The antigen stimulates the generation of anti-idiotype antibodies that neutralize the aberrant immune response causing the psoriasis. The method is used to treat psoriasis, especially chronic plaque, gluttate, pusque-type psoriasis or psoriatic arthritis. The compositions allow the individual's own immune system to act against psoriatic tissue. The present sequence represents a cDNA encoding the heavy chain variable region of monoclonal antibody 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCCAAAACGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein; intracellular immunization; gene therapy; single chain antibody; Fv; SFv; antibody engineering; resistance; cell immunity; HeLa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for conducting gene therapy - comprises using recombinant gene encoding antibody binding antigen associated with a disease; useful for providing cell immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 458 BP; 106 A; 132 C; 113 G; 107 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.5%; Score 76; DB 20; I 100.0%; Pred. No. 3.2e-25; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 23; 62pp; English
                                                                                                                                                                                        Disclosure; Fig 3; 48pp; English.
      (KENT ) UNIV KENTUCKY RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 76; Conservative
                                                                                                                                                 Treatment of psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sFv anti-rev sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-082039/11.
                                                                                    WPI; 1999-347407/29.
                                                                                                          P-PSDB; AAY21546.
                                             Chatterjee M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09503832-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-1994;
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30-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ81500
        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 TGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACGACACC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is the variable heavy chain region of monoclonal anti-idiotype antibody 1A7. The polypeptide encoded by this sequence has three CDRs (complementarity determining regions). When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The light chain variable region of the 1A7 antibody fAX28468) is also capable of eliciting an anti GD2 response in mammals. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 real and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours (e.g. melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma (including small cell lung cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Psoriasis; immunological response; anti-idiotype antibody; gluttate; chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis; monoclonal antibody; 1A7; ss.
                                                                                                                                                                                                                                                                                                           Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody 1A7 heavy chain variable region encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.5%; Score 76; DB 20; Length 458; larity 100.0%; Pred. No. 3.2e-25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                              Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                         Chatterjee M, Chatterjee SK,
                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig 2; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCACCGGTCTATCCA 441
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                                                                              96US-0752844.
95US-0372676.
96US-0591196.
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97US-0065774
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                                                                                                                                                              (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                   WPI; 1999-457600/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 76; Conserv
                                                                                                                                                                                                                                                                      P-PSDB; AAY28469
                                                                                                   17-JAN-1995;
16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jnidentified
                                         21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .7-NOV-1998;
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                                                                                  21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1998;
10-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX60630;
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Matches
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AAX60630 RESULT

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Gaps

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Length 458; Indels 425

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a single chain sFV anti-rev antibody constructed using variable domains of the heavy and light chains of a murine monoclonal antibody against (HIV-IIIB) rev (the parent artibody). This is incorporated into a viral vector where expression of the anti-rev gene causes inhibition of the rev function and so affects replication of the other viral (HIV). Rev is one of the sesential regulatory proteins of HIV, it binds to rev responsive element (RRE) and promotes the nuclear export, stabilisation and utilisation of the viral mRNA's containing RRE. A novel gene therapy method has been produced, where a recombinant (rec) gene is introduced into the cells of a mammal. The method is improved by using a rec gene encoding an antipedy (Ab) that is selectively specific for an intracellular (IC) antipody (Ab) that is selectively specific for an intracellular (IC) antipod a sociated with a disease. The method is used to prevent or halt the progress of a disease by IC immunisation. Specifically, the Ab can be used to inhibit the replication of a virus, such as human I-cell
                                                                                                                                                   ó
                                                                                                                                                                         Improved gene therapy using recombinant gene coding for an antibody – for intracellular immunisation against pathogens recognised by the antibody, esp. human immunodeficiency virus \rm HIV-1
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Gene therapy; antibody; immunisation; human immunodeficiency virus;
         The sequence given in AAQ81500 encodes an sFv anti-rev antibody consisting of the variable domains of the heavy and light chains of a mouse MAb against HIV-1 IIIB rev. The sFv specifically binds a highly conserved Rev domain. HeLa 14 cells expressing the SFv were resistant to all HIV-1 clinical isolates tested. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                     ö
                                                                                                                           Length 861;
                                                                                                                                                   Indels
                                                                                                  Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                             Single chain sFV anti-rev antibody encoding cDNA.
                                                                                                                                         4.4e-21;
                                                                                                                         DB 16;
                                                                                                                                  100.0%; Preu. ....
                                                                                                                          14.5%; Score 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                     HIV; human T-cell leukaemia virus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 54; 213pp; English.
                                                                                                                                                                                                                                                                                                                  AAT45347 standard; cDNA; 861 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1995; 95US-0447610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US07393
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                      Best_Local Similarity 100.0
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pomerantz RJ;
                                                                                                                                                                                                                           TCTATCC 440
                                                                                                                                                                                                                                                     TCTATCC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-020948/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                   08-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-1996
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                                                                                                                                                                                                                                                   852
                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                           RESULT 9
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The present sequence encodes a fusion of an anti-CD20 single chain antibody and streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs to expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively inked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence and a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.
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                                                                                                                                                                                                                                                                                                                                                                     374 ACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACGACACCCCCACCCG 433
                                                                                                                                                                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
leukaemia virus or especially HIV-1, or of other pathogens, e.g. bacteria, fungi. The method provides immunity before or after the development of the disease and can be used to control the severity the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding a fusion of a single chain antibody and streptavidin.
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                                                                                                                                                                                                                                        Length 861;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                            Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour cell; cancer; adenocarcinoma;
                                                                                                                                                                                                                                  Match 14.5%; Score 67; DB 18; I Local Similarity 100.0%; Pred. No. 4.4e-21; les 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schultz JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC86590 standard; DNA; 765 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hematological malignancy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137900.
99US-0168976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces avidinii.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTATCC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               852 TCTATCC 858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC86590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434
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                                                                                                                                                                                                                                                                                                            Matches
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Sequence 765 BP; 170 A; 201 C; 231 G; 163 T; 0 other;

XX SO

DB 22; L 7.5e-18;

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                                                                                                                                                                                                              145 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGCCTGGAATGGATTGGA 204
                                                                                                                                                                                                                                 is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                                                                                                                              Gaps
                                                                                                                                      Length 765;
                                                                                                                                                                          Indels
                                                                                             Sequence 765 BP; 169 A; .201 C; 230 G; 165 T; 0 other;
                                                                                                                                13.0%; Score 60; DB 22; I Similarity 100.0%; Pred. No. 7.5e-18; 0; Conservative 0; Mismatches 0;
                                                                                                                                                                        90;
                                                                                                                                  Query Match
                                                                                                                                                      Local
                                                                                                                                                                      Matches
 8888888
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DNA encoding a fusion of a single chain antibody and streptavidin. Streptavidin; tumour cell; cancer; adenocarcinoma; AAC86591 standard; DNA; 765 BP. hematological malignancy; ss 99US-0137900. 99US-0168976. 05-JUN-2000; 2000WO-US15595. (first entry) Streptomyces avidinii. Unidentified. (NEOR-) NEORX CORP. WO200075333-A1 07-JUN-1999; 03-DEC-1999; 02-APR-2001 14-DEC-2000 Synthetic. AAC86591; RESULT 11 AAC8659

The present sequence encodes a fusion of an anti-CD20 single chain antibody and streptavidin. The fusion protein is expressed using vectors of the invention. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively in a connoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour constructs of the protein and protein and process. e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host. New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with Example 5; Page 95; 100pp; English. cancer, e.g. adenocarcinomas -WPI; 2001-091213/10.

Sequence 1239 BP; 270 A; 392 C; 356 G; 221 T; 0 other;

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                                                                                                   145 ACCAGTTACAATATGCACTGGGTAAAGCAGACACTGGACAGGGCCTGGAATGGATTGGA 204
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                                                                                                                                                                                                                                                                                                       DNA encoding a fusion of anti-CD20 single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  these are useful as tools for medical diagnostics and therapeutic
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                        tumour cell; cancer; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin Y,
     13.0%; Scur.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                         malignancy; ss.
                                                                                                                                                                                                     AAC86563 standard; DNA; 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2000; 2000WO-US15595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0137900
99US-0168976
                                                                                                                                                                                                                                                                     02-APR-2001 (first entry)
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avidinii.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-091213/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200075333-A1.
                                                                                                                                                                                                                                                                                                                                        Streptavidin;
                                                                                                                                                                                                                                                                                                                                                       hematological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                      AAC86563;
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Reno JM;

Sanderson JA,

Lin Y,

Schultz JE,

Graves SS,

Goshorn SC,

C; 388 G; 228 T; 0 other;

Sequence 1280 BP; 267 A; 397

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                                                             The present sequence encodes a fusion of an anti-CD20 single chain antibody (B9E9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                                                                                                                                                                                                                       Anti-CD20 single chain antibody/streptavidin fusion protein cassette.
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                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "anti-CD20 scFv and streptavidin fusion"
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      Length 1239;
                                  Indels
                                                                                                                                                                                                                                                                                                         tumour cell; cancer; adenocarcinoma;
                  .2e-18;
DB 22;
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13.0%; Score 60; DB 100.0%; Pred. No. 7:2 Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Fig 11C; 100pp; English.
                                                                                                                                                                               BP
                                                                                                                                                                              AAC86564 standard; DNA; 1280
                                                                                                                                                                                                                                                                                                                         hematological malignancy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, e.g. adenocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0137900.
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                                                                                                                                                                                                                                           (first entry)
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     3..1274
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graves SS,
                                                                                                                                                                                                                                                                                                                                                                    Streptomyces avidinii. Homo sapiens.
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P-PSDB; AAB30695.
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                   Similarity
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                                                                                                                                                                                                                                                                                                       Streptavidin;
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 Query Match
Best Local Simi
Matches 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a synthetic CD20-specific chimeric receptor. The specification describes CD-20 specific redirected T cells which express and bear on the cell surface membrane a CD20-chimeric receptor comprising an intracellular signalling domain, a transmembrane domain and an extracellular domain, the extracellular domain comprising a CD20-specific receptor. The genetically engineered CD20-specific redirected T cells are useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a human patient having previously undergone myeoablative chemotherapy and stem cell rescue. The genetically, engineered CD20-specific redirected T cells are also useful for abrogating an untoward B cell function, such
                                            Gaps
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                                                                                                                                                                                                                                                                                                                         CD20-specific receptor; CD-20 specific redirected T cell; leukemia; CD20+ malignancy; non-Hodgkin's lymphoma; myeoablative chemotherapy; stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetically engineered CD20-specific redirected T cells useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, and autoimmune disease
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          Length 1280;
                                            Indels
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          Score 60; DB 22; Pred. No. 7.2e-18;
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13.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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27..1928
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     Ouery Match
Best Local Similarity 100.0
Matches 60; Conservative
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P-PSDB; AAY84965.
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Self-protecting chimeric polypeptide comprising biologically active sequence and single-chain antibody sequence - has resistance to e.g. disrupting temperature, presence of proteolytic enzymes, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       denaturing temperatures or pH conditions, protectlytic enzymes, oxidising agents or alcohol. The regions of the chimeric polypeptide interact to form a structure analogous to an antibody-antigen complex. A L-asparaginase-SCA fusion protein of the above type has better trypsin resistance than free
                                                                                                                                                                                                  cDNA for Ig heavy chain variable region of anti-asparaginase MAb.
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asparaginase II; monoclonal antibody; MAb;
recombinant chimeric polypeptide; ss.
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                                                                                               AAT96345 standard; cDNA; 360
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92US-0938505.
95US-0447422.
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Search completed: August 30, 2003, 19:57:04

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Job time : 203.688 secs

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Sequence 91, Applisequence 17, Applisequence 17, Applisequence 17, Applisequence 22, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 21, Applisequence 31, Applisequence 31, Applisequence 380, Applisequence 381, Applisequence 381, Applisequence 381, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 2, Applisequence 4, Applisequence 2, Applisequence 4, Applisequence 2, Applisequence 4, Applisequence 2, Applisequence 2, Applisequence 4, Applisequence 4, Applisequence 4, Applisequence 6, Applisequ

Seguence 17

Sequence 304, 1 Sequence 239, 1 Sequence 273, 1 Sequence 351, 1

Sequence 381,

US-10-207-655-273 US-10-207-655-351 US-10-207-655-381

ALIGNMENTS

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6286.388 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/DS07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_DUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_DUB.seq:*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_DUB.seq:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-153-401-3
US-10-244-821-44
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                                                                                                                                                                                                                                                                                                                                                                                                         1533700 seqs, 1147125425 residues
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seq length: 200000000
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             Sequence 3, Application US/09861294;
Patent No. US20020098190A1;
GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: WENNEY A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HARG AND CEA ANTIGENS;
FILE REFERENCE: 304142000620;
CURRENT APPLICATION NUMBER: US/09/861,294
CURRENT FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR APPLICATION NUMBER: 09/096,244

PRIOR APPLICATION NUMBER: 09/096,244

NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 6.9e-236;
Matches 461; Conservative 0; Mismatches 0;
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US-09-861-294-3
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US-09-861-294-3
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US-10-244-821-45 US-10-013-173-44 US-10-013-173-45 US-10-150-762-45 US-10-150-762-45 US-10-150-762-45 US-10-013-15-762-15 US-10-013-15-762-5

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GENERAL INFORMATION:
APPLICANT: FOOD, Kenneth A.
APPLICANT: CHATTERJEE, Malaya
APPLICANT: CHATTERJEE, Malaya
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501
CURRENT APPLICATION NUMBER: US/09/990,205
CURRENT PILING DATE: 2001-11-20
PRIOR PILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NOS: 5
   241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                                                   CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
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; Sequence 3, Application US/10153401
; Publication No. US20030114398A1
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US-09-990-205-3
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GENERAL LINEVERFILE
APPLICANT: MAIAYA CHATTERIEE
APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREI
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANT:
FILE REFERENCE: 30414200620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT FILING DATE: 2003-02-13
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 461; DB 12; Best Local Similarity 100.0%; Pred. No. 6.9e-236; Matches 461; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10367506 Publication No. US20030152575A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: mat_peptide
LOCATION: (58)...(461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: sig_peptide LOCATION: (1)...(57)
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LOCATION: (1)...(461)
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145 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGCCTGGAATGGATTGGA 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin OTHER INFORMATION: fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: C2B8 single chain antibody-genomic Streptavidin; OTHER INFORMATION: fusion construct
US-10-244-821-45
                      APPLICANT: Schultz, Joanne Blaine
APPLICANT: Schultz, Joanne Blaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT PILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Blaine
APPLICANT: Lin, Yukan
APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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. 8.8e-22;
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100.0%; Pred. No. 8.8e-22;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 13.0%; Score 60; DB Best Local Similarity 100.0%; Pred. No. 8.8 Matches 60; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILLING DATE: 2002-09-16
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goshorn, Stephen Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-244-821-45
; Sequence 45, Application US/10244821
; Publication No. US20030143233A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
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LENGTH: 765
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LENGTH: 765
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                                          FOOD, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: CUNROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:

NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
                                                                                                                                          NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                       ZIP: 24304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARATERISTICS:
LENGTH: 458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                             CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 706141
                                                                                                                                                                                                                                                                                               COUNTRY: USA
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LOCATION:
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Sequence 44, Application US/10013173; Publication No. US20030095977A1; GENERAL INFORMATION:

RESULT 7 : US-10-013-173-44

Sequence 44, Application US/10244821 Publication No. US20030143233A1 GENERAL INFORMATION: APPLICANT: Goshorn, Stephen Charles

US-10-244-821-44

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SEQ ID NO 45
LENGTH: 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin; OTHER INFORMATION: fusion construct
US-10-013-173-44
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Randerson, James A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBACE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 765
TYPE: NUMBER: NO.
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APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Blaine
APPLICANT: Sanderson, James A.
APPLICANT: Reno, John M.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FRASEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.0%; Score 60; DB 14; Length 765; 100.0%; Pred. No. 8.8e-22; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 765;
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8.8e-22;
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Publication No. US20030103948A1
GENERAL INFORMATION:
APPLICANT: Goshorn, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-013-173-45
; Sequence 45, Application US/10013173
; Publication No. US20030095977A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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145 ACCAGTTACAATATGCACTGGGTAAAGCAGACACCTGGACAGGGCCTGGAATGGATTGGA 204
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US-10-150-762-45
                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin ; OTHER INFORMATION: fusion construct US-10-150-762-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goshorn, Stephen C.
APPLICANT: Graves, Scott S.
APPLICANT: Schultz, Joanne E.
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: RENO, STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS FILE REFERENCE: 690022.54762
                                                                                                                             EXPRESSED GENE FUSIONS AND
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Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 14;
Pred. No. 8.8e-22;
                                        APPLICANT: Sanderson, James A.
APPLICANT: Reno, Jonh M.
APPLICANT: Reno, Jonh M.
APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C2
CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: AND 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.0%; Score 60; DB ilarity 100.0%; Pred. No. 8.6 Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/10150762; Publication No. US20030103948A1; GENERAL INFORMATION:
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Schultz, Joanne E.
Lin, Yukang
Sanderson, James A.
Reno, Jonh M.
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 60; Conserva
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us-08-836-455-3.oli.rnpb

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Lin, Yukang
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LENGTH: 1239
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                    APPLICANT:
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APPLICANT:
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APPLICANT:
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US/10/013
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US/10/244
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                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion US-10-244-821-5
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                                                                    APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
FAPPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 69012.5473
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1239
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TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.0%; Score 60; DB 12; Length 12
Best Local Similarity 100.0%; Pred. No. 8.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels
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8.7e-22;
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1239
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CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10013173
Publication No. US20030095977A1
GENERAL INFORMATION:
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Reno, John M.
Goshorn, Stephen Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10150762
Publication No. US20030103948a1
GENERAL INFORMATION:
APPLICANT: General, Stephen C.
APPLICANT: Graves, Scott S.
                                         Schultz, Joanne Elaine
Lin, Yukang
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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US-10-150-762-5
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OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion constru
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                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion US-10-150-762-5
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100.0%; Pred. No. 8.7e-22;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 60; DB 14; Length 1239; 100.0%; Pred. No. 8.7e-22; Live 0; Mismatches 0; Indels
APPLICANT: Sanderson, James A.
APPLICANT: Reno, John M.
APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 690022.547C2
CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT FILIG DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
FILLE REFERENCE: 690022.547C3
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/244,821 CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goshorn, Stephen Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10013173
Publication No. US20030095977A1
GENERAL INFORMATION:
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schultz, Joanne Elaine
Lin, Yukang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Matches 60; Conserve
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Best Local Similarity
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TYPE: DNA ORGANISM: Artificial Sequence PERTURE: PEATURE: 7 PEATURE: 7 OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion construct US/10/013,173-7
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                                                                     TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPERENCE: 690022.5470.

CURRENT APPLICATION NUMBER: US/10/013,173

CURRENT FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 69

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 1280
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Lin, Yukang
Sanderson, James A.
Reno, Jonh M.
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AK002875

K0748C01-K0746F08-

K0718G11

K0747G08-K0725B11-

K0729C06-K0724G04-

K0724C11 K0727C05 K0746G01

Word size :

Database

Searched:

Sednence:

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AGENCOURT BY703373

BF143948 BF583109 BQ929209 BY703373

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Run on:

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BE369087 676 bp mRNA linear EST 21-JUL-2000 601221765F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3590320 5',
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MH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can hfound through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM8758 row: b column: 17

High quality sequence stop: 580.
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                                                                                CA579143
CA580198
CA580106
CA578106
CA570834
CA570834
CA570854
CA570864
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CA57868
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BG966605
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BE915586
                           BF143948
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Mus musculus
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BE369087
BE369087.1 GI:9314450
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5540
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774
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BE369087
BE369087 601221765
BE371136 601218628
BF137216 601784466
BI455668 603173862
                                                                        (without alignments)
6984.224 Million cell updates/sec
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1 ATGGAÀTGCAGCTGGGTCTT......CTGGTCCCTGGAAGCTTGGG 461
                                                            August 30, 2003, 18:52:40 ; Search time 1604.24 Seconds
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                    22781392 seqs, 12152238056 residues
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BE371136
BF137216
BI455668

    nucleic search, using sw model

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Maximum DB seq length: 2000000000
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BG966605 602834440 BG966397 602832896 BG966355 602832843 BQ952276 AGENCOURT

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Result No.

K0518C07-K0741H07-602099628

NISC_ff15 601221857

BQ266826 BE367979

602828443 602096117

BF579001 BG963642 BF182141 BG968682 BE915586

601668633 602829160

BF168514 BG965088 BG966840

N

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FEATURES

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9253 row: c column: 17
High quality sequence stop: 697.
Location/Qualifiers
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/tlssue_type="tumor, metastatic to mammary"
/lab.host="DH0B"
/clone_lib="NCI_CGAP_Lu30"
/clone_lib="NCI_CG
                                                                                                                                                                                                                                                                                                                       BF137216 802 bp mRNA linear EST 24-OCT-2000 601784466F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4012360 5',
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.6e-14;
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Best Local Similarity 100.0%; Pred. No. 2.6
Matches 49; Conservative 0; Mismatches
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/organism="Mus musculus"
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BF137216.1 GI:10976256
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                                                                                    /mol_type="mush" mush.miscurus
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"
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601218628F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:3587742 5',
mRNA sequence.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone-"IMAGE:3587742"
/fissue_Lype-"spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMG751 row: g column: 07
High quality sequence stop: 552.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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100.0%; Pred. No. 1.5
:ive 0; Mismatches
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Contact: Robert Strausberg, Ph.D.
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/mol_type="mRNA"
/strain="CZECH II"

    .676
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Location/Qualifiers
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Mus musculus
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Best Local Similarity 100.C
Matches 59; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

DEFINITION

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RESULT 2 BE371136

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BASE COUNT ORIGIN

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BASE COUNT ORIGIN

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organism="Mus musculus"
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/cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: capabbs-remail.nih.gov

Email: capabbs-remant: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI1639 row: 1 column: 16
High quality sequence stop: 780.
Location/Qualifiers
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NIH-WGC http://mgc.ncl.nih.gov/.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arraped by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM1181 row: h column: 03
High quality sequence stop: 719.
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100.0%; Pred. No. 2.8e-14;
ive 0; Mismatches 0;
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/strain="C57BL/6J"
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                       bases 1 to 861)
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo II. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 711.
Location/Qualifiers
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_l: Sall;
Site_2: Notl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: glibert Smith, NIH"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1012)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/tisbe="taxon:netastatic to mammary"
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100.0%; Pred. No. 2.9e-14;
tive 0; Mismatches 0;
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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Query Match 10.4
Best Local Similarity 100.
Matches 48; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM9244 row: o column: 22

High quality sequence stop: 671.

Location/Qualifiers

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MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
a 186 c 181 g 168 t
                                                                                                                                                            BF136279 718 bp mRNA 11near EST 24-OCT-2000 601780988F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009197 5',
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11 H-MG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 862)
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BF143948
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Site_2: Sali; transgenic model WNT-1, expression driven by MMTV-IIR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed unidirectionally. Primer: Oligo dT. Library constructed samples: Gilbert Smith, NIH"

13 a 236 c 236 g 176 t lothers
                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
tolumn: 23
High quality sequence stop: 671.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9797 row: p column: 04
High quality sequence stop: 656.
Location/Qualifiers
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs r@mail.nih.gov

Email: crourement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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100.0%; Pred. No. 9.5e-14;
ive 0; Mismatches 0; Indels

    913
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    /mol_type="mRNA"
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                                                              Unpublished
Contact: Robert Strausberg, Ph.D.
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BF583109.1 GI:11656827
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Average insert size 1.6 kb. Constructed by Life
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
261 c 236 g 211 t 2 others
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rlate: LLAMA4019 row: d column: 24
High quality sequence sitop: 546.
Location/Qualifiers
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1. 933
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo df.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 261 c 250 g 219 t
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                                   /lab_host="DH10B (T1 phage-resistant)"
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ilarity 100.0%; Pred. No. 3.3e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                      Score 47; DB 10; I
Pred. No. 3.2e-13;
                                                                                                                                                                                                       10.2%; Scor.
100.0%; Pred. No. 3...
0; Mismatches
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                /clone-"IMAGE:4218099"
/db_xref="taxon:10090"
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/strain="FVB/N"
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RESULT 11

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Agazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yaqi,K., Tomatu,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Paldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Gojobori,T., Balake,J.A., Bradt.B., Kanapin,A., Matsuda,H., Batalov,S., Batse,J.K., Baratelli,R., Hill,D.P., Bult,C., Hume,D.A., Godzik,A., Brazer,K.S., Gasterlen,D., Brusic,V., Chothia,C., Corbani, J.E., Cousins,S., Dalla,E., Dragani,T.A., Hrokawa,N., Jackson,I.J., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanaj,A., Kawaji,H., Kawaswa,Y., Kedzierski,R.N., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lehnard,B., Lyons, P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pecole,G., Petrovsky,N., Pillai,R., Pontlus,J.G., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Rayasina,K., Sultana,R., Schoelder,C., Wang,Y., Watana,R., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wanner,L., Wahlestedt,C., Wang,Y., Watanada,K., Shiraki,T., Wahlestedt,C., Wang,Y., Arakawa,T., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Yang,I., Waninada,S., Ravasi,I., Mayazaki,A., Sakai,R., Kawai,J., Alzawa,K., Arakawa,T., Kayawa,T., Ka
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10.(11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
BY703373 RIKEN full-length enriched, adult male kidney Mus musculus CDNA clone 0610041A01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITE GENOME-TESSESCITIKEN.90.jp,
URL: http://genome.gsc.riken.90.jp,
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
A.S., Hashlzume,W. Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Now,S., Miyazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,M., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct
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                                                                                                                                                                                                                                                                                                                                                                  /issue_type="kidney"
/dev_stage="adult"
/dev_stage=
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610041A01 product:immunoglobulin heavy chain 6 (Meavy chain of 1gM), full insert sequence.

AK002875.1 GI:12833178
HTC; CAP tranner
Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                         Please visit our web site (http://genome.gsc.riken.go.jp) for
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                             /clone="0610041A01"
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                                                        prepare mouse tissues
                                                                                                                                                                                                                                                                                                                                                  /sex="male"
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                                                                                                                                                     FEATURES
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Yendamoto, R., Matsumoto, R., Sakaquin, S., Kaenia, P., Matsunta, S., Wathhiki, W., Yoneda, Y., Ishikawa, T., Cawa, X., Taraka, T., Wathiki, W., Yoneda, Y., Ishikawa, T., Cawa, X., Taraka, T., Watsunta, S., Kawai, J., Okazak, Y., Watsunta, S., Kawai, J., Shingawa, A., Shibata, K., Yooni, M., Adohi, J., Yahii, Y., Azakawa, T., Hara, A., Fukuishi, Y., Konno, H., Adadhi, J., Yahii, Y., Azakawa, T., Hara, A., Fukuishi, Y., Konno, H., Adadhi, J., Yahii, Y., Azakawa, T., Hara, A., Fukuishi, Y., Okazak, M., Salto, Y., Yakai, Y., Ya
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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ORIGIN
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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                                                                                                                   FEATURES
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                                                                                                                                                                                                                                                                                                              53. .1333
Anote-"unnamed protein product; immunoglobulin heavy chain 6 (heavy chain of Igyl) (WGD|MGT:96448, GB|AK008342, evidence: BLASTN, 100%, match=137)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uy34h12.yl NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:3661511 5/
similar to SW:HV02_MOUSE P01746 IG HEAVY CHAIN V REGION 93G7
PRECURSOR. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="Bab22422.1"
/db_xref="G1:12833179"
/db_xref="G1:19646#
/dc_xref="G1:9646#
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LSSLTSEDSAVYFCARSDYYGPYAMDYWGQGTSVTVSSESARNPTIYPLTLPRALSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMSSQLTLPAVECPE
GESVKCSVQHDSNAVQELDVKCSGPPPPCPPCPPSCHPSLSLQRPALEDLLLGSDASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTLNGLRNPEGAVFTWEPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFK
CTVTHPESDTLTGTIAKITVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNDKEVL
VRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAELWKQGDQYSCMVGHEA
                                                                                                                                                                                                                                        /tissue_type="kidney"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 406)
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 406)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.2%; Score 47; DB 11; 100.0%; Pred. No. 3.8e-13; Live 0; Mismatches 0;
                                                                                                                                                  /db_xref="FANTOM_DB:0610041A01"
/db_xref="MGI:1907162"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 308 t
                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                       /clone="0610041A01"
                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 g
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/note="putative"
1384
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BF016722.1 GI:10748054
                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                      /sex="male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 47; Conservative
                                                                          .1384
                                                                                                                                                                                                                                                                                                                                                                                              putative
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Unpublished
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COMMENT
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BF016722
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KEYWORDS
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                                                     FEATURES
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/note=_organ: lug; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI: transgenic model MNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo MT Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" a 102 c 98 g 97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K0733D01-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
CDNA Library (Long) Mus musculus CDNA clone NIA:K0733D01
IMAGE:30076740 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 429) to 429. Pio 0. Y., Rargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H. Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) cDNA Library (Long) Other_ESTS: K0733D01-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="niaEST:K0733D01-5N"
Adb_xxref="taxon:10090"
/clone="N1A:K0733D01 INAGE:30076740"
/tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Genetics

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

Mational Institute on Aging/National Institutes of Health

Mational Institute on Aging/National Institutes of Health

Batis Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

Plate: K0733 row: D column: 01

Seq primer: M13 Reverse

High quality sequence stop: 429

POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3661511"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 43; DB 10; I 100.0%; Pred. No. 3.1e-11; rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Lu30"
                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
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/strain="C57BL/6NCr"
                                                                                 MGI:1422279
Seg primer: -40RP from Gibco.
                                                                                                                                             Location/Qualifiers
1..406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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0.9 ug of total RNA, treated with 74 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/Chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/Chloroform and Centricon 100. The CDNAs were digested with Sal1 and NoII enzymes and cloned into Sal1/NoII site of pSPORTI plasmid vector. The DHIUB E. Coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K0748C01-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
CDNA Library (Long) Mus musculus CDNA clone NIA:K0748C01
IMAGE:30078168 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
/clone_lib="NIA Mouse Hematopoietic Stem Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.1%; Score 42; DB 14; Length 429; Best Local Similarity 100.0%; Pred. No. 1e-10; Matches 42; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG 394
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/mol_type="mRNA"
/strain="C57BL/6NCr"
/db_xref="niaEST:K0748C01-5N"
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Plate: K0748 row: C column: 01
Seq primer: M13 Reverse
High quality sequence stop: 451
POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by Yulan Piao (NIA)."
112 c 108 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Mus musculus
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ORIGIN
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CA580198
LOCUS
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COMMENT
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KEYWORDS
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tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-
                                                                                                                                                                                                                                                                                    mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."
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                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                 Length 451;
'clone-"NIA: K0748C01 IMAGE: 30078168"
                        /dev_stage="Age approx.10 weeks old"
/lab host="DH10m"
                                                                                                                                                                                                                                                                                                                                                9.1%; Score 42; DB 14; I
100.0%; Pred. No. 1.1e-10;
tive 0; Mismatches 0;
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Matches 42; Conservative
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Search completed: August 30, 2003, 21:57:09 Job time : 1606.24 secs

371 TGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG 412

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

5777422 Total number of hits satisfying chosen parameters: 2888711 seqs, 20454813386 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		AR164506 Sequence RD085738 Methods o	snm sn	sn.	AII/8830 Mus Muscu BC002121 Mus muscu	U39899 Mus musculu	BD092129 Diagnosti D14625 Mus musculu	~ (e re	105921 Sequence 37	υo	M17953 Mouse Ig re	E08434 cDNA encodi	U49832 Synthetic s E35543 Transgenic	AB050071 Mus muscu	BDU218/6 Humanized X65773 M.musculus	E33134 Humanized a	A22261 M.musculus A77138 Sequence 6	U39900 Mus musculu	AJSSS622 Mus muscu BC018280 Mus muscu	A78881 Sequence 1	AR029102 Sequence	BC019489 Mus muscu	A23165 Artificial L02346 Mus musculu	M24785 Mouse anti-	AF466769 Mus muscu	AJ416332 Mus muscut	BC018315 Mus muscu	X79907 M.musculus	164458 Sequence 23	BC028249 Mus muscu AJ012555 Mus muscu		linear PAT 17-OCT-2001					G-associated tumors using
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Mus musculus immunoglobulin heavy chain mRNA, partial cds.
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Tripathi, P. K., Oli, H., Bhattacharya-Chatterjee, M., Ceriani, R.L., Foon, K.A. and Chatterjee, S.K.
Construction and characterization of a chimeric fusion protein consisting of an anti-idiotype antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF
Hybridoma 18 (2), 193-202 (1999)
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Mismatches 0;
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1. 461
/organism="unidentified"
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/do_type="genomic DNA"
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Chatterjee, S.K. and Tripathi, P.K.
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Patent: JP 2001523269-A 2 20-NOV-2001;
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PN JP 2001523269-A/2
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PN JP 2001523269-A/2
PD 20-NOV-2001
PF 12-JUN-1998 JP 1999503252
PR 13-JUN-1997 US 60/049540,11-JUN-1998 US
MALAYA CHATTERJEE, KENNETH A FOON
PC ACIR39/395, AGIR39/39/PC07R16/42
CC Strandedness: Single;
CC Topology: Linear;
CC Methods of delaying development of HMFG-ass
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GYTLTSYNMIWVKOTPGGGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mol. Immunol. 19 (2), 257-266 (1982)
6178956
                                                                             /note="anti-idiotype antibody 11D10; mimics a breas
cancer-associated antigen, human fat globule (HMFG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 мысолово 471 bp mRNA linear ROD 02-
Mus musculus VH9H8 mRNA for anti-A/U antibody, partial cds.
AB050080
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                                                                                                                   /product="immunoglobulin heavy chain"
/protein_id="AAK55119.1"
/db_xref="G1:14164545"
                                                                                                                                                                                                                                         Score 409.4; DB 10;
Pred. No. 8.5e-129;
0; Mismatches 1;
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anti-dsRNA (A/U) Ab VH region VH9H8
              musculus"
                                                    /db_xref="taxon:10090"

    >411
    note="anti-idiotype"

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Mus musculus
            /organism="Mus mu
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                         tch 88.8%;
al Similarity 99.8%;
410; Conservative
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/translation="MGWTGVFLILLSITTGVHSQAYLQQSGAELVRSGASVKMSCKAS

GYTFTSYNMHWYRQPEQGEBNIGYIFLNAGTNYNQKFKGKATLTADTSSSTAYMQIS

SITSEDSAVYFCARESPENFFYWGQGTLVTVSAAKTTAQPVYPLAPGSL"

126 11 9 110 t
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Mus musculus clone 13G10 antiporphyrin immunoglobulin G heavy chain variable region mRNA, partial cds.
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Direct Submission
Submitted (17-007-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; Minami 2-2, Ogata, Akita
PRE: 181-185-45-2026(ex.400),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGAATGCAGCTGGGTCTTTCTCTTCTTCTTCTACAATAACTACAGGTGTCCACTCCCAG
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Pred. No. 3.6e-110;
0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="anti-A/U antibody"
/protein_id="BAB87192.1"
/db_xref="GI:19909936"
                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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1. 471
                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
Published Only in Database (2002) (bases 1 to 471)
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                    /gene="VH9H8"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.0%;
88.4%;
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11. .>469
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/protein_id="AAO20092.1"
/db_xref="G1:27763666"
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GYTFTSYNMHWVRQPEGGGEWIGVIYPGNGDTSYSOKFKGKATLTAAKSSSTAYMQL
SSLTSEDSAVYYCSRGGAGIMAYWGQGTSVTVSSAKTTPPSVYPLARD
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                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                         8 .>457
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                                                            1 (bases 1 to 457)
Sari,M.-A., Quilez,R. and Mahy,J.-P.
Antiorho-carboxy-substituted tetraarylporphyrin antibodies Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                         rue des Saints-Peres, Paris 75006, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 353.6; DB 10, Pred. No. 1.3e-109;
                                                                                                                         2 (bases 1 to 457)
Sari,M.-A., Quilez,R. and Mahy,J.-P.
Sariect Submission
Submitted (12-NOV-2002) UMR8601-CNRS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                     /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                         122 g
                          Mus musculus (house mouse)
AY178830.1 GI:27763665
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88.4%;
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MARINETIME MASS AND SECURITION HEADY CHAIR 4 (SETUM 1967), MRNA (CONNACCESSION ECOURTY)

MARINETIME MASS AND MASS AND MASS AND SECURITION HILLIANS (CONNACCESSION ECOURT) 1 (1112035108)

MASS AND MAS
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/translation="MENTWVILFLLSVTEGVHSQVOLQQSGAELVRPGSSVKISCKAS GYAFSGYWINWVKQRPGGGLEWIGQIYPGDGDTDYNGKFKGKATLTADKSSSTAYMQL SSLTSEDSAVYFCARGYDEVDYYFAMDYWGGGTSVTVSSAKTTPPSVYPLAFVCGDKL G"
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                                          Antibodies specific for the antigenic domain 1 of glycoprotein B (gpUL55) of human cytomegalovirus bind to different substructures Virology 216 (1), 133-145 (1996) 96187797 8614980
                                                                                                                                                                2 (bases 1 to 483)
Schoppel.K.
Direct Submission
Submitted (02-NOV-1995) Michael Mach, Institute of Virology,
University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen,
Schoppel, K., Hassfurther, E., Britt, W., Ohlin, M., Borrebaeck, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human Cytomegalovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oŧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 328.2; DB 10;
Pred. No. 6.9e-101;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="ant1-glycoprotein-B
immunoglobulin Vh chain"
/protein_id="AAB26552.1"
/db_xref="G1:1680667"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                               1. .483
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="Balb/c"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 bp
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .>483
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.2%;
Best Local Similarity 83.8%;
Matches 388; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 c
                                                                                                                                                                                                                                                                                                                                  .483
                           Mach, M.
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                                                                                                                                                                                                                                                                                             Germany
                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                                                                                                                                                                          source
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ORIGIN
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PUBMED
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BD092129
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT 180
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Mus musculus
Busaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae, Murinae; Mus-
1 (bases 1 to 483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 AGACAGGCCTTGAGTGGATTGGAGAGATTTATCCTGGAAGTGGTAACACTTACTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACAGGTGTCCACTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 337.8; DB 10; Length 1542;
Pred. No. 4.2e-104;
); Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACCCCCATCTGTCTATCCACTGGCCCCTGGA 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325
                                                                                                                                                             /product="Igh-4 protein"
/protein_id="AAH02121.1"
/db_xref="G1:12805309"
/db_xref="LocusID:16017"
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/note="synonym: IgG1"
/db_xref="LocusID:16017"
                                                                                       /db_xref="MGI:96446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 g
                                                                                                                   33. .1418
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.3%;
Best Local Similarity 84.1%;
Matches 381; Conservative
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ORIGIN
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/product="immunoglobulin gamma-3 heavy chain precursor"
/product="immunoglobulin gamma-3 heavy chain precursor"
/protein_id="BAA03476.1"
/db_xref="fg11304160"
/translation="MEMSQTVIPLESVTAGVHSQVOLQQSGAELVRPGTSVKMSCKAA
/translation="MEMSQTVIPLESVTAGVHSQVOLQQSGATTARATADTSSSTAYMQL
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SSITSBAITYCARENGGGYYAMOYGALSSGVRTVSSATTARATADTSSSTAYMPSG
SYTCONVAHPASKTELIKTERRIPKBSTPPGGSSCPPGNILGGFSVFIPPRKDALMI
SIJPKYTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTOPREAQYNSTFRVVSALPIQHQ
DWMRGKEFKCKVNNKALDAPIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSITCLV
TNFFSEAISVEWERKGELEQDYKNTPPILDSDGTYFLYSKLTVDTDSWLQGEIFTCSV
VHEALHNHHTQKNLSRSPGR"
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1514)
Takahashi, S., Itoh, J., Nose, M., Ono, M., Yamamoto, T. and Kyogoku, M. Cloning and cDNA sequence analysis of nephritogenic monoclonal antibodies derived from an MRL/Ipr lupus mouse Mol. Immunol. 30 (2), 177-182 (1993)
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                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-MAR-1993) Masato Nose, Tohoku University School of
Submitted (10-MAR-1993) Masato Nose, Tohoku University School of
Medicine, Dept. of Pathology: 2-1 Seiryo-cho Aoba-ku, Sendai,
Miyagi 980, Japan (E-mail:d22181@cctu.cc.tohoku.ac.jp,
Tel:81-22-273-9042, Fax:81-22-234-1986)
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1446. .1544
1514. .1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 .1445
/note="precursor of C and V-D-J regions from 7B6.8"
                                                                                                                                                                                                                               Ono,M., Yamamoto,T., Kyogoku,M. and Nose,M.
Sequence analysis of the germ-line VH gene corresponding to nephritogenic antibody in MRL/lpr lupus mice
Clin. Exp. Immunol. 100 (2), 284-290 (1995)
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/product="lmmunoglobulin gamma-3 heavy chain"
90. .452
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1.1e-99;
ches 70; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="immunoglobulin V-D-J region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="pBluescript KS(+)"
/dev_stage="adult"
1. .32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="mRNA"
/strain="MRL/MpJ-lpr/lpr"
/db_xref="taxon:10090"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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83.0%; Pred. No. 1.
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                    musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                    musculus
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SOURCE
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                                                                                                                  Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Matheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E 1 (bases 1 to 409)
Shitara, K. and Shibuya, M. Diagnostic and therapeutic agents for the diseases related monocytes and macrophages
AL RYOWA HAKKO KOGYO CO LTD, KENYA SHITARA, MASABUMI SHIBUYA
S Mus musculus (mouse)
PP WO 0079275-A/3
PD 28-DEC-2000
PP 16-JUN-2000 WO 2000JP003957
PR 17-JUN-1999 JP 99P 171709
PI KENYA SHITARA, MASABUMI SHIBUYA
PC G01N33/53, A61K45/00, A61K39/395//C12N15/06, C12N15/12, C07K16/28
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D14625.
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88.8%; Pred. No. 1.5e-100;
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/organism="Mus musculus"
/mol_type="genomic DNA".
/db_xref="taxon:10090"
/ 105 c 99 g 106
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                                                                    WO 0079275-A/3.
Mus musculus (house mouse)
Mus musculus
                                                   BD092129.1 GI:22637740
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chain (anti-Pseudomonas aeruginosa lipoprotein I end.
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Gytftaywmhwykorpgoglewigyinphtgyteynonfkdkatltadkssstaywol
SSLTSEDSAVYYCTRSYYNYEGAMDYWGOGTSVTVSSAKTTAPSVYPLAPVCGDTTG"
                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
Marget,M., Eckhardt,A., Ehret,W., von Specht,B.U., Duchene,M. and
                CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                           Cloning and characterization of cDNAs coding for the heavy and light chains of a monoclonal antibody specific for Pseudomonas aeruginosa outer membrane protein I Gene 74 (2), 335-345 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Nov 28, 1994 this sequence version replaced gi:342018. Original source text: Mus musculus (strain BALB/c, sub_species domesticus) hybridoma cDNA to mRNA.
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                              M28834.1 GI:576597
V-segment; anti-lipoprotein antibody; immunoglobulin G2a gamma
chain; immunoglobulin heavy chain.
                                                                    GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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/protein_id="AAA53291.1"
/db_xref="GI:576598"
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4.3e-99;
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0; Mismatches
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/db_xref="taxon:10090"
/cell_line="MAb 6A4"
/tissue_type="hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .525
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
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/codon_start=1
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83.4%;
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106. .>525
/gene="Igg"
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antibody) mRNA, 5'
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Best Local Similarity 83.4
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 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC
                                                     TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                   121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
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Pred. No. 1.2e-99;
0; Mismatches 74;
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Eda Y., Maeda, H., Makizumi, K., Shios,
Higuchi, H., and Toklyoshi, S.
Anti-HIV monoclonal antibody
Patent: US 6114143-A 33 05-SEP-2000;
Location/Qualifiers
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AR109947
AR109947.1 GI:12826223
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369; Conservative
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Robinson, R.R., Liu, A.Y., Horwitz, A.H., Wall, R. and Better, M.
MODULAR ASSEMBLY OF ANTIBODY GENES, ANTIBODIES PREPARED THEREBY AND
                                                                                                 PAT 02-DEC-1994
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279 CAGAAGTTCAAGGGCAAGGCCACACTGACTGTAGACAAATCCTCCAGCACAGCCTACATG 338
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Robinson, R. R., Liu, A. Y., Hellstrom, K. E., Hellstrom, I. and Ledbetter, J. A.
Patent: WO 884936-A 12 14-JUL-1988;
Location/Qualifiers
                   Length 458
                                                                                                                                                                                                                                                                                                                 20; Indels
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Pred. No. 9.2e-99;
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Sequence 12 from Patent WO 8804936.
108811.1 GI:588489
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109199
109199.1 GI:588126
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94.4%;
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Matches 334; Conservative
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Score 322; DB 6;
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he : 2092.91 secs
 69.8%;
94.4%;
                 Best Local Similarity 94.4
Matches 334; Conservative
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August 30, 2003, 16:05:49; Search time 202.202 Seconds (without alignments) 6154.444 Million cell updates/sec
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1 ATGGAATGCAGCTGGGTCTT......CTGGTCCCTGGAAGCTTGGG 461
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ne monoclonal	body 11D10 hea	e liblo antibo	-human VEGF re	-human Flt-1 m	e DNA encoding	y chain of mon	2H7 Vh sequence.
Descr	Muri	Anti	Mous	Anti	Anti	Mous	Heav	2H7
SUMMARIES	AAT85150	AAV83773	AAL51274	AAZ87715	AAF70192	ABX16571	AAN91645	AAN91146
DB	18	20	25	21	22	25	10	10
å Query Match Length DB ID	461	461	461	409	409	736	540	458
% Query Match	100.0	100.0	100.0	71.0	71.0	70.8	70.1	8.69
Score	461	461	461	327.2	327.2	326.6	323	322
Result No.	-	7	m	4	2	9	7	89

7	2H7 heavy	œ r		AAV18593 Mouse 2H7	AAT36316	AAT51042	AAQ79930	AAX61084	AAV20085	AAQ12637 Monoclonal	AAQ48037	AAN70971	0	AAQ43385	AAT62936	AAT62935	AAT62937 3F4 human G2/G	SANIO2938 SEA NUMBER 1964 EXP	AAA43821	AAQ94037	AAV22074	AAQ15164 VH186 region of	AAT88869	5 Anti-human	Anti-huma	 	Antibody C2B8 (AAA63531	24 AAD45752 Human C2B8 antibod		AAQ65629	3 TCAE8 expressi	9 AAV61793
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69.8 459 20	9.8 459 2	69.8 491 1	9.8 491 1	69.8 491 1	69.8 518 1	22 69.8 520 1	69.5 1553 1	20 69.4 1683 2	68.3 494 1	67.6 1570 1	67.3 1581 1	67.1 459 8	66.9 420 2	66.9 588	66.9 1392	66.9 1395	6.9 3400	66.9 5300	6.2 725	66.0 1582	8 65.0 440	99 64.9 458	.4 64.5 1773	.4 64.5 1773	4.5	.2 64.5 1	4.5	97.2 64.5 1413	.2 64.5 1413	.2 64.5 1	.2 64.5	.2 64.5	2 64 5 1

ALIGNMENTS

AAT85150 AAT85150 XX AC AAT85150; AC AAT85150; DT 25-MAR-2003 (updated) DT 04-JAN-1998 (first entry) XX Murine monoclonal anti-idiotype antibody; mucin; XX Muman milk fat globule; HMFG; tumour; breast cancer; vaccine; XX XX Mus musculus. XX FT sig_peptide 157 FT Sig_peptide 58461 FT Mat_peptide 58461 FT Mat_peptide 58461 FT Mat_peptide 58461 FT Mat_peptide 96WO-US20757. XX PN W09722699-A2. XX PN W09726699-A2. XX PN W09722699-A2. XX PN W09722699-A3. XX PN W0972669-A3. XX
4 C

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Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss;
human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the coding sequence for the murine antibody 11D10 heavy chain variable region. This anti-lidicype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for treating breast tumours.
                                                                                                                                                                                                   /*tag= a /*tag= a //product= "antibody 11D10 heavy chain variable region" //note= "no stop codon is given at the 3' end of the sequence"
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                                            Antibody 11D10 heavy chain variable region coding sequence.
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100.0%; Pred. No. 1e-117;
11ve 0; Mismatches 0;
                                                                                                                                                                 Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 461; Conservative C
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97US-0049540.
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13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                               This cDNA sequence encodes the heavy chain variable region VH (AAWB5150) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFC). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are allagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMFG-
                                                                                                                               Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours, especially breast cancer
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                                               Foon KA;
                                                                                                                                                                                                   Claim 12; Page 94; 130pp; English.
                                              Chatterjee SK,
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/product= "Mouse 11D10 anti-idiotype antibody heavy chain
variable region"
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Use of anti-idiotypic antibodies for human milk fat globules (HMFG)- or carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g. breast tumor) in humans.
                                                GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG
                                      CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                                                                                                                Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                             Mouse 11D10 antibody heavy chain variable region coding sequence.
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                                                                                                                            ACACCCCCACCCGTCTATCCACTGGTCCCTGGAAGCTTGGG 461
                                                                                                                  ACACCCCCACCCGTCTATCCACTGGTCCCTGGAAGCTTGGG
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1..459
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P-PSDB; AA016293.
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present DNA sequence encodes the heavy chain variable region of the mouse 11D10 anti-idiotype antibody.
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                                                                                                                                   Gaps
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                                                                                            Score 461; DB 25;
Pred. No. 1e-117;
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(KYOW ) KYOWA HAKKO KOGYO KK
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                                                                           The invention relates to a gene recombinant antibody that has specific reaction with human vascular endothelial growth factor (VEGF) receptor Plt-1. The antibodies are useful for diagnosis and as remedies for diseases due to abnormal neovascularisation such as proliferation or metastasis of solid tumor, arthritis in rheumatoid arthritis, diabetic retinopathy, premature retinopathy and psoriasis.
                                                                                                                                                                                                                                       1 ATGGGATTCAGCAGGATCTTTCTCTTCCTCTGTCAGTGACTACAGGTGTCCACTCCCAG
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           diseases due to abnormal neovascularization e.g. proliferation or metastasis of solid tumor, rheumatoid arthritis, diabetic retinopathy
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recombinant antibodies, useful for diagnosis and as remedies
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                                                         Disclosure; Page 155-156; 210pp; Japanese.
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les 366; Conservative
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                                   and psoriasis
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monocytes and macrophages from haematopoletic stem cells, containing a substance which binds to human vascular endothelial growth factor (VEGF) receptor Fit-1. The invention also includes a method for diagnosing a disease in which the differentiation of monocytes and macrophages is implicated, using the reagent, and an agent for the treatment of diseases implicated, using the method, containing a substance which binds to Fit-1 or a substance which inhibits the signal transduction of Fit-1. Diseases hypersensitivity, malignant tumours and arterioscleorosis.

Mycrosonsitivity, malignant tumours and arterioscleorosis.

Mycrosonsitivity, malignant tumours and arterioscleorosis.

Concoding anti-human Fit-1 monoclonal antibody fragments, and construction of the antibody. The monoclonal antibody is used in the reagent of the invention. PCR primers AMF70255 antibody is used in the reagent of the invention of the antibody by sequences. Protein sequences AMB78878 each in the isolation of the antibody of the antibody is used in the reagent of the invention of the antibody antibody is sequences. Protein sequences AMB78878 each of the antibody of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody by the monoclonal antibody is used in the reagent of the invention of the antibody of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the invention of the antibody is used in the reagent of the antibody is used in the reagent of the antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 AGACAGGGCCTGGAATGGATTGGAGCTATTTTTCCAGGAAATGGTTTTACTTCCTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of inflammatory diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Indels
                                                                                                                                                                 arteriosclerosis, cancer and delayed hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 409 BP; 99 A; 105 C; 99 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 327.2; DB 22;
Pred. No. 1e-80;
0; Mismatches 43;
                                                                                  Substances binding to human vascular endothelial
                                                                                                                                                                                                                                               Example 3; Page 124-125; 164pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the anti-human Flt-1 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                         1, used for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.0%;
88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366; Conservative
WPI; 2001-080847/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX16571 standard;
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300 313 354 373 414

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reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa. It is used for therapy and diagnosis of infection, and as a carrier for darugs. The antibody is 1962a subclass. (Updated on 31-0CT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence has a variable and constant region. Monoclonal antibody 6A4
                                                                                                                  CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
                                                                                                                                                                                                              314 CAGCTCAGTAGCCTGACTTCTGAGAACTCTGCAGTCTATTTCTGTGCAAGAGGGGGGTAAC
                                                                                                                                                                                                                                                    355 AACTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
                                                                                                                                                                        301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG
                                                                                                                                                                                          Sequence 540 BP; 145 A; 144 C; 130 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                AAAACGACCCCCCCCCCCTTATCCACTGGTCCCTGGA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody to Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heavy chain of monoclonal antibody 6A4.
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64..540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; page 6; 7pp; german.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN91645 standard; DNA; 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88DE-3813023
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domdey H, Marget M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-310861/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAP93079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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15-MAR-1990
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AAN91645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a chimaeric molecule comprising the GD3 (ganglioside antigen) binding domain of antibody MB3.6, with any of 3 variable gene sequences, or the PSMA (prostate-specific membrane antigen) binding domain of antibody 3D8, 4D4 and 3E11, with variable gene sequences, the zeta signalling chain of the T cell receptor and an intervening CD8alpha hinge in which cysteine residues have been mutated. The chimaeric molecules expressed in T cells or NK cells or other effector cells are useful in treating patients with cancers expressing the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives), and/or together with each other or with heterologous constructs to engage additional stimulatory and functional properties of the effector cells to enhance the antitumour therapeutic efficacy (claimed). They are particularly useful in disorders including melanoma, neuroendocrine constructs and prostate and small cell lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; T-cell receptor; gene; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E1; prostate-specific membrane antigen; zeta signalling chain; CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGAATGCAGCTGGGTCTTTCTTTCTTCTTCTTCAATAACTACAGGTGTCCACTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence encodes the mouse antibody 4D4 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                "4D4 heavy chain variable region""
Mouse DNA encoding antibody 4D4 heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.8%; Score 326.6; DB 2
83.7%; Pred. No. 1.7e-80;
iive 0; Mismatches 69
                                                                                                                                                                                                                                                                    /partial
/note= "No stop codon shown"
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 4F; 35pp; English.
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2000US-250089P.
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/product=
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                                                                                                                                                                                                                14..430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JUNG/) JUNGHANS R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG74245
                                                                                                                                                                                                                                                                                                                              US2002132983-A1
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30-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Junghans RP;
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Matches
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1989-061144/08
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            P-PSDB; AAP94780
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30-MAR-1999
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Best Local
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                                            GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC 120
                                                        183
                                                                    TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT 180
                                                                                                                      CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                   363
                                                                                                                                               354
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                                                                                                                                               1 ATGGAATGCAGCTGGGTCTTTCTCTTCTCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                            AACTGGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCC
       Gaps
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      Indels
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398..408
/*tag= b
/note="Sequence homologous to DSP.2"
360..406
                                                                                                                                                                                                        AAAACAACCCCCATCGGTCTATCCACTGGCCCCTG: 520
                                                                                                                                                                                                 AAAACGACACCCCACCGTCTATCCACTGGTCCCTG 451
Pred. No. 1.6e-79;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                    Antibodies; passive immunisation; pH3-6a;
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39..458
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/note="JH1 region"
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                                                                                                                                                                                                                                             ВР
83.48;
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                                                                                                                                                                                                                                                                      (updated)
(first entry)
Best Local Similarity 83.4 Matches 381; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu AY,
                                                                                                                                                                                                                                                                                      2H7 Vh sequence.
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                                                                                                                                                                                                                                                                     25-MAR-2003
06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 IGCAAGGCTICTGGCTACACATITACCAGTTACAATATGCACTGGGTAAAGCAGACACT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGAAGTITAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
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                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                      Sequence carries 2H7 VH region of the chimeric immunoglobulin sequence. The antibodies are useful in passive immunisation avoiding negative immune reactions. They are also useful in assaying and in vitro imaging (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                            99 ATGGGATTCAGCAGGATCTTTCTCTTCTTCTTCTTCAGTAACTACAGGGTGTCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse antibody 2H7 heavy chain variable region encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                            Length 458;
                          or
Polynucleotide(s) encoding Immunoglobulin molecules - used for efficient prodn. of chimeric human or non-human class switched antibodies.
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pelB pectate lyase, secretion signal; chimeric antibody;
heavy chain; B-cell antigen; antibody 2H7; ss.
                                                                                                                                                                                                                                                             Sequence 458 BP; 113 A; 120 C; 112 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                         Score 322; DB 10;
Pred. No. 2.9e-79;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
40.459
/*tag= a
/note= "partial CDS"
                                                                                               Disclosure; Page ?; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                            69.8%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV82357 standard; DNA; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0472696
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(first entry)
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                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTATCTACAGCAGTCTGGGGCTGAGCTGGGGGTCTGGGGGCCTCAGTGAAGATGTCC 120
                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the mouse antibody 2H7 heavy chain variable region. Antibody 2H7 is specific for human B-cell antigen. The antibody sequence was used to construct a chimeric human-mouse antibody. In the course of the invention. The chimeric antibody is expressed in a secretion vector comprising a pelB pectate lyase secretion signal producing a protein such as a chimeric antibody in a bacterial host. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                      TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 AGACAGGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTCCTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pelB pectate lyase signal sequence - and vector for expression of secreted proteins in Gram-negative bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                 Query Match
69.8%; Score 322; DB 20; Length 459;
Best Local Similarity 94.4%; Pred. No. 2.9e-79;
Matches 334; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mouse; chimeric immunoglobulin; chimeric antibody;
                                                                                                  Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                Sequence 459 BP; 113 A; 121 C; 112 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2H7 heavy chain variable region gene sequence.
                                                                                                                                                                              Example 4; Fig 21; 98pp; English
                                                                                                 Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                          86WO-US02269.
87US-0077528.
88US-0142039.
                                   85US-0793980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH22070 standard; DNA; 459
        900S-0501092
93US-0020671
                          94US-0357234
                                                                                                i, Horowitz AH,
Wilcox GL;
                                                                                                                          WPI; 1999-059072/05
                                                                               (XOMA ) XOMA CORP.
                                                                                                                                   P-PSDB; AAW89540
                                 01-NOV-1985;
27-OCT-1986;
24-JUL-1987;
11-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2001
                 22-FEB-1993;
09-DEC-1994;
                                                                                                Better M,
Wall R, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH22070;
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that is capable of binding antigen involves modular assembly of
that is capable of binding antigen involves modular assembly of
antibodies through gene cloning and expression of light and heavy
chains. The cloned immunoglobulin gene can be produced by expression in
genetically engineered organisms. The method comprises: (a) expression in
genetically engineered organisms. The method comprises: (a) expression in
genetically engineered organisms. The method comprises: (a) expression
in a bacterial cell, of a first nucleic acid that encodes a bacterial
signal sequence operably linked to either the heavy chain or heavy chain
fragment, and a second nucleic acid that encodes a bacterial signal
sequence operably linked to either the light chain or light chain
fragment, and obtaining the immunoglobulin from the periphasmic space or
culture medium; or (b) operably linking a nucleic acid encoding a
bacterial signal sequence to a nucleic acid encoding the heavy chain
variable region or the light chain variable region or both of the
variable regions, and obtaining the immunoglobulin from the periplasmic
space or culture medium. The bacterial signal sequences bring about the
transport of the heavy chain or heavy chain fragment, and the light chain
con light chain fragment, or the variable regions through the cytoplasmic
membrane of a bacterial cell. The immunoglobulin comprises: (a) a heavy
chain or heavy chain fragment, and a light chain or light chain fragment,
who mashod is useful fragment, and a light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method is useful for producing genetically engineered antibodies of desired variable region specificity and constant region properties. The method is also useful large scale production of human antibodies. AAH21985 to AAH22082 and AAB98085 to AAB98097 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ATGGGATTCAGCAGGATCTTTCTCTTCCTCTGTCAGTAACTACAGGTGTCCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGAATGCAGCTGGGTCTTTCTTTTCTCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing immunoglobulins or genetically engineered antibodies for that scale production of antibodies involves modular assembly of antibodies through cloning and expression of light and heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lei S;
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Pred. No. 2.9e-79;
0; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robinson RR, Liu AY, Horwitz AH, Better M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 21; 100pp; English.
genetic engineering; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0299085.
90US-0501092.
92US-0987555.
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85US-0793980.
86WO-US02269.
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Best Local Similarity 94.4%;
Matches 334; Conservative
                                                                                                                                                                                                                                                                                                                                               95US-0472691
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                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1995;
01-NOV-1985;
27-OCT-1986;
24-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XOMA ) XOMA
                                                                                                                                                                                       JS6204023-B1
                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1992
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us-08-836-455-3.rng

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72 ATGGGATTCAGCAGGATCTTTCTCTTCCTCCTGTCAGTAACTACAGGTGTCCACTCCCCAG 131
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                                                                                                                                                                                                                                                                                                                                       CAGAAGTTTAAGGGCCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGAATGCAGCTGGGTCTTTCTCTTCTCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                  TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGG 354
                                                    A cDNA clone (AAT70868) codes for the heavy chain variable region (AAW16343) of the 2H7 mouse monoclonal antibody, which recognises human B-cell surface antigen Bp35. The sequence was isolated from a 2H7 cell line cDNA library by PCR amplification. The 2H7 light chain variable sequence (AAT60869) has also been isolated. The sequences have been used to construct a human-mouse chimaeric antibody with specificity for the human B-cell antigen. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                               Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; murine; heavy chain; variable region; immunoglobulin fragment production; Ig fragment production; monoclonal antibody 2H7; human B-cell surface antigen; ss.
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                   Sequence 491 BP; 113 A; 153 C; 112 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse 2H7 antibody heavy chain variable region cDNA
                                                                                                                                                                                                          Ouery Match
69.8%; Score 322; DB 18;
Best Local Similarity 94.4%; Pred. No. 2.9e-79;
Matches 334; Conservative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
72..128
                             Example 4; Fig 21; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
 immunisation, diagnosis, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV18557 standard; cDNA; 491
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sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1990;
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                                                                                                                           CAGAAGITIAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
              Antibody engineering; heavy chain; light chain; chimaeric antibody; passive immunisation; diagnosis; hybridoma; monoclonal antibody; 2H7; B-cell antigen; Bp35; ss.

    capable

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                                                                                                                                                                                   CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secretable immunoglobulin heavy and light chain fragments - cap; of assembling into chimeric antibodies, useful for e.g. passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= d
note= "DSP.2 sequence element"
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393..439
/*tag- c
/note- "JH1 sequence element"
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/note= "primer JHBstEII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                2H7 heavy chain variable sequence.
                                                                                                                                                                                                                                                                   BP.
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85US-0793980.
86WO-US02269.
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88US-0142039.
92US-0870404.
94US-0235225.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-225473/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (XOMA ) XOMA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1988;
17-APR-1992;
29-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1994;
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04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
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27-OCT-1986
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121
                                                      181
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AAV03926 standard; cDNA; 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACT 180
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                                                                                                                                                                                                                                                                                                                                                   The present sequence was used in the development of a novel method for the production of an immunoglobulin (1g) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the 1g fragment, under conditions so that the 1g fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences encoding; (a) pectate lyase secretion signal sequence operably inked to a DNA sequence encoding at least the variable region of an 1g Fd molecule; and (b) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of an 1g 1ght chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable region of an 1g 1ght chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic region of a single prokaryotic promoter to form a dicistronic molecules, e.g. derived from murine monoclonal antibody 2H7 raised gainst human B-cell surface antigen. The invention provides a novel approach for producing genetically engineered antibodies of contents. The cloned Ig gene products can be produced by expression in genetically engineered organisms. The application of specific Ig chains in various organisms provides a solution to the reflicient large scale production of human monoclonal antibodies. The invention also provides a solution to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 AGACAGGCCTGGAATGGATTGGAGCTATTTATCCAGGAAATGGTGATACTTGCTACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGAATGCAGCTGGGTCTTTCTCTTCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGG 354
                                                                                                                                                                                                                                                                        DNA encoding secretable immunoglobulin fragments - comprising at least the variable regions of light or heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.8%; Score 322; DB 19; Length 491; 94.4%; Pred. No. 2.9e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;
                                                                                                                                                                        Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the problem of class switching antibody molecules
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                                                                                                                                                                        Liu AY,
                                                                                                                                                                                                                                                                                                                          Example IV; Fig 21; 98pp; English.
                                                                                                                                                                        Lei S,
85US-0793980.
86WO-US02269.
87US-0077528.
88US-0142039.
92US-0299085.
95US-0467140.
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                                                                                                                                                                        Horwitz AH,
                                                                                                                                                                                                                      WPI; 1998-051492/05
                                                                                                                                                                                        Wilcox GL;
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                                                                                                                                      (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                          P-PSDB; AAW47513
                                                                                     18-AUG-1994;
06-JUN-1995;
                                                   11-JAN-1988
08-DEC-1992
                 27-OCT-1986
24-JUL-1987
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                                                                                                                                                                                          Wall R,
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The present sequence was used in the development of a novel method for the production of an immunoglobulin (1g) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the. Ig fragment, under conditions so that the Ig fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences concoding: (a) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of an Ig Fd molecule; and (b) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable coperably linked to a DNA sequence encoding at least the variable coperably linked to a DNA sequence and (b) are operably linked to a single prokaryotic promoter to form a dicistronic region of an Ig light chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic conscription unit. The method is used to produce channeric Fab molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a novel approach for producing genetically engineered antibodies of desired variable region specificity and constant region properties. The cloned Ig gene products can be produced by expression in genetically engineered organisms. The application of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli
                                                                                                                        Mouse; murine; heavy chain; variable region;
immunoglobulin fragment production; Ig fragment production;
monoclonal antibody 2H7; human B-cell surface antigen; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu AY, Robinson RR;
                                                              Mouse 2H7 antibody heavy chain variable region cDNA.
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88US-0142039.
92US-0987555.
94US-0299085.
95US-0450731.
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85US-0793980.
86WO-US02269.
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(first entry)
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129..491
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01-JUN-1998
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08-DEC-1992;
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Wall R, W
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95US-0466203

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06-JUN-1995;
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Best Local S
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                                          Wall R,
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                                                                                                                  72 ATGGGATTCAGCAGGATCTTTCTCTTCCTCCTGTCAGTAACTACAGGTGTCCCCAG 131
                                                                                                                                     GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 120
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                                                                                                                                              TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT 180
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                                                                                    Gaps
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chemical gene synthesis, recombinant DNA cloning and production of
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       specific Ig chains in various organisms provides an effective solution for the efficient large scale production of human monoclonal antibodies. The invention also provides a solution the problem of class switching antibody molecules.
                                                                  Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; murine; heavy chain; variable region; immunoglobulin fragment production; Ig fragment production; monoclonal antibody 2H7; human B-cell surface antigen; ss.
                                                                                    Indels
                                                  Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                     Mouse 2H7 antibody heavy chain variable region cDNA
                                                                 Score 322; DB 19;
Pred. No. 2.9e-79;
0; Mismatches 20;
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92US-0987555.
94US-0299085.
95US-0450731.
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ilarity 94.4%;
Conservative
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sig_peptide
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Best Local Simi.
Matches 334; (
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27-OCT-1986;
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18-AUG-1994;
25-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence was used in the development of a novel method for the production of an immunoglobulin (1g) fragment capable of binding an antigen. The method comprises culturing an E. coil host that has been transformed with a nucleic acid molecule encoding the and secreted. The nucleic acid molecule encoding the and secreted. The nucleic acid molecule comprises DNA sequences and secretion is produced and secretion pertably inked to a DNA sequence encoding at least the variable region of an Ig Handle to an DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a Single prokaryotic promoter to form a dicistronic region of an Ig light chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic ranscription unit. The method is used to produce chimeric Fab molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antipen. The invention provides a covel approach for producing genetically engineered antibodies of estred variable region specificity and constant region properties. The cloned Ig gene products can be produced by chemical gene synthesis, recombinant DNA cloning and production of specific Ig chains in various organisms. The application of specific Ig chains in various organisms provides a solution to monoclonal antibodies. The invention are producted a solution to
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                                                                                                                                                                                                                                                            Production of recombinant immunoglobulin fragment - comprising Fd
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Pred. No. 2.9e-79;
0; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;
                                                                Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the problem of class switching antibody molecules.
                                                             Liu AY,
                                                                                                                                                                                                                                                                                                                                                            Example IV; Fig 21; 98pp; English.
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                                                                                                                                                             WPI; 1998-051487/05
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                                                                                            Wilcox GL;
                                                             Horwitz
(XOMA ) XOMA CORP.
                                                                                                                                                                                           P-PSDB; AAW47520
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                                                                                                                                                                                                                      Immunoglobulin G; IgG; heavy chain; recombinant production; antibody; passive immunisation; serum sickness; anaphylactic shock; immunoassay; imaging; reagent; complement mediated lysis; therapy; variable region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encodinding immunoglobulin fragment - comprising discistronic transcription unit with pectate lyase signal sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The polynucleotide molecule is used for the production of recombinant antibodies, which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging purposes when coupled to a toxin or other therapeutic agent. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes the heavy chain variable region of the 2H7 antibody. The 2H7 CDNA was used in the preparation of a novel polynucleotide molecule encoding an Ig fragment. The DNA molecule comprises 2 DNA sequences encoding 2 pectate lyase secretion signal sequences respectively linked to a DNA sequence encoding an Ig Fd molecule or Ig light chain, operably linked to a single prokaryotic promoter so as to form a dicistronic transcription unit, provided that the Ig fragment can bind an antigen and is produced and secreted by an E. coli host cell, the nucleic acid molecule is expressed in the host cell.
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                                                                                                                                                                       2H7 antibody heavy chain variable region cDNA.
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71..127
/*tag- a
128..490
/*tag- b
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AAT36316 standard; cDNA; 518
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86WO-US02269.
87US-0077528.
88US-0142039.
92US-0987555.
94US-0299085.
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                                                                                                  (updated)
(first entry)
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P-PSDB; AAW10588.
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11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
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21-OCT-1997
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27-OCT-1986
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                                                 AAT36316;
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                  61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC
                                                                          1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCCTGTCAATAACTACAGGTGTCCACTCCCAG
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(without alignments)
6267.222 Million cell updates/sec
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1 ATGGAATGCAGCTGGGTCTT......CTGGTCCCTGGAAGCTTGGG 461
                                                                                                                                 August 30, 2003, 17:29:10 ; Search time 168.759 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                              1533700 seqs, 1147125425 residues
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/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* Published_Applications_NA:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	Sequence 3. Appli		Sequence 12. Appl	Sequence 6. Appli		'n	7	'n	7	7	Sequence 8, Appli	Sequence 19, Appl	91		1,	
. di	US-09-861-294-3	US-10-367-506-3	US-10-160-232-7	US-10-006-773-12	US-09-795-515-6	US-09-911-692-3	US-09-911-703-3	US-09-905-928-2	US-10-238-681-3	US-10-096-964-2	US-10-109-853-2	US-10-216-484-8	US-09-881-823-19	US-10-040-739-911	US-09-903-327A-5	US-09-903-327A-1	
gth DB	461 9	461 12	409 14	736 13	570 11	11 661	9209 10	209 11	209 12	209 14	8986 13	392 14	482 9	478 13	1314 10	516 10	
Query Match Length DB ID	100.0	100.0	71.0	70.8											63.2 1		
Score	461	461	327.2	326.6	310	297.2	297.2	297.2	297.2	297.2	297.2	296.4	295.2	292	291.4	291.4	
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99-753-436-77 10-244-821-8 110-150-762-8 10-150-762-8 10-911-703-9 10-9911-703-9 10-90-911-692-9 110-207-655-2 110-207-655-2 110-207-655-3 110-207-655-3 110-207-655-3 110-207-655-3 110-207-655-3 110-207-655-3 110-207-655-3	US-10-207-655-273 US-10-207-655-381 US-10-207-655-381 US-10-207-655-394 US-10-207-655-394 US-10-207-655-395 US-09-897-006-11
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ALIGNMENTS

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           Sequence 3, Application US/09861294

Patent No. US2002098190A1

GENERAL INFORMATION:

APPLICANT: Malaya CHATTERJEE

APPLICANT: Kenneth A. FOON

TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS

TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS

FILE REFERENCE: 304142000620

CURRENT FILING DATE: 1907-06-13

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 100.0%; Score 461; DB 9; I Similarity 100.0%; Pred. No. 5.4e-142; 61; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(461)

NAME/KEY: sig_peptide

LOCATION: (1)...(57)

NAME/KEY: mat_peptide

LOCATION: (58)...(461)

US-09-861-294-3
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Mus musculus
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US-09-861-294-3
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APPLICANT: 1TO, MIKITO
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, VOKO
APPLICANT: NAKAMURA, YOKO
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: SHIBUTA, MASABUMI
TITLE OF INVENTION: ANTI-HUMAN VEGF RECEPTOR FLT-1 MONOCLONAL ANTI-BODY
FILE REPERENCE: 249-107
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Pred. No. 8.6e-98;
0; Mismatches 43; I
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CURRENT FILING DATE: 2002-06-04
PRIOR PAPLICATION NUMBER: US/09/453,718
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-06-20
PRIOR APPLICATION NUMBER: 09/315,051
PRIOR APPLICATION NUMBER: 09/315,014
PRIOR FILING DATE: 1998-07-20
PRIOR PILING DATE: 1998-07-20
PRIOR FILING DATE: 1998-07-20
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10160232
Publication No. US20030088075A1
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88.8%;
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LOCATION: (1)..(57)
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): LOCATION: (58)..(408)
US-10-160-232-7
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Matches 366; C
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 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10367506
Publication No. US2003015257541
GENERAL INFORMATION:
APPLICANT: Malay CHATTERJEE
APPLICANT: Reneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142006620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT PILING DATE: 2003-02-13
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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; LOCATION: (58)...(461)
US-10-367-506-3
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Decided Deci	Oy 241 CAGAGGGAGGGCTATTAGGGGAGACACCCCCCCCCCCCC
GENERAL INFORMATION: APPLICANT: Junghans, Richard P. TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antiplies EPERENES. TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antiplies. TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antiplies. TITLE OF INVENTION: 2001-11-2.0 OURRENT FILING DATE: 2001-11-30 PRIOR FILING DATE: 2000-11-30 SOFTWARE: Patentin version 3.1 SEQ ID NOS: 19 SOFTWARE: Patentin version 3.1 SEQ ID NOS: 19 SOFTWARE: Patentin version 3.1 SOFTWARE: Patentin version 3.1 CORRAISM: Mus sp. FEATURE: NAME/KEY: CON ORGANISM: (44)(430) OUTHER INFORMATION: 404 OUTHER INFORMATION: 404 OUTHER INFORMATION: 404 ATGGAATGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	THE BELLING THE STREET

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LEONARD, John E.
NEWAMN, Roland A.
REFF, Mitchell E.
RASTETTER, William H.
THERAPEUTIC APPLICATION OF CHIMBRIC AND
RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
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CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 297.2; DB 11;
Pred. No. 2.7e-87;
0; Mismatches 83;
   012712-014
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                      ase pairs
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANDERSON, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09911703 Publication No. US20020197255A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             64.58;
79.98;
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                                                                                                                       INFORMATION FOR SEQ ID NO: 3
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US-09-911-703-3
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Best Local (
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HANNA, Nabil
LEONARD, John E.
NEWMAN, Roland A.
REFF, Mitchell E.
RASTETTER, William H.
THERAPEUTIC APPLICATION OF CHIMERIC AND
RADIOLABELED ANTIGODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
                                                                                                                                                                                                                                                                                                                                                                                      ATGGAAAGGCACTGGATCTTTCTACTCCTGTTGTCAGTAACTGCAGGTGTCCACTCCCAG
                                                                                                                    GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
   ATGGAATGCAGCTGGGTCTTTCTCTTTCTCTGTCAATAACTACAGGTGTCCACTCCCAG
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MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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BILING DARE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09911692 Publication No. US20030095963A1 GENERAL INFORMATION:
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COUNTRY: United States
ZIP: 22313-1404
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CORRESPONDENCE ADDRESS:
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2570

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Score 297.2; .DB 11;
Pred. No. 2.7e-87;
0; Mismatches 83;
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                                                                                                                                                                                                                       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince St. CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
POSITION IN GENOME:
CHROMOSOME/SEGMENT: anti-CD20 in TCAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/DOCKET NUMBER: 012712-158
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/475,813
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/905,928 FILING DATE: 17-JUL-2001
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   Anderson, Darrell R.
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ilarity 79.9%;
Conservative
 Publication No. US20030021781A1
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                   Hanna, Nabi
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Best Local Similarity
Matches 366; Conserv
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MOLECULE TYPE: DN
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                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Indels
                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,703
FILING DATE: 25-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 297.2; DB 10;
Pred. No. 2.7e-87;
0; Mismatches 83;
                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-6620
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                         COMPUTER READDBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/149,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-911-703-3
                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 9209 base pairs
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; Sequence 2, Application US/09905928
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
COUNTRY: United States
                                                                                                                                                                                                                                FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 64.5%;
Best Local Similarity 79.9%;
Matches 366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NO
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APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Refit Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphom
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 2401 ATGGGTTGGAGCCTCATCTTGCTTTGTCGCTGTTGCTACGCGTGTCCTCTCCCAG 2460 121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT 180 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCTGTCAATAACTACAGGTGTCCACTCCCAG Length 9209; 6

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Newman, Roland A.
Reff, Mitchell E.
Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
Radiolabeled Antibodies to Human B Lymphocyte Restricted
Differentiation Antigen for the Treatment of B-Cell Lymp
                                                                                                                 2641 CAGAAGTICAAAGGCAAGGCCACATIGACIGCAGACAAAICCICCAGCACAGCCIACAIG 2700
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    241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                              361 GAGGGTGCT-----CTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCAA 411
                                                                                          CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGGTCTATTTCTGTGCAAGAGGGAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                           412 GCCAAAACGACACCCCCACCGTCTATCCACTGGTCCC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 012712-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/475,813
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/096,964
FILING DATE: 14-Mar-2002
CLASSIFICATION: <a href="https://doi.org/10.10/10/10/10/10/">CLASSIFICATION: <a href="https://doi.org/10/">CDM://doi.org/10/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
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TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Anderson, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10096964 Publication No. US20030082172A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leonard, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
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ADDRESSEE: BURNS,
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ANTI-SENSE: NO
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                      US-10-096-964-2
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APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWMAN, FOLAND A.
APPLICANT: REFF, MITCHELL E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: RASTETTER, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED
TITLE OF INVENTION: LYMPHONA
TITLE REFERENCE: 37003/0291808
CURRENT APPLICATION NUMBER: US/10/238,681
CURRENT PILING DATE: 1997-08-29
PRIOR PILING DATE: 1997-08-29
PRIOR PILING DATE: 1993-11-03
PRIOR PILING DATE: 1993-11-13
                              2581 GGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAAT 2640
                                                                                                                                                                                                                                                                                        2520
                                                                                                          2641 CAGAAGTTCAAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG 2700
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                                                                                                                                                                       301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGAACTGG 360
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                                                                                   241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
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Pred. No. 2.7e-87;
0; Mismatches 83; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                              412 GCCAAAACGACACCCCCACCGTCTATCCACTGGTCCC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10238681
Publication No. US20030147885A1
GENERAL INFORMATION:
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79.98;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 9209
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Best Local Similarity 79.9
Matches 366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HANNA, NABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Murine sp. US-10-238-681-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-238-681-3
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181
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US-10-216-484-8
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APPLICANT:
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MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
                                                                                                                                                                                                       2520
                                                                                     1;
                                                                                                                                                                                                                                                  2401 ATGGGTTGGAGCCTCATCTTGCTTTCCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAG 2460
                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                                                                      241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                                                                                                                                                                                                                                                              301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
                                                                                                                                                                          GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GAGGGTGCT------CTGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCA 411
                                                                                                                 09
                                                                                                               ATGGAATGCAGCTGCTTTTCTCTTCCTCTCTCATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                        TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                                                                                                                                                           Gaps
                                                        Length 9209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. BOX 1404
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAAAACGACACCCCCACCCGTCTATCCACTGGTCCC 449
                                                          DB 14;
                                                       Score 297.2; DB 14;
Pred. No. 2.7e-87;
0; Mismatches 83;
CHROMOSOME/SEGMENT: anti-CD20 in TCAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/023,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/819,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/109,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
            SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10109853 Publication No. US20020192820A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: REFF, Mitchell E.
                                                       tch 64.5%;
al Similarity 79.9%;
366; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                          US-10-096-964-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-109-853-2
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                                                       Query Match
Best Local S
Matches 366
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301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
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Pred. No. 3.6e-87;
0; Mismatches 83;
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tamaki, Kuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR PELICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-109-853-2
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10216484 Publication No. US20030103976A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                       STRANDEDNESS: single
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Best Local Similarity 79.9
Matches 366; Conservative
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9552

120

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180

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TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT 180
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416 AAACGACACCCCACCGTCTATCCACTGGTCCCTG 451
                                                                                                                                 Score 295.2; DB 9
Pred. No. 3.5e-87;
0; Mismatches 88
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APPLICATION NUMBER: US/10/040,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 911, Application US/10040739
Publication No. US20020173635A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy Disk
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Racie, Lisa
Merberg, David
Treacy, Maurice
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COUNTRY: U.S.A
                                                                                                                                 64.0%;
illarity 79.6%;
Conservative
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COMPUTER READABLE FORM:
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                                                ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(482)
US-09-881-823-19
                                                                                                                                                   Similarity
                TYPE: DNA ORGANISM: Murine
                                                                                                                                   Query Match
Best Local Simi
Matches 363;
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Patent No. US2020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: SHORRISON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: TRINH, RYAN
APPLICANT: TRINH, RYAN
APPLICANT: TRINH, SHORY
APPLICANT: TITLE OF INVENTION: Method for the Treatment and Prevention of Dental of File Reference: 22851-032
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                                                                                                                                                                                                                                                                                                         86;
                                                                                                                                                                                                                                                                       Score 296.4; DB 14
Pred. No. 2.2e-87;
0; Mismatches 86
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                     Query Match 64.3%;
Best Local Similarity 79.4%;
Matches 367; Conservative
SEQ ID NOS: 165
                                                                ORGANISM: Mus musculus
                                                                                                                                                 NAME/KEY: mat peptide
LOCATION: (58)..(1392)
                                                                                                                                                                                  FEATURE:

NAME/KEY: sig peptide

LOCATION: (1)..(57)
US-10-216-484-8
                                                                                                                 LOCATION: (1)..(1392)
FEATURE:
                                                                                                   NAME/KEY: CDS
                                1392
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Best Local
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              SEQ ID NO LENGTH:
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61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 120
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                                                                                                                                                       LOCATION: (0)...(1314)
OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
OTHER INFORMATION: bifunctional antibody
                                                                                                                                                                                                                                                                                                                                      1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                           1 ATGGGATGGAGCTGGATCTTTCTCTTCCTCTGTCAGGAACTGCAGGCGTCCACTCTGAG
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                                                                                                                                                                                                                                                   Score 291.4; DB 10; Length 1314;
Pred. No. 9.6e-86;
0; Mismatches 76; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGA 453
  SEQ ID NOS: 33
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: August 30, 2003, 19:50:22 e : 170.759 secs
                                                                                                                                                                                                                                                       Query Match 63.2%;
Best Local Similarity 79.9%;
Matches 362; Conservative (
                                                                                                 ORGANISM: Mouse
                  SOFTWARE: Fasts
SEQ ID NO 5
LENGTH: 1314
                                                                                                                                    NAME/KEY: CDS
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                                                                            TYPE: DNA
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TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 292; DB 13;
Pred. No. 4e-86;
0; Mismatches 70;
                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDRES: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 911:
                                                      APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998
                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09903327A
Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
APPLICANT: Li, Erguang
DATE: 07-Jan-2002
                                                                                                                                                                                                                                                     LENGTH: 478 base pairs
                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 911:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.3%;
Best Local Similarity 82.2%;
Matches 350; Conservative
                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACG 420
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CA574907 BG968682 BG962137

K0731A04-

CA578968 CA579750

BF168514

501782916

BF136093 BF138460

K0644A12

BF136397

imageqc_6 K0718G11-

K0725B11

CA578116 CA578534 BE286958

602832896

23a08.y

BF165486 BF015548 CA580087

BF168856

CA570382

BG966397 BQ109114

601777393

601092470 K0733D01-.

CA579143

602096127

3F580337

CA577080 CA580316

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Run on:

Sequence:

Searched:

Database

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BE284158 739 bp mRNA linear EST 13-JUL-2000 601099428F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov.

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://lmage.llnl.gov

Plate: LLAN8636 row: h column: 07

High quality sequence stop: 535.
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BF579009
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                                                                                           (without alignments)
6988.707 Million cell updates/sec
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                                                                                                                                                      1 ATGGAATGCAGCTGGGTCTT......CTGGTCCCTGGAAGCTTGGG 461
                                                                              August 30, 2003, 16:08:05; Search time 1603.21 Seconds
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                  22781392 seqs, 12152238056 residues
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Listing first 45 summaries
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BY724721 BY724721 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530011123 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Lu29"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
106 c 211 g 198 t
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                CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://mage.lln.gov h column: 07
                                                                                                                                                                                                                                                                             tumor, metastatic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 892;
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Tissue Procurement: Gilbert Smith, Ph.D.
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/clone="IMAGE:3491766"
/fissue_type="spontaneous f
Stem cell origin."
/lab_host-"DH10B"
                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                      High quality sequence stop: 771.
Location/Qualifiers
                                                                                                                                                                                                       /mol_type="mRNA"
/strain="CZECH II"
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                            /organism="Mus musculus"
/mol_type="mRRA"
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/clone="IMAGE:3491766"
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Stem cell origin.
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/clone_lib="NCI_CGAP_Lu29"
/clone="Organ: lung; Vector: pcWV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
84 a 210 c 184 g 161 t
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.7e-85;
0; Mismatches 72;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
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Best Local Similarity 84.1%;
Matches 381; Conservative
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                                                                                               Manualais Eutreria; Kodentia; Sciurognathi; Muridae; Murinae; Mus. Manualais; Eutreria; Kodentia; Sciurognathi; Muridae; Murinae; Musado, N. Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nixaido, T., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Haseqawa, Y., Nogami, A., Schonbach, C. Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schrini, L.M., Kanapin, A., Matsda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bursic, V., Chothia, C., Corbani, J.L. E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garboldi, M., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jackson, I.J., Kongaya, A., Kurcokhin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Majott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Majott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Magotti, S., Parasia, M., Shimada, K., Sultana, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Renda, J.U., Qi, D., Ramachandran, S., Ravasi, T., Nahlais, L., Marki, M., Yangi, L., Yang, Y., Watanabe, Y., Wells, C., Wilmig, L.G., Wynshaw-Boris, R., Yang, L., Yang, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Genome Sequences Mamu. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant CDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resegsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Adachi.J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Innotani,K., H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Salto,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                     Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 81-45-503-9216
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                                                                                                                                                              AUTHORS
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/organism="Mus musculus"

Location/Qualifiers

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source

FEATURES

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                                                                                                                                                                                                                                                                                                                      contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGAGAAGAGACTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCAGCTGCAGCAGTCTGGAGCTGAGCTGGTAAGGCCTGGGACTTCAGTGAAGGTGTCC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 GAGAAGTTCAAGGGCAAGGCAACACTGACTGCAGACAAATCCTCCAGCACTGCCTACATG 351
                                                                                                                                                                                                     /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                            /clone_lib="RIKEN full-length enriched, adult male aorta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ATGGAATGGAGCAGAGTCTTTATCTTTCTCCTATCAGTAACTGCAGGTGTTCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGAATGCAGCTGGGTCTTTCTCTTTCCTGTCAATAACTACAGGTGTCCACTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 70.8%; Score 326.6; DB 14; Best Local Similarity 82.6%; Pred. No. 2.5e-82; Matches 374; Conservative 0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACACCCCCACCCGTCTATCCACTGGTCCCTGGA 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 t
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 g
                                                                                                              /dev_stage="adult"
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RESULT 5

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1. 941

/organism="Max musculus"
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/strain="CZECH II"
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Site_2: Sali; transgenic model WNT-1, expression driven by
MMNY-LTR enhancer; cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
32 a 266 c 248 g 195 t
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                                                                         Murinae; Mus
                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CCAP clone distribution information can bittp://image.llnl.gov
Plate: LLAM9245 row: k column: 04
High quality sequence stop: 637.
Location/Qualifiers
                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                     1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.4e-80;
0; Mismatches 6?
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
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84.2%;
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Best Local Similarity 84.29
Matches 377; Conservative
                Mus musculus
Mus musculus
                                                                                                                                          Unpublished
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COMMENT
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Buseroutus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Maxadi, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,

Yagi, K., Tomau, Y., Hasegawa, Y., Nogama, A., Schonbach, C.,

Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,

Gojobori, T., Baldarelli, R., Mill, D.P., Bult, C., Hume, D.A.,

Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest

A., Frazer K.S., Gaasterland, T., Gariboldi, M., Glssi, C., Godzik, A.,

Gough, J., Grimmond, S., Gustinotich, S., Hirokawa, N., Jackson, I. J.,

Jarvis, E.D., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons

A., Majott, D.R., Maltais, I., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,

Ramachandran, S., Ravasi, T., Reed, J.C., Semple, C.A., Setou

M., Shimmada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale

R.D., Tomita, M., Verardo, R., Wangner, L., Wahlestedt, C., Wang, Y.,

Watcanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yang, I., Yang, I., Yang, I., Yang, I., Wanger, I., Wahlestedt, C., Wang, I., Watchabe, Y., Walls, C., Wanger, I., Wahlestedt, C., Wang, I., Watcher, R., Markaya, T., Romo, H., Nakawa, T.,

Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komo, H., Nakawu, K.,

Arakava, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, R., Isahi,

Y., Itoh, M., Kagawa, I., Miyazaki, A., Sasaki, D., Yanger, L., Sasaki, D., Sasaki, Sasaki
                                     BY724790 BY724790 667 bp mRNA linear EST 17-DEC-2002 BY724790 RIKEN full-length enriched, adult male aorta and vein Musmusculus CDNA clone A530085L22 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp,
Adachi.j., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi.j., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi.j., Aizawa,I., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9212
Fax: 81-45-503-9216
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/note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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/lab_host="bh108"
/clone_lib="RIKEN full-length enriched, adult male aorta
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishli, Y.,
Alzawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Alzawa, T., Ishai, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Mikaido, I., Pesole, G.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Toyo-oka, K., Wang, K.H., Weltz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Stem cell origin."
/lab_host="DH10B"
                                                                    56 ATGGAATGGAGCTGGGTCTTTCTCTTCCTCCTGTCAGTAACTGCAGGTGTCCACTGCCAG
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM9270 row: m column: 12
High quality sequence stop: 695.
Location/Qualifiers
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  74; Indels
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Tissue Procurement: Gilbert Smith, Ph.D.
    Mismatches
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/clone="IMAGE:4019123"
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Mus musculus
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  377; Conservative
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                                   Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanaqaki, T., Hayata, N., Hiamoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Hiramoto, K., Kobuda, M., Kasukawa, T., Kato, H., Kadi, Y., Ishii, Y., Itoh, M., Izawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Shibata, Y., Shinaqawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Shibata, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Shibata, M., Muranatsu, M. and Hayashizaki, Y. Direct Submission

L. Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research Group, RIKEN Genomic Schences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0405, Japan (E-mail:genome-reségsc.riken.go.jp, Fax:81-45-503-9216, Please visit our web site (http://genome.gsc.riken.go.jp/) for further details
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; immunoglobulin heavy chain 6 (heavy chain of IgM) (MGDIMGI:96448, GB|AK008342, evidence: BLASTN, 100%, match=137)
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VTLGCLVKGYFPEPYTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTYTSNTWPSQTI
TOTVAHDASSTKVDKK IEPRYDITQNPCPPLKECPPCAAPDLLGGESSVFIFPRKTKDY
IMISLSPWTCYVVVNSEDDPDYQISWFVNNVEVHTAQTQTHREDYNSTLRVYSALFI
QHQDKWSGKEFKCYKVVNNRALDSPIEKTISKPRGPYRAPOYYLLPPAEDMYKRFSLT
CMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFA
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/translation="mEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKAS
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/clone_lib="RiKEN full-length enriched mouse cDNA library"
/dev_stage="10 day old"
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/organism="Mus musculus"
/organism="Mus musculus"
/orlan="C57BL/6J"
/db_xref="FANTOM_DB:1810060009"
/db_xref="faxon:10090"
/db_xref="taxon:10090"
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/protein_id="BAB25349.1"
/db_xref="G1:12841781"
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/clone_lib="NCI_CGAP_Lu29"
//note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"
               /mol_type="mRNA"
/strain="CaECH II."
/db_xref="taxon:10090"
/clone="IMAGE:5065801"
/tissue_type="spontaneous tu
Stem coll origin "
/lab_host="DH108"
   /organism="Mus musculus"
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can
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Email: cgapbs remail.nih.gov
Itssue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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                                                                                                        Length 767;
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http://image.llnl.gov
Plate: LLAM11177 row: 1 column: 02
High quality sequence stop: 794.
Location/Qualifiers
1. 794
                                                                                                      Score 316.6; DB 10;
Pred. No. 2e-79;
0; Mismatches 69;
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llarity 84.0%;
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                             121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                                                                                                                                                                                                   282 GAGAAGTTCAAGGGCAAAGGCCACACTGACGGCAGACACATCCTCCAGCACAGCCTACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 -GGGAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAA
                                                                                                                                           1 ATGGAATGCAGCTGGGTCTTTCTCTTCTTCCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                            GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACT--
                                                                                                      Gaps
                                                                                                  3;
                                                      Score 316.4; DB 12; Length 794;
Pred. No. 2.3e-79;
0; Mismatches 76; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffreg E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 ACAACAGCCCCATCGGTCTATCCACTGGCCCCTG 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 ACGACACCCCCACCCGTCTATCCACTGGTCCCTG 451
200 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG871607.1 GI:14222147
                                                        68.6%;
82.6%;
                                                                                                    Conservative
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/lab_nost=~billus*
//lab_nost=content by the laborates of careful chin-/c-kit-/Sca-1+) cDNA Library (Long)*
//note=_lob="Note: pSPORT! Invitrogen; Site_l: Sall; Site_2: Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA project by the Laboratory of Genetics, Not!; Mouse cDNA; Downerse, 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Drs. Dennis Taub. Dan Longo (National Cancer Institute on Aging, USA), Jonathan Relier (National Cancer Institute, USA). Downle-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were digested with Apiner Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with Sal1 and Not! enzymes and cloned into Sal1/Not! site of psPORT! plasmid vector. The DHIOB E. Coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Plao (NIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GTTCAGCTGCAGCAGCTGGAGCTGAGCTGAGCCTGGGGCCTCAGTGAAGCTTTCC 144
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                       Luo, A., Carter, M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTATCTACAGCAGTCTGGGGCTGAGCTGGGGTCTGGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                                Contact: Dawcod B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Sassall Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@ligau.grc.nia.nih.gov
Plate: K0647 row: B. column: 06
Seg primer: M13 Reverse
High quality sequence stop: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
1 (bases 1 to 546)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Car
Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 311.2; DB 14; Length
Pred. No. 5.7e-78;
0; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="NIA:K0647B06 IMAGE:30073265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Age approx.10 weeks old"
/lab_host="DH10B"
                                                                                            (Lin-/c-Kit-/Sca-1+) cDNA Library (Long) Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref-"niaEST:K0647B06-5N"
/db_xref-"taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6NCr"
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .546
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                                                                                                                                                     Other_ESTs: K0647B06-3
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82.1%;
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371; Conservative
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                              AUTHORS
                                                                                                                              JOURNAL
       REFERENCE
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                                                                                                                                                                                                                                                                    /strain="rybB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="TwAGE:4921295"
/lab_host="DH10B (Tl phage-resistant)"
/clone_11b="NOI_CGAP_SG2"
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NOI_CGAP Library."
a 222 c 181 g 163 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGC-CAAAAC 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAGGTCTGGGGGCCTCAGTGAAGATGTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 GAGAAGTTCAAAGACAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACATG:335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI0839 row. c column: 24
High quality sequence stop: 582.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 315.6; DB 12; Length
Pred. No. 3.8e-79;
0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420 GACACCCCCACCGTCTATCCACTGGTCCCTGGA 453
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                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
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CA576594.1 GI:25121296
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ilarity 82.4%;
Conservative (
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/lab_host=nbHi0B:
/clone_lib="NIA Mouse Hematopoietic Stem C
(Lin-/c-Kit;/Sca-1+) cDNA Library (Long)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="NIA: K0644A12 IMAGE: 30072971"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Lin-/c-Kit-/Sca-1+) cDNA Library (Long)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/db_xref="niaEST:K0644A12-5N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAGCCCCATCGGTCTATCCACTGGCCCCTG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 ACACCCCCACCCGTCTATCCACTGGTCCCTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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                    61
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nl. gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM9260 row: h column: 21
High quality sequence stops: 648.
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/rote="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
// Site_2: SalI; transgenic model WNT-1, expression driven by
// WMY-LTR enhancer; Cloned unidirectionally. Primer: Oligo
// Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
// Site_195 g 182 t
                                                                                                                                                                                                                                                                                                                                                                                                                BF140551 771 bp mRNA linear EST 24-OCT-2000 601787584F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015172 5',
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                                                                                                                                         CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
                                                                                                                                                                                                               GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACG 420
241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGGCTACATG 300
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 711)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 ATGGGATGGGGTCTTTTTCTTTTCTTTGTCAGTAACTGCAGGTGTCCACACGCG 74
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/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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Pred. No. 1e-77;
0; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                      421 ACACCCCCACCCGTCTATCCACTGGTCCCTGG 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
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Mus musculus
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82.3%;
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CA576389 S29 bp mRNA linear EST 19-NOV-2002 K0644A12-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) cDNA Library (Long) Mus musculus cDNA clone NIA:K0644A12 LIMAGE:30072971 5', mRNA sequence CA576389
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Musaryotas Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 529)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
Systematic Analyses of NIR Mouse Hematopoietic Stem Cell
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134
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                                                                                                                                                                                                                                                 195 GGACAGGGCCTTGAGTGGATAGGATACTTTTCTCCTTACAATGATGATACTAAATGCAAT
                                                                                                                                                                                                                                                                                                              241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
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                                                                 TGCAAGGCTTCTGGCTACACTTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                 Other_ESTS: K0644A12-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
Sassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0644 row: A column: 12
Seq primer: M13 Reverse
High quality sequence stop: 529
POLYA-No.
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   BF136295 616 bp mRNA linear EST 24-OCT-2000 601781413F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009443 5',
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pSPORT1 (Invitrogen); Site_1: Sall; Site_2
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81.9%; Pred. No. 1...
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Mus musculus (house mouse)
/note="Vector:
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G. E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9245 row: j column: 04
High quality sequence stops: 613.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Lu30"
//clone_lib="NCI_CGAP_Lu30"
//note="Organ: lung; Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: Sall; transgenic model WNT-1, expression driven by
MMV-LRR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
170 c 160 g 148 t
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae, Murinae; Mus
1 (bases 1 to 616)
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                                                            AINH WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:4009443"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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Pred. No. 3.4e-77;
0; Mismatches 69; Indels
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/strain="CZECH II"
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82.8%;
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      ð
                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9251 row: f column: 07
High quality sequence stop: 717.
Location/Qualifiers
1.748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Lu30"
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: SalI; transgenic model WMT-1, expression driven by
MMY-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
a 198 c 191 g 176 t lothers
                                 BF136397 748 bp mRNA linear EST 24-OCT-2000 601783927F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4011654 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CAGATCAGCAGCCTGACATCTGAAGACTCTGCGGTCTATTTCTGTGCAAGAGGGAACTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 TGCAAGGTTTCTGGCTACACCTTCACTACCATGCTATTCACTGGTGATTCAGAGGCCT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 748)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308.6; DB 10; Length
Pred. No. 3.8e-77;
0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/clone="IMAGE:4011654"
                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                 BF136397.1 GI:10975437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.9%;
80.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.9
Best Local Similarity 80.3
Matches 362; Conservative
                                                                 mRNA sequence.
BF136397
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                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                DEFINITION
                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                           TITLE
RESULT 14
BF136397
LOCUS
                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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```
1. 700

/organism="Mus musculus"
/mol_type="mrNa"
/strain="rwBAN"
/db_xref="taxon:10090"
/clone="twAGE:4189350"
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/clone_lib="Not_GGAP_SG2"
/clone_lib="not_GGAP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF540088 700 bp mRNA linear EST 11-DEC-2000 602050325F1 NCI_CGAP_SG2 Mus musculus CDNA clone IMAGE:4189350 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9515 row: b column: 07
High quality sequence stop: 675.
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                                                                                      424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
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    361 GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGAATGCAGCTGGGTCTTTCTTCTTCCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 ATGGAATGGACCTGGGTCTTTCTCTTCCTCTCTCGTCAGTAACTGCAGGTGTCCACTCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TGCAAGGCTTCTGGCTACACATTGACCAGTTACAATATGCACTGGGTAAAGCAGACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TGCAAGGCTACTGGCTACACATTCAGTAGCTACTGGATAGAGTGGGTAAAAGCAGAGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 700)

NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Pred. No. 1.4e-76;
0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                 425 ACAGCCCCATCGGTCTATCCACTGGCCCCTG 455
                                                                                                                                                                                 ACACCCCCACCCGTCTATCCACTGGTCCCTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF540088.1 GI:11627469
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80.2%;
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Search completed: August 30, 2003, 19:44:51 Job time : 1608.21 secs

fusion of anti-C fusion of anti-C

ritle:
Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Database :

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A fusion of anti-Camino acid sequence Anti-carcinoembryo Anti-carcinoembryo Murine COL1 VH cha Mouse Monse COL-1 variab Maria anti-Pab-42 Heavy chain amino Anti-idiotype anti-Sequence of the va Monoclonal antibod
                                                                                                                                                                                                                                                                          Anti-idiotype anti-
Sequence encoded b
2 H7 VH gene. Syn
2H7 antibody heavy
BH7 antibody heavy
CH7 antibody
Wouse 2H7 antibody
Wouse 2H7 antibody
Wouse 2H7 antibody
Mouse antibody
2H7 heavy chain va
Anti-CA125 bifunct
Heavy chain (VH) g
Anti-CA125 bifunct
Heavy chain (VH) g
Anti-CA125 bifunct
Heavy chain (VH) g
Mouse anti-idiotyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse monoclonal a
TSH receptor antib
TSH receptor antib
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Mouse anti-idiotyp
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55..68
/label= FR2
/note= "framework region 2"
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine monoclonal anti-idiotype antibody 11D10 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
AAB30694

AAB30695

AAR60565

AAR60566

AAR39528

AAB39341

AAU7632

AAU7632

AAU7633

AAU70791

AAY70791

AAX70791

AAX70791
                                                                                                                                                                                                                                                                                                                                                                      AAW10242
AAW41070
AAW47513
AAW47520
AAB98092
AAB98092
AAB98092
AAW19577
AAW19577
AAW19577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW01752
AAR77306
ABP96771
ABP96772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20..153
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW27120 standard; Protein; 153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50..54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20..49
/label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
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04-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW27120
 Heavy chain variab
Monoclonal antibod
Anti-STX1 heavy ch
Anti-idiotype mono
Gamma-glutamyl tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody 11D10 hea
Mouse 11D10 antibo
MAD 1A7 heavy chai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine monoclonal
                                                                                                                                           (without alignments) 927.461 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 **SIDSI./gcgdata/geneseqp/embl./AA1980.DAT:**

**SIDSI./gcgdata/geneseqp/embl.AA1981.DAT:**

**SIDSI./gcgdata/geneseqp-embl.AA1981.DAT:**

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**SIDSI./gcgdata/geneseqp-embl.AA1985.DAT:**

**SIDSI./gcgdata/geneseqp-embl.AA1989.DAT:**

**SIDSI./gcgdata/geneseqp-embl.AA1999.DAT:**

**SIDSI./gcgdata/geneseqp-embl.AA1999.DAT:**

**SIDSI./gcgdata/geneseqp-embl.AA1990.DAT:**

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**SIDSI./gcgdata/geneseqp-embl.AA1991.DAT:**

**SIDSI./gcgdata/geneseqpeneseqp-embl.AA1991.DAT:**

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**SIDSI./gcgdata/geneseqgpeneseqpeneseqpenentl.AA1991.DAT:**

**SIDSI./gcgdata/geneseqgpeneseqpeneseqpenentl.AA1991.DAT:**

**SIDSI./gcgdata/geneseqgpeneseqpeneseqpenentl.AA1991.DAT:**

**SIDSI./gcgdata/geneseqgpeneseqpeneseqpenentl.AA1
                                                                                                                                                                                                                                    MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153
                                                                                                                          August 30, 2003, 22:04:11 ; Search time 26.1846 Seconds
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               5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                              1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
               GenCore version
Copyright (c) 1993 - 2003
                                                                                      OM protein - protein search, using sw model
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AAY21546
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Score

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Murine; mouse; antibody; heavy chain; variable region; anti-idiotype; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the heavy chain variable region of the murine antibody 11D10. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delaying development of, or treating, HMFG-associated tumours -using anti-idiotype antibody 11D10 raised against antibodies to human milk fat globule protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= CDR3
/note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 153; DB 20;
100.0%; Pred. No. 1.8e-130;
ive 0; Mismatches 0;
                                                                                                                                      Antibody 11D10 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                              20..153
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                 /note= "signal peptide"
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= framework_2
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/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                              /label= framework_1
                    standard; Protein; 153 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR2
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/label= CDR1
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97US-0049540.
                                                                                               (first entry)
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Best Local Similarity
Matches 153; Conserva
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                                                                                               16-MAR-1999
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                    AAW87594
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                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide sequence comprises the heavy chain variable region (VH) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATC 12020. 11D10 was obtained by immunising naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polymucleotides (see also AATBS119-50) are claimed. Also claimed are diagnostic kits and methods of using 11D10, 11D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating HMFG-associated tumours. 11D10 is also used in a claimed method of palliating HMFG-associated disease and in claimed kits to detect or quantify anti-HMFG antibody. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Also claimed are diagnostic kits and methods of using 11D10, 11D10 tolypepildes and/or 11D10 polynucleotides, including methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours,
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                                                                                             /label= CDR3
/note= "complementarity determining region 3"
"complementarity determining region 2"
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                                                         region 3"
                                                                                                                                                                             region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chatterjee M, Chatterjee SK, Foon KA;
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                                                                                                                                127..137
/label= FR1
/note= "framework
                                                       "framework
                                                                                                                                                                                            138..153
/label= Constant
              86..117
/label= FR3
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96US-0766350.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KENT ) UNIV KENTUCKY.
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N-PSDB; AAT85150.
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13-DEC-1996;
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1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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1..19
/label- signal_peptide
20..153
/note- "Mature murine 11D10 antibody heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for delaying the development, of or treating HMFG/CEA-associated tumours. The present amino acid sequence represents the heavy chain variable region of the mouse 11D10 anti-idiotype antibody.
                                                       GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
 MECSWVFLFLLS1TTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
            Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g. breast tumor) in humans
                                                                                                                                                                                                                                                    Mouse; murine; vaccine; tumour; human milk fat globules; HMFG; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 153; DB 24; Best Local Similarity 100.0%; Pred. No. 1.8e-130; Matches 153; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                               Mouse 11D10 antibody heavy chain variable region.
                                                                                                EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
                                                                                                                                                                AA016293 standard; Protein; 153 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Fig 2; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001; 2001US-0861294.
                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2002; 2002WO-US15840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chatterjee M, Foon KA;
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                                                                                                                                                                                                          20-MAR-2003
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                                                                                                                                                                                     AA016293;
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                                                                                                        61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
Monoclonal antibody 1A7 which elicits an anti-GD2 immunological response, useful for the development of products for the detection and treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                          DB 20;
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Pred. No. 3.96
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAb 1A7 heavy chain variable region.
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor-associated antiqen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KENT ) UNIV KENTUCKY.
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Best Local Similarity
Matches 31; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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(including small cell lung cancer).
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                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                               17-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                   16-NOV-1998;
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                                                                                                                                                                                                                                                                                                           27-MAY-1999.
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                                                                                                                                                                      AAY21546;
                     Sequence
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                                                                                                                                         AAY21546
                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide is the variable heavy chain region of monoclonal anti-idiotype antibody 1A7. The polypeptide has three CDRs (complementarity determining regions) and four frame work regions. When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The light chain variable region of the 1A7 antibody (AAY28468) is also capable of eliciting an anti GD2 response in mammals. Both the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 T cell and antibody responses. The peptides antibodies may be useful for the modulation of gangliaside GD2, and particularly for the treatment of GD2-associated tumours e.g. melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma
                                                                                                 Heavy chain variable region; antibody 1A7; T cell response; carcinoma; ganglioside GD2; CDR; complementarity determining region; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
                                                                                                                                                                                                                                                                    69..84
/label= "CDR 2"
/note= "Complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                  1177..125
|/label= "CDR 3"
|/note= "Complementarity determining region 3"
                                                                                                                                                                                                                                         "Complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                    137..152
/label= "Constant region"
                                                                                                                                                             1..19
/label= "Signal peptide"
                                                                                                                                                                                20..152
/label= "Mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chatterjee M, Chatterjee SK, Foon KA;
                                                                              Heavy chain variable region of MAb 1A7.
                                                                                                                                                                                                                                                                                                                                              .
.136
.al= "Framework 4"
                                                                                                                                                                                                                                                                                                  35..116
/label= "Framework 3"
                                                                                                                                                                                                    20..49
/label= "Framework 1"
                                                                                                                                                                                                                                                  55..65
/label= "Framework 2"
                                                                                                                                                   Location/Qualifiers
                   AAY28469 standard; Protein; 152 AA.
                                                                                                                                                                                                                      50..54
/label= "CDR 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 2; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0752844.
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96US-0591196.
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                                                           (first entry)
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/label=
137.
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N-PSDB; AAX89553.
                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1995;
16-JAN-1996;
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                                                           06-OCT-1999
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                                       AAY28469;
                                                                                                                                                            Peptide
                                                                                                                                                                                Protein
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                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                      Domain
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          AAY28469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Psoriasis; immunological response; anti-idiotype antibody; gluttate; chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis; monoclonal antibody; 1A7.
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   Length 152;
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                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody 1A7 heavy chain variable region.
DB 20; I
. 3.9e-20;
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100.0%; Pred. No. 3.9e-20;
Live 0; Mismatches 0;
                                                                                                                                                   122 ALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 152
                                                                                                                     123 ALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
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20.3%; Score 31; DB 100.0%; Pred. No. 3.9: ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                            AAY21546 standard; Protein; 152 AA.
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Query Match 20.3
Best Local Similarity 100.
Matches 31; Conservative
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Best Local Similarity 100.
Matches 31; Conservative
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N-PSDB; AAX60630.
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Length 122;

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The invention relates to humanised monoclonal antibodies (MAb) against
Shiga toxins. The humanised MAb that binds to Shiga toxin comprises a
constant and a variable region, where: (a) the constant region contains
at least part of a human immunoglobulin (Ig) constant region, and (b) the
variable region contains at least part of a non-human Ig variable region.
String toxin type 2 is useful for treating a patient with an infection
caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin
producing bacteria. The humanised MAb can also be used to reduce illness
caused by EHEC or other Shiga toxin producing bacteria. EHEC are
associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic
colitis) and the hemolytic uremic syndrome. In particular, the humanised
MAbs ameliorate edema, thrombocytopenia and uremia associated with EHEC-
cantellar diasease. The present sequence represents an anti-STX1 heavy
                                                                                                                         Humanised; monoclonal antibody; MAb; Shiga toxin; immunoglobulin;
ig constant region; enterchemorrhagic Escherichia coli; EHEC; uremia;
edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic syndrome;
thrombocytopenia; EHEC-mediated disease; anti-STXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanized monoclonal antibodies against Shiga toxins, useful for
protection against enterohemorrhagic Escherichia coli or other Shiga
                                                                                                                                                                                                                                                                                     31.35
/note= "complementarity determining region (CDR) 1;
specifically claimed for in claim 10"
                                                                                                                                                                                                                                                                                                                                                   /note= "complementarity determining region (CDR) 2; specifically claimed for in claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                  /note-"complementarity determining region (CDR) 3; specifically claimed for in claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinson JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schmitt CK,
                                                                                                                                                                                                                                                                      'note= "encoded by AAG"
                                                                                           Anti-STX1 heavy chain variable region.
                                                                                                                                                                                                                               Location/Qualifiers
23
AAY21816 standard; Protein; 122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 3; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Welton-Celsa A, O'Brien AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0215163.
97US-0068635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US27267
                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MELT/) MELTON-CELSA A. (OBRI/) O'BRIEN A D. (SCHM/) SCHMIT C K. (STIN/) STINSON J L. (WONG/) WONG H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coxin producing bacteria
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                                                                                                                                                                                                        Shigella dysenteriae
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                                                                                                                                                                                                                                                       Misc-difference
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                                                             10-SEP-1999
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma
                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                               "complementarity determining region 1"
                                                                                                                                                                                               Anti-idiotype monoclonal antibody 1A7 variable heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity determining region
17.6%; Score 27; DB 20; I 100.0%; Pred. No. 1.3e-16; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "corresponding codon TAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                      55..68
/note= "framework region 2"
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                                                                                                                                                                                                                                                                                                                                                                         'note= "framework region 1"
                                           89 LTADISSTAYMQISSLTSEDSAVYFC 115
                                                        LTADTSSSTAYMQISSLTSEDSAVYFC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foon KA;
                                                                                                                                                                                                                                                                                                                                           1..19
//label= sig_peptide
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                     AAW03200 standard; Protein; 152
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96US-0591196.
95US-0372676.
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                                                                                                                                                                (updated)
(first entry)
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126..136
                     27; Conservative
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/note=
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N-PSDB; AAT31333.
           Similarity
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                                                                                                                                                                                                                                                                                                           Aus musculus
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17-JAN-1995;
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26-FEB-1997
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Query Match
Best Local S
Matches 27
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                                                                                                                                                                                                                                                                                                                                          Peptide
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WPI; 2002-000467/01.

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The present sequence is that of the murine anti-idiotype monoclonal antibody (MAb) 1A7 variable heavy chain. MAb 1A7 was raised against the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2. As the glycosphingolipid GD2 is expressed at high density by human neuroectodermal tumours, e.g. malignant melanoma. Concernoted and small cell carcinoma of the lung, MAb 1A7, or its CDM can be used in a vaccine to treat or palliate such diseases. They can also be used to reduce the anti-GD2 Ab bound to a tumour cell.

MAb 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 Ab (humoral response) and CD2-specific cells (cellular response). It can be used to purify anti-GD2 in a sample or measure the level of cellular anti-1A7 or anti-GD2 (AD1') or 14G2a (AD1') or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen binding region; antibody; 138H11; VH region; VL region; human; gamma-glutamyl transferase; gamma-glutamyl transpeptidase; EC 2.3.2.2; kidney cell; carcinoma; renal cell; cytostatic; tumour; antitrheumatic; antiarthritic; liver; stomach; ovary; breast; glioma; melanoma; autoimmune disease; rheumaticid arthritis; metabolic disorder; leukotriene biosynthesis; mercaptoacid; glutathione; metastasis; differentiation; adenocarcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gamma-glutamyl transferase antibody 138H11 antigen binding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the prepn. of probes and primers to respectively assay for 1A7 cDNA, and amplify desired polynucleotides for use in gene therapy. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                               he cDNA can be used in expression systems for 1A7 prodn., and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.6%; Score 27; DB 17; Length 152; 100.0%; Pred. No. 1.6e-16; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/label- VL
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/label- VH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmiedl A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FISC/) FISCHER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUEBEL S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE10020034-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG80224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUEB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
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                                               This invention describes a novel agent (A) for diagnosis and treatment of
            Agent for diagnosis and treatment of carcinoma, especially renal cell carcinoma, comprises binding partner for gamma-glutamyl transferase
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                        Length 279;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                            A fusion of anti-CD20 single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                         Streptavidin; tumour cell; cancer; adenocarcinoma;
hematological malignancy; B9E9.
                                                                                                                                                                                                                                       13.7%; Score 21; DB 23; I
100.0%; Pred. No. 7.1e-11;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "streptavidin"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                          109 ALDYWGQGTSVTVSSAKTTPP 129
                                                                                                                                                                                                                                                                                                                  AAB30694 standard; Protein; 412 AA
                                                                                                                                                                                                                                                                   123 ALDYWGQGTSVTVSSAKTTPP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                      "VL chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "VH chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249..253
/note= "linker"
254..412
                                                                                                                                                                                                                                                                                                                                                                                                                                               109..126
/note= "linker"
                                  Claim 5; Fig 2; 12pp; German.
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             127..248
                                                                                                                                                                                                                                                                                                                                                                                                                                1..108
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                      avidinii.
                                                                                                                                                                                                                                              Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200075333-A1
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                              02-APR-2001
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                AAB30694;
                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                            AAB30694
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07-JUN-1999; 03-DEC-1999;

14-DEC-2000

Goshorn SC,

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The present sequence represents a fusion of an anti-CD20 single chain antibody (BBE9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin fusion proteins. The vector comprises a linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 minno acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD20-specific receptor; CD-20 specific redirected T cell; leukemia; CD20+ malignancy; non-Hodgkin's lymphoma; myeoablative chemotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a CD-20 specific chimeric receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.1%; Score 20; DB 22; I 100.0%; Pred. No. 8.1e-10; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lin Y,
                                         /note= "VL chain"
260.264
/note= "linker"
265.423
/note= "streptavidin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schultz JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 11C; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY84965 standard; Protein; 633 AA.
                                    "VL chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 TSYNMHWVKQTPGQGLEWIG 68
/note= "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer, e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 TSYNMHWVKQTPGQGLEWIG
                                                                                                                                                                                                                                                                                                                           99US-0137900.
                                                                                                                                                                                                                                                                               05-JUN-2000; 2000WO-US15595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 20; Conservative
                 151..259
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                                                                                  (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC86564
                                                                                                                                                                                  WO200075333-A1.
                                                                                                                                                                                                                                                                                                                         07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                 03-DEC-1999;
                                                                                                                                                                                                                                 14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soshorn SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY84965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                      Protein
                                                                  Peptide
                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a fusion of an anti-CD20 single chain antibody (BPE9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector constructs nucleic acid encoding streptavidin nor its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second concline acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detecting the presence or absence of, or treating, a
                                                                                                                                                                                                                                 Reno JM;
                                                                                                                                                                                                                                                                                                                                               New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                            Sanderson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A fusion of anti-CD20 single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin; tumour cell; cancer; adenocarcinoma; hematological malignancy; B9E9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 13.1%; Score 20; DB 22; 1
1 Similarity 100.0%; Pred. No. 7.9e-10;
20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              Schultz JE, Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ourposes, e.g. for detecting the pre-
arget site within a mammalian host,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 11B; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB30695 standard; Protein; 423 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 TSYNMHWVKQTPGQGLEWIG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..126
/note= "VH chain"
127..150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 TSYNMHWVKQTPGQGLEWIG 68
                                                                                                                                                                                                                                                                                                                                                                                              cancer, e.g. adenocarcinomas -
                                                        05-JUN-2000; 2000WO-US15595
                                                                                                      99US-0137900
99US-0168976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                            Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avidinii.
Homo sapiens.
                                                                                                                                                                                                                                                                          WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                             (NEOR-) NEORX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA;
                                                                                                                                                                                                                                                                                                   N-PSDB; AAC86563
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Sequence

Query Match

Matches

ŏ g

Sanderson JA, Reno JM;

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Gaps

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Indels

02-APR-2001

AAB30695;

Synthetic.

Peptide Protein

Length 423;

Synthetic.

Mus sp.

Key Peptide

Peptide

Region Region Region

Region

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murine-human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be used in in vitro immunoassays for the detection of CEA, and monitoring of tumour-associated antigen during therapy. It can also be used in vivo diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the gastrointestinal tract, lung, ovary and pancreas. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis and therapy of carcinoma, e.g. breast or colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ71395 codes for AAR60565 the antibody heavy chain region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-carcinoembryonic antigen chimeric antibodies; CEAS; chimeric human-murine; breast or colorectal carcinoma;
                                                                                          Anti-carcinoembryonic antigen chimeric antibodies; CEAS; chimeric human-murine; breast or colorectal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-carcinoembryonic antigen chimeric heavy chain Ab.
                                                         Anti-carcinoembryonic antigen chimeric heavy chain Ab.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 15;
Pred. No. 2.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rixon MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR60566 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mezes PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; SCC_
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 51; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LQQSGAELVRSGASVKMSC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LOOSGAELVRSGASVKMSC
                                                                                                                                                                                                                                                                                                       94WO-US01709
                                                                                                                                                                                                                                                                                                                                          93US-0017570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.4
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gourlie BB, Kaplan DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric Mus muscaris.
Chimeric Homo sapiens.
                                                                                                                                                                       Chimeric Mus muscaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-294331/36.
                                                                                                                                                                                                                                                                                                                                                                                (DOWC ) DOW CHEM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ71395
                                                                                                                                                                                                                                                                                                       16-FEB-1994;
                                                                                                                                                                                                                              WO9419466-A2
                                                                                                                                                                                                                                                                                                                                            16-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
25-APR-1995
25-MAR-2003
25-APR-1995
                                                                                                                                 heavy chain.
                                                                                                                                                                                                                                                                   01-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR60566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR60566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a synthetic CD20-specific chimeric receptor. The specification describes CD-20 specific redirected T cells which express and bear on the cell surface membrane a CD20-chimeric receptor comprising an intracellular signalling domain, a transmembrane a CD20-specific receptor. The genetically engineered CD20-specific receptor. The genetically engineered CD20-specific redirected T cells are useful for treating a CD20+ malignancy, such human patient having previously undergone mycoablative chemotherapy and stem cell rescue. The genetically engineered CD20-specific redirected T cells are useful for always modergone mycoablative chemotherapy and stem cell rescue. The genetically engineered CD20-specific redirected T cells are also useful for abrogating an untoward B cell function, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetically engineered CD20-specific redirected T cells useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphôma or CD20+ acute or chronic leukemia, and autoimmune disease –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as autoimmune disease (lupus or rheumatoid arthritis) in a patient.
                                                                                            Location/Qualifiers
27..86
/note= "signal peptide from murine T86.66 antibody
kappa 11ght chain"
 stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 20; DB 21; Length 633; 100.0%; Pred. No. 1.1e-09; ative 0; Mismatches 0; Indels
                                                                                                                                                                     21..126
/note= "anti-CD20 variable regions"
                                                                                                                                                                                                                                                                                                                       500..521
/note= "CD4 transmembrane region"
/note= "zeta chain"
                                                                                                                                                                                                                                                                 "hinge region"
                                                                                                                                                                                                                                                                             ..499
.te= "CH3 region"
                                                                                                                                                                                                                            "GS18 linker"
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N-PSDB; AAA15019.
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WO9419466-A2

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RESULT 13 AAR60565

Sequence

Query Match

Length 124; 0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                           murine-human anti-carcinoembryonic antigen (CEA) chimeric antibody. Which can be used in in vitro immunoassays for the detection of CEA, and monitoring of tumour-associated antigen during therapy. It can also be used in vivo diagnostically, or in therapy for the treatment of tumours associated with colorectal and breast carcinomas, as well those of the gastrointestinal tract, lung, ovary and pancreas. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                      Anti-carcinoembryonic antigen chimeric antibodies - for diagnosis and therapy of carcinoma, e.g. breast or colorectal carcinoma
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                                                                                                                                                                                                                                 AAQ71396 codes for AAR60566 the antibody heavy chain region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody specific for treatment and diagnosis of cancer
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                                                                                                                 Schlom J;
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Pred. No. 2.3e-09;
0; Mismatches 0;
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                                                                                                                 Gourlie BB, Kaplan DA, Mezes PS, Rixon MW,
                                                                            (DOWC ) DOW CHEM CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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100.0%; Pre
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Best Local Similarity 100.0
Matches 19; Conservative
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N-PSDB; AAQ71396.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 16, Appl	Sequence 16, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli	Sequence 121, App
SUMMARIES		aı	US-09-861-294-4	US-10-367-506-4	US-09-861-294-16	US-10-367-506-16	US-09-990-205-4	US-10-153-401-4	US-09-861-294-12	US-10-367-506-12	US-10-244-821-6	US-10-013-173-6	US-10-150-762-6	US/10/244	US/10/013	US/10/150	US-10-194-975-121
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		Match Length DB	153	153	32	32	152	152	30	30	412	412	412	423	423	423	119
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ALIGNMENTS

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Sequence 4, Application US/09861294

Patent No. US20020098190A1

GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: Malaya CHATTERJEE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BERRING HAFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 05/049,540
PRIOR PAPLICATION NUMBER: 09/096,244
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR PELING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-13

SPIOR FILING DATE: 1997-06-13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 5.3e-131;
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; LOCATION: (1)...(19)
US-09-861-294-4
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Sequence 4, Application US/09990205
Patent No. US20020150572A1
GENERAL INFORMATION:
APPLICANT: FOON, Kenneth A.
APPLICANT: FOON, Kenneth A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501
CURRENT APPLICATION UNMBER: US/09/990,205
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: US. 09/192,838
PRIOR FILING DATE: 1998-11-16
PRIOR FILING DATE: 1998-11-17
NUMBER: OF SEQ. DI NOS: 5
COMMINDED: US. 05/10-11-17
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Malaya CHATTERJEE
APPLICANT: Renneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT APPLICATION NUMBER: US/09/861,294
PRIOR PILING DATE: 2003-02-13
PRIOR PLING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 09/09,540
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR PILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
SPRIOR FILING DATE: 1907-06-13
SROTUMBER OF SEQ ID NOSS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 6e-22;
Matches 32; Conservative 0; Mismatches 0;
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                                                            20.9%; Score 32; DB 9;
100.0%; Pred. No. 6e-22;
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; Publication No. US20030152575A1
; GENERAL INFORMATION:
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SEQ ID NO 4
LENGTH: 152
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Best Local Similarity 100..
These 32; Conservative
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US-09-990-205-4
; ORGANISM: Mus musculus
US-09-861-294-16
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                                                                                                                                                             Sequence 4, Application US/10367506; Dublication No. US20030122575A1
GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: Malaya CHATTERJEE
APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT APPLICATION NUMBER: US/09/861,294
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR FILING DATE: 1997-06-13
PRIOR PELICATION NUMBER: 60/049,540
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US2002098190al

GENERAL INDORMATION:

APPLICANT: Malaya CHATTERJEE

APPLICANT: Kenneth A. FOON

TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS

FILE REFERENCE: 304142000620.

CURRENT APPLICATION NUMBER: US/09/861,294

CURRENT FILING DATE: 1997-06-13

PRIOR FILING DATE: 1997-06-13

PRIOR FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0
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                121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-367-506-4
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Length 30;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS CURRENT APPLICATION NUMBER: US/09/861,294
CURRENT APPLICATION NUMBER: 00/09,540
PRIOR APPLICATION NUMBER: 00/09,540
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/10367506
; Boulcation No. US2003015257541
; GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Memeth A. FOON
; TITLE OF INVENTION: TUDMORS BEARING HMFG AND CEA ANT
FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1999-06-11
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 30
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3.7e-20;
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Pred. No.
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APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Bero, John M.
APPLICANT: Dearstyne, Erica A.
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100.0%; Pre
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Best Local Similarity 100.0
Matches 30, Conservative
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Best Local Similarity 100.
Matches 30; Conservative
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US-10-367-506-12
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US-10-367-506-12
                                                                                                                                                                                                                                                   SEQ ID NO 12
LENGTH: 30
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Publication No. US20030114398A1
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Chatterjee, Sunil K.
TITLE OF INVENTION: MONCELONAL ANTIBODY 1A7 AND USE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/153,401
FILING DATE: 27-Aug-2002
CLASSIFICATION: <unknown>
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100.0%; Pred. No. 1.8e-20;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Catherine M. Polizzi
REGISTATION UNDHABER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
TELECOMMUNICATION INFORMATION:
                           123 ALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
                                                       122 ALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 152
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APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 09/293,533
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ADDRESSEE: WORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-153-401-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09861294 Patent No. US20020098190A1 GENERAL INFORMATION:
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TELEX: 706141
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATA:
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Best Local Similarity 100.
Matches 31; Conservative
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ZIP: 94304-1018
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; OTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- g US/10/244,821-8
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APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Sanderson, James Allen
APPLICANT: Sanderson, James Allen
APPLICANT: Randerson, James Allen
APPLICANT: Randerson, James Allen
APPLICANT: REPERFORE, Etica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                         Length 412;
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APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Reno, Jonh M.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
     TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 3.9e-10;
0; Mismatches 0;
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                                           FILE REFERENCE: 690022.54762
CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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100.0%; Pre
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Publication No. US20030143233A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                           LENGTH: 412
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APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Scott Stoll
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Randerson, James A.
APPLICANT: Randerson, James A.
APPLICANT: Randerson, James A.
APPLICANT: Randerson, James A.
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.54701
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                         Length 412;
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TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPERENCE: 690022.547C3
CURRENT APPLICATION UNDER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pred. No. 3.9e-10;
Live 0; Mismatches 0;
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Publication No. US20030103948A1
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                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 20; Conserva
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1.1e-09;
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  ; SEQ ID NO 121
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus SP.
US-10-194-975-121
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COTHER INFORMATION: Predicted amino acid sequence of B9E9 single chain antibody- gend

US/10/013,173-8
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US/10/150,762-8
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                                                                                                                                                                                                                                                                                            13.1%; Score 20; DB 15; Length 423; ilarity 100.0%; Pred. No. 3.9e-10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: COSMOLIA, SCOUTES.
APPLICANT: Graves, ScouteS.
APPLICANT: Schultz, Joanne E.
APPLICANT: Lin, Yukang
APPLICANT: SanderSon, James A.
APPLICANT: Rend. Jonh M.
APPLICANT: Rend. Jonh M.
APPLICANT: Rend. John M.
APPLICANT: RENG. STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPERBINES: 690022.547C2
CURRENT APPLICATION NUMBER: 08/10/150,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 423;
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FULE NEPRENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
TITLE OF INVENTION: METHODS OF USE THEREOF
               FILE REFERENCE: 690022.547C1
CURRENT PAPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
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Publication No. US20030039649A1
GENERAL INFORMATION:
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/10150762
Publication No. US20030103948A1
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                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Goshorn, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.1
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserva
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US-10-194-975-121
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 30, 2003, 22:07:01; Search time 10.7819 Seconds Run on:

(without alignments)
1364.679 Million cell updates/sec

US-08-836-455-4

153 1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153 score: Title: Perfect sc Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

length: 0 length: 200000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Listing first 45

1: pirl:* 2: pirl:* 3: pir2:* 4: pir4:* PIR_76:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

;		æ			SUMMAKIES		
Result No.	Score	Query Match	Length	DB	ΔΙ	Description	
1	22	14.4	119	7	PL0089	Iq heavy chain V r	
N	22	14.4	15	~	PL0011		
m	20	13.1	93	7	S42182	gamma chain	
4	20	13.1	94	7	S42177		
ഹ	20	13.1	95	~	S42178		
9	20	13.1	97	7	S42181	gamma	
7	20	13.1	101	7	S42179		
8	20	13.1	101	7	S42184		
σ	20	13.1	102	'n	S42180		
10	19	12.4	140	7	S14238		
11	19	12.4		~	S30752	heavy	
12	19	12.4	150	~	PN0444	heavy chain	
13	19	12.4		7	B26471		
14	19	12.4	178	~	S29594	Ig gamma chain (WM	
12	18	11.8	124	7	S06824	Ig heavy chain V r	
16	17	11.1	112	7	S26473	heavy	
17	17	11.1	246	7	838950	Ig gamma chain - m	
18	17	11.1	446	~	S40295 ·		
13	16	10.5	109	N	PH1001	Ig heavy chain V r	
20	16	10.5	111	~	PH0998	heavy	
21	16	10.5	116	N	S09962	Ig heavy chain V-D	
22	16	10.5	119	~	PH1512	Ig heavy chain V r	
23	16	-:	140	7	809216	Ig heavy chain pre	
24	15	٠	43	~	S11111	heavy chain	
22	15	9.8	67	N	H28833	Ig kappa chain V r	
56	15		91	N	PL0242		
27	15		94	~	G32513	Ig heavy chain V r	
58	15	9.6	96	N	H28195		
59	15	9.8	106	~	PH1002		

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V r	V r	۲ ۲	νr	Vr	V r	V r	v r	V-D	v r	v r	V r	Vr	٧r	V r	v V
chain	chain	chain	chain	chain	chain	chain	chain	chain							
heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy	heavy							
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PL0240	PL0241	S26316	PH0997	S26317	PH1000	S25033	\$25034	S09957	S55535	PL0238	A54378	PL0237	PL0235	PL0234	S19966
7	~	~	N	N	N	~	N	~	ď	N	~	7	~	~	7
107	107	108	109	110	110	111	111	112	113	115	115	117	117	117	117
8.6	8.6	8.6	9.6	8.6	8.6	8.6	9.6	8.6	9.6	9.6	9.6	8.6	8.6	8.6	8.6
15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C; Accession: PL0089
R; Meek, K.; Häsemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; J. Exp. Med. 169, 519-533, 1989
A; Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s A; Reference number: PL0080; MUID:89094248; PMID:2492056
A; Accession: PL0089
                                                                                                                                                                                                                                                                                    A Molecule type: MRNA A; Residues: 1-119 <MEE>
A; Residues: 1-119 <MEE>
A; Cross references: GB.X58580; GB:Y00794; NID:951591; PIDN:CAA41456.1; PID:9930150
A; Cross references shown here is from the VH region of an antidiotypic monoclonal A; Note: the sequences from two other clones (18528-16 and 12584-3) were almost identical C; Superfamily: Immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö.
Ig heavy chain V region (12518-1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.4e-14;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.4%; Scor
100.0%; Pred
0; N
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Best Local Similarity 100.0
Matches 22; Conservative
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92 DTSSSTAYMQISSLTSEDSAVY 113 73 DISSSTAYMQISSLTSEDSAVY 94 qq

Ig heavy chain precursor V region (4C11) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000 C;Accession: PL0011

R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H. Mol. Immunol. 25, 33-40, 1988 A;Title: Structural basis of stimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424

A; Accession:

A; Molecule type: mRNA A; Residues: 1-151 <CRES A; Experimental source: cell line 4C11 C; Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl C; Superfantly: Immunoglobulin V region; immunoglobulin homology C; Reywords: heterotetramer; immunoglobulin E; 1-19/Domain: signal sequence #status predicted <SIG>

F;20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;34-117/Comain: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-125/Region: complementarity-determining 3

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ig gamma chain V region - mouse (fragment)
(5) Specias: Mus musculus (house mouse)
(5) Date: 28-Sep-1994 Requence_revision 21-Jul-1995 #text_change 23-Jul-1999
(5) Accession: 542181
(6) An .: Bona, C.A.: Holmdahl, R.
(7) A.A.: Bona, C.A.: Holmdahl, R.
(8) Eur. J. Immunol. 23, 2503-2510, 1993
(6) A; Title: Variable region gene selection of immunoglobulin G-expressing B cells with shifteners unmber: 542176; MuID:94009207; PMID:7691608
(7) A; Status; preliminary
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with shreference number: S42176; MuID:94009207; PMID:7691608
A;Reference number: S42176
A;Reference number: S42176
A;Rolecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Coross-references: EMBL:225445; NID:9407814; PIDN:CAA80932.1; PID:9407815
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin homology < IMM>
F;8-91/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Iggamma chain V region - mouse (fragment)
C;Species: Mus musculus (house.mouse)
C;Species: 28-58p-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: 542179
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with A;Reference number: 542176; MUID:94009207; PMID:7691608
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A;Residues: 1-101 <MOJ>
A;Residues: 1-101 <MOJ>
A;Cross-references: EMBL:225447; NID:g407816; PIDN:CAA80934.1; PID:g407817
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:225451; NID:9407820; PIDN:CAA80938.1; PID:9407821 C;Superfamily: immunosplobulin V region; immunosplobulin homology C;Reywords: immunosplobulin homology <IMM>
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ilarity 100.0%; Pred. No. 1.2e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                            13.1%; Score 20; DB 2;
100.0%; Pred. No. 1.2e-1:
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.1%; Score 20; DB 100.0%; Pred. No. 1.3 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 TSYNMHWVKQTPGQGLEWIG 68
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserva
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Best Local Similarity
Matches 20; Conserv
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A; Residues: 1-97 <MOJ>
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                                                                                                                                                                                                                                                                                                                                                 Query Match
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S42179
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C;Species: Mus musculus (house mouse)
C;Date: 28-8pe-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42177
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Bur, J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42177
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <MOJ>
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C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: $42182
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Bir. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cel
A;Reference number: $42176; MUD:94009207; PMID:7691608
A;Accession: $42182
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C;Accession: S42178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule Type: DNA
A.Molecule Type: DNA
A.Cross-references: 1-93 <MOJ>
A.Cross-references: EMBL: Z25453; NID: g407822; PIDN: CAA80940.1; PID: g407823
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: immunoglobulin homology <IMM>
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                                                           Length 151;
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                                                      Score 22; DB 2; Length 151
Pred. No. 1.7e-14;
0; Mismatches 0; Indels
  F;137-151/Domain: C region (fragment) #status predicted <COR>
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100.0%; Pred. No. 1.1e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                         121 GALDYWGQGTSVTVSSAKTTPP 142
                                                                                                                                                              122 GALDYWGQGTSVTVSSAKTTPP 143
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                                                      Query Match

Best Local Similarity 100.0%; Pa
Matches 22; Conservative 0;
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Best Local Similarity 100.0
Matches 20; Conservative
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C; Species: Homo sapiens (man)
C; Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C; Accession: PNO444
R; Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A; Title: A general method for chimerization of monoclonal antibodies by inverse polym A; Reference number: PNO444; MUID:93138402; PMID:1339379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain precursor V region - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999 C; Accession: 330752 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999 R; Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W. Nucleic Acids Res. 15, 5496, 1987 A; Tile: Improved RNA sequencing method to determine immunoglobulin mRNA sequence. A; Reference number: S30751; MUID:87260030; PMID:3601683
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                                                 A;Cross-references: EMBL:X56392; NID:951619; PIDN:CAA39803.1; PID:9747853 C. Superfamilty: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin homology <a href="https://documentoglobulin-nomology">https://documentoglobulin-nomology</a> <a href="https://docum
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A.Residues: 1-149 <GRA>
A.Residues: 1-149 <GRA>
A.Cross-references: EMBL:X05878; NID:g52526; PIDN:CAA29302.1; PID:g52527
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>
F;33-116/Domain: c region (C-gamma 2b) (fragment) #status predicted <CRI
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heteroterramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-150/Product: Ig heavy chain V region #status predicted <MAT>F;20-117/Domain: variable region <VRG>F;34-117/Domain: immunoglobulin.homology <IMM>
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Pred. No. 1.7e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 DYWGOGTSVTVSSAKTTPP 143
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Matches 19; Conservative
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A; Molecule type: mRNA
A; Residues: 1-150 <KAL>
         A; Residues: 1-140 <VAN>
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PN0444
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Spate: 28.58p-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999
C; Accession: 842180
R; Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A; Reference number: 842180
A; Accession: 842180
A; Accession: 842180
A; Accession: S42180
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-102 <AOJ>
A; Cross-references: EMBL: 225449; NID: 9407818; PIDN: CAA80936.1; PID: 9407819
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Keywords: immunoglobulin homology <IMM>
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(5.5pecies: Mus musculus (house mouse)
(5.5pecies: Musculus (house mouse)
(5.5pecies: Musculus (house mouse)
(5.5pecies: Musculus (house mouse)
(5.4pecies: Musculus (house mouse)
(5.4pecies: Musculus (house mouse)
(6.4pecies: Musculus (house mouse)
(7.4pecies: Musculus (house)
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R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
R; Vandamme, 192, 767-775, 1990
A; Title: Construction and characterization of a recombinant murine monoclonal antibody A; Reference number: S14236; MUID:91006173; PMID:2209622
A; Accession: S14238
A; Molecule type: mRNA
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C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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A; Residues: 1-101 <MOJ>
A; Residues: 1-101 <MOJ>
A; Cross references: EMBL:225457
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: immunoglobulin homology <IMM>
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1.2e-12;
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    68
                                                     30 TSYNMHWVKQTPGQGLEWIG 49
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49 TSYNMHWVKQTPGQGLEWIG
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.(
Matches 20; Conservative
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Gaps ö

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A; Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-m A; Reference number: $06815; MUID:90064531; PMID:2555519
A; Accession: $06824
A; Molecule type: mRNA
A; Residues: 1-124 < MILL>
A; Residues: 1-124 < MILL>
A; Residues: EMBL: X17166; NID:951918; PIDN:CAA35044.1; PID:9930156
A; Cross references: EMBL: X17166; NID:951918; PIDN:CAA35044.1; PID:9930156
A; Note: the authors did not translate the codon TGG for residue 36
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; S2-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 11.8%; Score 18; DB 2; Length 124; Best Local Similarity 100.0%; Pred. No. 1.5e-10; Matches 18; Conservative 0; Mismatches 0; Indels
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Job time : 10.7819 secs
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                                                                                               C; Species: Mus musculus (house mouse)
C; Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C; Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C; Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
R; Buckel, P: Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A; Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A; Reference number: A91572; MUID:87248058; PMID:3110009
                                                                                                                                                                                                                                                                                                                                                                       A; Wolecule type: mRNA
A; Residues: 1-152 <BUC>
A; Cross-retences: GE-MI6163; NID:g195405; PIDN:AAA38292.1; PID:g195406
A; Cross-retences: G.; Gearhart, P.J.
J. Exp. Med. 172, 1717-1727, 1990
J. Exp. Med. 172, 1717-1727, 1990
A; Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary
A; Reference number: S70410; MUID:91079775; PMID:2258702
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C;Accession: S06824
C;Accession: S06824
S;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-178 <SEY>
A; Cross-references: EMEL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C; Keywords: immunoglobulin
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1.8e-11;
thes 0; Indels
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                                                                      Ig heavy chain precursor V region (MAK33) - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.4%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 19; Conservative 0; Mismatches
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A; Residues: 1-19 <LEB>
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:
August 30, 2003, 22:04:41; Search time 9.24161 Seconds
(without alignments)
778.553 Million cell updates/sec
Title:
US-08-836-455-4
Perfect score: 153
Sequence: 1 MECSWVFLFLISTTGVHSQ......TVSSAKTTPPPVYPLVPGSL 153
Scoring table: OLIGO
Gapop 60.0, Gapext 60.0
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Word size : 0 Total number of hits satisfying chosen parameters: 127863

127863 seqs, 47026705 residues

Searched:

Total number of Alts Satisfying on Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

		Description		P01757 mus musculu	_	P01746 mus musculu	9 mus	P01783 mus musculu	P01812 mus musculu	P01748 mus musculu	P01749 mus musculu	P01750 mus musculu	P01754 mus musculu	P01758 mus musculu	P06328 mus musculu	P01745 mus musculu	P01755 mus musculu	P01751 mus musculu	P01753 mus musculu	P06330 mus musculu	P01741 mus musculu	P06327 mus musculu	P06329 mus musculu	P06321 mus musculu	P01735 mus musculu	Snur 6	P03980 mus musculu	P19180 carassius a	P01743 homo sapien	homo	mus m	6 homo	homo	7 homo	P01744 homo sapien
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SUMMARIES		ID	HV12_MOUSE	HV13_MOUSE	HV03_MOUSE	HV02_MOUSE	HV43_MOUSE	HV16_MOUSE	HV42_MOUSE	HV04_MOUSE	HV05_MOUSE	HV06_MOUSE	HV10_MOUSE	HV14_MOUSE	HV49_MOUSE	HV01_MOUSE	HV11_MOUSE	HV07_MOUSE	HV09_MOUSE	HV51_MOUSE	HV00_MOUSE	HV52_MOUSE	HV50_MOUSE	TVB8_MOUSE	TVB2_MOUSE	HV15_MOUSE	HV48_MOUSE	HV03_CARAU	HV1B_HUMAN	HV1G_HUMAN	TVA1_MOUSE	TVA1_HUMAN	TVB1_HUMAN	TVA2_HUMAN	HV1C_HUMAN
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		Match Length	117	117	120	140	144	136	117	117	117	117	117	117	117	121	137	139	117	118	114	117	120	130	133	136	138	117	117	117	130	131	135	139	147
d	Query	Match	9.2	•	٠	٠		8.5	٠	7.2	٠	٠								•		•	•		•	•				•			2.5		
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34 7 4.6 111 1 HV35_MOUSE P01804 mus musculu 35 7 4.6 116 1 HV31_HEPTR P01919 P01804 mus musculu 36 7 4.6 116 1 HV31_HEPTR P01919 P	DR InterPro; IPR007110; Ig-11ke. DR InterPro; IPR007306; Ig_MHC. DR InterPro; IPR003596; Ig_W. DR PAGE: PR003596; Ig_W. DR PAGE: PR0047; IG'Y. DR SNART; SM0040; IGY: 1. DR PR051TE; PS50835; IG_LIKE; 1. DR MUMUNOJLOULIN V region; Glycoprotein. FT CARBOHYD 25 55 BY SIMILARITY. FT CARBOHYD 55 55 BY SIMILARITY. FT CARBOHYD 55 55 BY STMILARITY. FT CARBOHYD 55 55 BY STMILARITY. OUETY MATCH 117 AA; 12983 MW; 3CP8ACE4BE447E41 CRC64; AC SEQUENCE 117 AA; 12983 MW; 3CP8ACE4BE47E41 CRC64; OUETY MATCH 95 BSST CONSETVATIVE 0; Mismatches 0; Indels 0; Gaps 0 AGASVKMSCKASGYT 47
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NCBI_TaxID=10090;
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ID HV43_MC
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DT 21-JUL
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MEDINE-80078170; PubMed-6765983;
Schilling J., Clevinger B., Davie J.M., Hood L.;

"Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";

"Mature 283:35-40(1980).
"In RICELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
HICH OCCUR IN THE D AND J SEGMENTS.

"HICH OCCUR THE PROTEIN BINDS DEXTRAN."
"IN STATE AS 242; MHMSJ5.
"IN HICH POSITIONS, MANKS J.
"IN HICH POSITIONS, MANKS J.
"IN THEFPOSITIONS, MANKS J.
"IN THEFPOSITIONS, J. J.
"IN THEFPOSITIONS, 
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Eur. J. Immunol. 12:1023-1032(1982).

-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER

DIFFERENTIATED GENES THATH HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus..
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 14; Conservative 0; Mismatches 0; Indels
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117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
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HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILINE-83131846; PubMed-6186498;
Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marabak-Rothstein A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
18 heavy chain V region 36-65.
Mus musculus (Mouse)
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BY SIMILARITY.
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Pfam; PF00047; 1g; 1.
SMRFT; SM00406; 1g; 1.
PROSITE: PS50835; 1G_LIKE; 1.
Immunoglobulin V region; Hybridoma.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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P01747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDINE-82152818; PubMed-6801765;
Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
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100.0%; Pred. No. 5.9e-07;
ive 0; Mismatches 0; Indels
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                                                                                                                 0; Indels
120 AA; 13307 MW; FF04E4A167B654AF CRC64;
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                                                                   Score 14; DB 1; L Pred. No. 5.1e-07;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003106; Ig_MRC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SMO406; IGY, 1.
IMMUNO910bulin V region; Hybridoma; Signal.
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                                                  9.2%; Suc.
100.0%; Pre
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                  MEDLINE-81012133; PubMed-6774258;
MEDLINE-81012133; PubMed-6774258;
Sakano H., Waki R., Kurosawa Y., Roeder W., Tonegawa S.;
"Two types of somatic recombination are necessary for the generation of complete immunoglobulin heavy-chain genes.";
Nature 286:676-683(1980).
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DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBL_TaxID=10090;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 21 precursor (Fragment).
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Pred. No. 6.1e-07;
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 141 precursor.
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SMARY; SM00406; IGv. 1.
PROSITE; PS50835; IG_LKE; 1.
Immunoglobulin V region; Signal.
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                                                                                          Mus musculus (Mouse)
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P01783;
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Best Local S
Matches 14
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      ACCOCC OCT REPRESENT THE PROPERTY OF THE PROPE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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H4 cyanogen-bromide
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DN -> ND (IN REF. 2).

W -> H (IN REF. 2).

Y -> W (IN REF. 2).
                   Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
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Pred. No. 6.1e-06;
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Immunoglobulin V region; Signal; 3D-structure.
NON_TER 1 1 1
SIGNAL <1 16
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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MEDLINE=76091933; PubMed-812695;
Rocca-Serra J., Millil M., Fougereau M.;
"Determination of the primary structure of a immunoglobulin. Amino-acid sequence of the l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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JH4 SEGMENT.
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100.0%; Pred
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MEDLINE-77100368; PubMed-401950;
                                                                                                                                                                                                                                                                                                                                                PDB; 1150.03-500-95.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W-V.
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SMART; SM00406; IGv; 1.
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These 13; Conserve
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P01812;
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117 1
117 AA;
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-1- MISCELLANDOUS: THIS GERMINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR; A02030; HVMS23.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                               Bourgois A., Fougereau M.;
"Partial amino acid sequence of the variable region of a mouse"
gammaG2a immunoglobulin heavy chain. Evidence for the existence of
third sub-group of variability for the heavy chain pool.";
FEBS Lett. 8:65-268(1970).
-I- MISCELLANEOUS: THIS GAMMA-2A CHAIN WAS ISOLATED FROM A MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                         15.1.1...
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 23 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musi.
                   Gough N.M., Bernard O.; "Sequences of the joining region genes for immunoglobulin heavy chains and their role in generation of antibody diversity."; Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
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                                                                                                                                                                                                                                                                                                                      Length 117;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                 117 AA; 13051 MW; 156DCCC259380F19 CRC64;
                                                                                                                                                   -1- SIMILARITY: Contains 1 immunoglobulin-like domain. PRI; A91190; G2M873.

HSSP, P011010; ZFBJ.

InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                   Query Match 7.8%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 12; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                          IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
SEQUENCE OF 96-117 FROM N.A. MEDLINE=81223769; PubMed=6787590;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                         SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                             126 YWGQGTSVTVSS 137
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                                                                     DISULFIDE BOND.
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P01748;
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata, Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                 COMPLEMENTARITY - DETERMINING - 1.
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COMPLEMENTARITY - DETERMINING - 1.
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COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                 Score 11; DB 1; Length 117;
Pred. No. 0.00058;
                                                                                                                                                                                                                                                                                                     0; Indels
IG HEAVY CHAIN V REGION 23. FRAMEWORK-1.
                                                                                                                                                                                                  12772 MW; C530F829C906F69B CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ig heavy chain V region 3 precursor.
                                                                                                                                                                                                                                  7.2%; Scor.
100.0%; Pred. No. v.
0; Mismatches
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BY SIMILARITY
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HSSP; P01810; 2FBJ.
MGD; MGI:96486; Igh-VJ558.
InterPro: IPR007110; Ig-1ike.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Ffam; PF00047; Ig; 1.
FMAM: SMOM46; Ig; 1.
PROSITE: PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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Mammalia; Eutheria; Rodentia;
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Best Local Similarity
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13016 MW; 427C861C53975EDC CRC64;

BY SIMILARITY.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE
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MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
PIR; A02032; HVWS02.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-2.
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100.0%; Pred. No. 0.00058;
ive 0; Mismatches 0; Indels
             7.2%; Score 11; DB 1; Length 117; 100.0%; Pred. No. 0.00058; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 102 precursor.
Mus musculus (Mouse).
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InterPro, IPR007110, Ig-like.
InterPro, IPR003006, Ig_MHC.
InterFro, IPR003596, Ig_V.
           Query Match 7.2
Best Local Similarity 100.
Matches 11; Conservative
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P01750;
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 0.00058;
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100.0%; Pre-
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PIR, C90809, HVMS45.
HSSP, P01810, 2FBJ.
MGD, MIT:96486, Igh-VJ558.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig-MC.
InterPro; IPR003596; Ig-V.
SMART; SM00440; Ig, Ig, I.
PROSITE; PS50835; IG_LIKE; I.
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117 AA;
                                                              SEQUENCE FROM N.A.
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NCBI_TaxID=10090;
                                                                                                                                                                                 Baltimore D.;
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HV01_MOUSE
P01745;
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SEQUENCE
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   SELETTE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-85099340; PubMed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                     7.2%; Score 11; DB 1; Length 117; 100.0%; Pred. No. 0.00058; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                      IG HEAVY CHAIN V REGION 108A.
IG-LIKE.
                                                                                                                                                                                                                                                                                  117 117
117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region VH558 B4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA.
                                                                                                  EMBL; J00488; AAA38519.1; -. PIR; A02041; HVMSA. HSSP, P01810; 2FB. MGD, MGD; MG1:96486; Igh-VJ558. InterPro; IPR0070110; Ig-11ke. InterPro; IPR0070110; Ig-11ke. InterPro; IPR003066; Ig_MHC. InterPro; IPR003506; Ig_V. Pfam; PF00047; ig; 1. SMART; SM00406; iGV; 1. SMART; SM00406; iGV; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin V region; Signal
SIGNAL 1 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                   Query Match 7.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                        SSLTSEDSAVY 113
                                                                                                                                                                                                                                                                                                                                                                                     103 SSLTSEDSAVY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                      >117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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ID HV49_MOUSE
AC P06328;
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NON_TER
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A Zakut R., Cohen J., Givol D.;

A Zakut R., Cohen J., Givol D.;

B Zakut R., Cohen J., Givol D.;

C I C A STANDART SECRETES IGG2B.

C I SIMILARITY: Contains 1 immunoglobulin-like domain.

PIR, 393708; GYMS11.

R HSSP, PO1810, 2FBJ.

R InterPro; IPR001306; Ig_MC.

InterPro; IPR003006; Ig_MC.

R InterPro; IPR003006; Ig_MC.

R SMART; SM04406; IGv: 1.

PROSITE; PS50835; IG_LIKE; 1.

R Immunoglobulin V region.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-81053741; PubMed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPCII.";
Nucleic Acids Res. 8:3591-3601(1980).
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IG HEAVY CHAIN V REGION VH558 B4
                     FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                       FRAMEWORK - Z.
COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                        7.2%; Score 11; DB 1; Length 117; 100.0%; Pred. No. 0.00058; Live 0; Mismatches 0; Indels
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                                                                                                                                                                     12834 MW; B8862FAC67ABD345 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-SEP-2003 (Rel. 42, Last annotation update)
1G heavy chain V region MPC 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AA
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                                                                                                  FRAMEWORK-3.
BY SIMILARITY.
                                                            FRAMEWORK-2
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                             103 SSLTSEDSAVY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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117 AA;
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ID HV11_MC
AC P01755;
DT 21-JUL-
DT 21-JUL-
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                                                                                                                                                                                                                                            -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                        "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                      WEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 11; DB 1; Length 137; 100.0%; Pred. No. 0.00067; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG HEAVY CHAIN V REGION S43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15200 MW; ADD5881BF44B8EC9 CRC64;
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region S43 precursor.
Mus musculus (Mouse).
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JH2 SEGMENT.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 1. SMART; SM04060; IGV; 1. PROSITE; PSS6835; IG_LKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro: IPR007110; Ig-like.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                  (NPB ANTIBODIES).
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137 AA;
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                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P01810; 2FBJ
                                                                                                                                                                          Baltimore D.;
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Best Local Simi
Matches 11;
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Search completed: August 30, 2003, 22:10:22 Job time : 9.24161 secs

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0924r3
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0924r0
0924q6
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0924r4
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Q8k172
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08k0f2
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0924r6
0924p8
0924q4
091va2
0924q5
091v67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488.1;
RMGD; MGI:96486; Igh-VJ558.
R InterPro; IPR007110; Ig-11ke.
R InterPro; IPR007306; Ig_MHC.
R InterPro; IPR003596; Ig_V.
R Pfam; PF00047; Ig; 4.
R SMART; SM00406; IG, 11
R PR0SITE; PS00209; IG_LIKE; 4.
R PROSITE; PS00209; IG_MHC; 2.
Hypothetical protein.
Q SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 kba protein.
IGH-VJ558 OR AI893585.
Mus musculus (Mouse).
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Pred. No. 7.1e-08;
0; Mismatches 0;
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0924P6
0924R0
0924Q6
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0924R1
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0924R4
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081X172
08K074
08K074
08CX4
0924R6
0924P8
091V47
091V67
0924P9
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100.0%; Pr
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   Conservative
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nes 16; Conserv
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   Query Match
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1671.732 Million cell updates/sec
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                                                                                                               August 30, 2003, 22:06:06; Search time 23.6174 Seconds
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0991C4
0991R14
099dxe9
099xe0
0925x3
08873h6
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099177
092442
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                                                                                                                                     830525 seqs, 258052604 residues
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                                                                               protein search, using sw model
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09DD9BB
099CCD9
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090EC4
090EC4
092AC0
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091C77
091C77
092AC0
092AC0
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Gapop 60.0 , Gapext 60.0
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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sp_bacteriap:*
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sp_phage:*
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                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
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sp_bacteria:*
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sp_mhc:*
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   Arakawa T., Hara A., Fukunishi Y., Koshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sak Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rasaid K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Browstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rordone P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Stoch K.-F., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Marsareli V., Wanghi, V., Wang K., Wang K., Wawaji H., Kohtsuki S., Marsareli V., Wang K., Wang K., Wawaji H., Kohtsuki S.,
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                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:885-504(2001). EMBL; AKO07163; BAB24877.1; -. HSSP; PO1810; 2FBJ.
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                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Adult male testis cDNA, RIKEN full-length enriched library,
clone:1700110L11, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-JUNR-2003 (TrEMBLrel. 23, Last annotation update)
Adult male kidney CDNA, RIKEN full-length enriched library, clone:0610041A01, full insert sequence.
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 111 AA; 11976 MW; 874DDF7BD98BD7B2 CRC64;
                               111 AA.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
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MEDLINE-21085660; PubMed-11217851;
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STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-21085660; Pubmed-11217851;
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100.0%; Pre-
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity 100.0
Matches 15; Conservative
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                                 PRELIMINARY;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                 Q9D9B8;
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                               Q9D9B8
RESULT 2
Q9D9B8
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ra Fleischmann W., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Browstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Gustinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
Ryons P., Marchlonni L., Mashima J., Mazzarelli J., Mombarts P.,
Ryons P., Marchlonni L., Mashima J., Mazzarelli J., Mombarts P.,
Ryons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK002075; BAB22422.1; -.
HSSP; P01810; 2FBJ.
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PROSITE; PSS0835; IQ_LIKE; 4.
PROSITE; PS00290; IG_MC; 1.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
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100.0%; Pred. No. 6.9e-07;
ive 0; Mismatches 0;
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IGLIKE; 3.
PROSITE; PS60290; IG_MHC; 2.
SEQUENCE 426 AA; 45819 MW;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; Ig; 4.
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Best Local Similarity 100.0%
Matches 15; Conservative
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Matches 15; Conserv
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STRAIN=BALB/C;
MEDLINE=20448942; PubMed=10992488;
Malkiel S., Liac L., Cunningham M.W., Diamond B.;
Malkiel S., Liac L., Cunningham M.W., Diamond B.;
"T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin.";
Infect. Immun. 68:5803-5808(2000).
Infect. Immun. 68:5803-5808(2000).
HSSP; P01810; 2FBJ.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ225174; CAB65237.1; -.
HSSP: P01810; 2PBJ.
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117 AA; 13000 MW; CDDE2AF84D499734 CRC64;
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100.0%; Pred. No. 2.3e-06;
ative 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last seg
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMARY; SM0406; IGv; I.
PROSITE; PS50835; IG_LIKE; I.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserv
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                                                                          SEQUENCE FROM N.A.
                                         NCBI_TaxID=10090;
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ID Q9QXF0
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Q90XE9
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Hayashizaki Y.;
Henderional annotation of a full-length mouse cDNA collection.";
Hencerional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).

EMBL: AK007918; BAB25349.1;
HSSP; P01842; 7FAB.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
(Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                             473 AA
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                                                                                                                                                                Created)
                                                                                                                             PRT;
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STRAIN-C57BL/6J; TISSUE-Pancreas;
MEDLINE-21085660; PubMed-11217851;
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100.0%; Pre-
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
103 SSLTSEDSAVYFCAR 117
                      103 SSLTSEDSAVYFCAR 117
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IGH-1 OR 1810060009RIK.
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Best Local Similarity
Matches 15; Conserv
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SMART; SM00406; IGv
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PubMed-11819679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/c;
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Q925S3
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Pulrect Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl) Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069915; BAB63931.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                              Mus mušculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
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Pred. No. 2.4e-06;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                Clemens A., Rademaekers A., Specht C., Koelsch E.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ22517; CAB65236.1; -.
HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA; 13060 MW; D816AD0858A47E4C CRC64;
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143 AA; 15704 MW; C99D2433F2BADBAO CRC64;
              01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pre
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V165-D-J-C MU.
                                                                                                                                                                                                                                                                                              Interpro; IPR007110; Ig-like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003506; Ig_V.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGV; I.
PR0SITE; PS50835; IG_LIKE; I.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                         NCBI_TaxID=10090;
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Strain D., Zeng G., Yan X., Li X., Su C.;
Cui D., Zeng G., Yan X., Li X., Su C.;
"Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same 'strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240166; AAK43731.1; -.
InterPro; IPR003106; 1g_MHC.
InterPro; IPR003596; 1g_V.
InterPro; IPR003596; 1g_V.
SMART; SM00406; 1G; 1.
PROSITE; PS50835; IG_LIKE; 1.
SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;
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the repair of intestinal epithelium after irradiation in mice.";
World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Hypothetical 51.7 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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llarity 100.0%; Pred. No. 3e-06;
Conservative 0; Mismatches 0; Indels
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO55447; AAH2447.1; -
InterPro; IPR00345; CytC_heme_bind.
InterPro; IPR003105; Ig_AHC.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_W.
PROSITE; SMO0407; igy; 3.
PROSITE; PS00190; CYTOCHROME_C; 1.
                           0925S3;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
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147 AA
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PRT;
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Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L., Bautsch W., Kola A., Klos A., Koehl J.;
Bautsch W., Kola A., Klos A., Koehl J.;
"Site-Directed Cla-Receptor Antibodies from Phage Display Libraries.";
J. Immunol. 160:2947-2958[1998].
EMBL; AJ222590; CAA10890.1;
-...
HSSP; PO1825; TRAB.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_W.C.
InterPro; IPR003596; Ig_W.C.
SMART; SMO406; Ig; 1.
SMART; SMO4066; Ig; 1.
      MEDLINE=98169018; PubMed=9510199;
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"T-Call-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin...
Infect. Immun. 68:5803-5808(2000).
EMBL: AF206029; AAF69327.1; -.
HSSP; PO1810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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                                                                      9.2%; Score 14; DB 11; Length 474; 100.0%; Pred. No. 8.2e-06; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.5e-05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-myosin immunoglobulin heavy chain variable region
                            Hypothetical protein.
SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
51ngle chain Fv (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                  110 AA.
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PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 19; 1. SMART; SM00406; 1Gv; 1. PROSITE; PS50835; IG_LIKE; 1.
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                                                                                     Best Local Similarity 100.
Matches 14; Conservative
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Rozono Y., Kozono H., Azuma T.;

"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of B Cell Antigen Receptors in Response to (4-
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

InterPro; IPR067788; BAB63273.1;

InterPro; IPR003006; Ig_Mic.
InterPro; IPR003596; Ig_V.

Pfam; PF00047; ig; 1.

SWART: SW00406; IGV; 1.

SWART: SW00406; IGV; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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121 121
121 AA; 13255 MW; D293E4EBC8C59D5B CRC64;
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1 Similarity 100.0%; Pred. No. 3.1e-05;
13; Conservative 0; Mismatches 0;
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SCAOOD V., KOZONO H., AZUMB T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
V23-D-J-C mu protein (Fragment).
V23-D-J-C MU.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
VCBI_TaxID-10090;
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8.5%; Score 13; DB 11; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB069913; BAB63929.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; ig; 1.
SMART; SM0046; IGy; 1.
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142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
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Search completed: August 30, 2003, 22:11:19 Job time : 24.6174 secs

105 DYWGQGTSVTVSS 117

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U39900 Mus musculu

AB050070 Mus musculu

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A77138 Sequence 6

BC003888 Mus musculus

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X79907 M.musculus
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-MODEL-frame+-p2n.model -DEV-xlh
-MODEL-frame+-p2n.model -DEV-xlh
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-NO_MARP -LARGEQUERY -NGG_SCORES=-0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TINEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                   August 30, 2003, 22:10:26; Search time 3130.85 Seconds (without alignments) 1999.191 Million cell updates/sec
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816
1 MECSWVFLFLLSITTGVHSQ ......TVSSAKTTPPPVYPLVPGSL 153
                         Compugen Ltd
                                                              - nucleic search, using frame_plus_p2n model
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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BC033451 Mus muscu AB050073 Mus muscu AB069863 Mus muscu

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GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
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        Chatterjee, M. and Foon, K.A.
Methods of delaying development of HMFG-associated tumors using methods of delaying development of HMFG-associated tumors using anti-idictype antibody 11010
L. Patent: JP 2001523269-A 2 20.NOV-2001;
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PN JP 2001523269-A/2
PP 12-UNN-1998 UP 199503252
PR 13-UNN-1998 US 60/049540,11-JUN-1998 US 09/096244 F
MALAYA CHATTERJEE, KENNETH A FOON
PC AGIR39/395, AGIR39/39//CO7K16/42
CC Strandedness: Single;
CC TOPOLOGY: Linear;
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Key Location/Qualifiers
CDS 1. .459
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
/121 c 119 g 109
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TITLE
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BD085738.1 GI:22631348
JP 2001523269-A/2.
unidentified unidentified unclassified.
            PAT 17-0CT-2001
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                                                                                     T (bases 1 to 461)
Chatterjee, M. and Foon, K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11b10
Patent: US 6274143-A 3 14-AUG-2001;
Location/Qualifiers
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Matches:
Conservative:
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Indels:
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            DNA
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         AR164506 461 bp
Sequence 3 from patent US 6274143.
AR164506
AR164506.1 GI:16237556
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                                                                                                                                                            /organism="unknown"
121 c 119 g
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Unclassified.
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/product="anti-A/U antibody"
/protein_id="BAB87192.1"
/db_xref="G1:19909936"
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SITSEDSAVYFCARGEFGNPWFAYWGQGTLVTVSAAKTTAQPVYPLAPGSL"
a 126 c 121 g 110 t
                                                                                                                                                         ROD 02-APR-2002
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                     The Separation of three antibody populations from anti-poly(A).poly(U) antibodies elicited in mice or rabbits and antigenic features of poly(A).poly(U))
MOL Immunol. 19 (2), 257-266 (1982)
82245325
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Published Only in Database (2002)
3 (bases 1 to 471)
Kitagawa,Y.
Direct Submission
Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural University, Biotechnology Institute; Minami 2-2, Ogata, Akita OIO-0444, Japan (E-mail:kitagawa@qri.akita-pu.ac.jp, UKL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
                                                                                                                                                                     cds
                                                     авоэсово 471 bp mRNA linear ROD
Mus musculus VH9H8 mRNA for anti-A/U antibody, partial
AB050080
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Mismatches:
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Matches:
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/cell_line="hybridoma 9H8"
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/organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="VH9H8"
11. .>469
/gene="VH9H8"
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AB050080
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GYLLTSYNMHWYKQTPCQGLENIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQI
SSLTJSEDSAVFCARGNWEGALDYWGQGTSVTVSS"
101 c 101 g 101 t
      ROD 22-MAY-2001
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 411)

Tripathi, P.K., Qin, H., Bhattacharya-chatterjee, M., Ceriani, R.L., Poon, K.A. and Chatterjee, S.K.

Construction and characterization of a chimeric fusion protein consisting of an anti-idiotype antibody mimicking a breast

Hybridoma 18 (2), 193-202 (1999)
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Chatterjee S.K. and Tripathi,P.K.
Direct Submission
Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .>411
/note-"anti-idiotype antibody 11D10; mimics a breast
cancer-associated antigen, human fat globule (HMFG)"
      24720 411 bp mRNA linear ROD 23 musculus immunoglobulin heavy chain mRNA, partial cds.
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136
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/product="immunoglobulin heavy chain"
/protein_id="AAK55119.1"
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/mol_type="mRNA"
/strain="BALB/c"
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                                                                                     Mus musculus (house mouse)
Mus musculus
                                                    AF124720.1 GI:14164544
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725.00
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MMU39899 11-NOV-1996 483 bp DNA linear ROD 21-NOV-1996 Mus musculus anti-glycoprotein-B of human Cytomegalovirus immunoglobulin Vh chain gene, partial cds.
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                                                                                                                                                                                                                                                   116 GTTCAGCTCCAGCAGTCTGGGCTGAGCTGGCAAAACTGGGGCTTCAGTGAAGTTGTCC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 118
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Schoppel, K., Hassfurther, E., Britt, W., Ohlin, M., Borrebaeck, C.A. and Mach, M.
                                                                                                                                                                                                                                                                                                                                         Antibodies specific for the antigenic domain 1 of glycoprotein B (gpUL55) of human cytomegalovirus bind to different substructures Virology 216 (1), 133-145 (1996) 96187797
                                                                                                                                                                                                                                    21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-NOV-1995) Michael Mach, Institute of Virology, University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen.
                                                                                                                                                                                                                                                                                          1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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Matches:
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 /db_xref="taxon:32644"
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Schoppel, K.
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75.64%
76.10%
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                                                                                                                                                                                                                                                                                                                                                                                                 PAT 29-SEP-1997
                                                                                                                                                                                                             362 GAGTATGGTAACCCCTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGTA 421
119 AsnTrpGluGlyAla---LeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1553)
Saito,Y., Kogiku,T., Kamishiro,T., Murafuji,H., Takami,M. and Fumino,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .55
56. .1453
/product='H-chain of anti-TMV-antibody'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1993 JP 1993131208
SALTO YASUTO, KOGIKU TOSHIHIKO, KAMISHIRO TAKASHI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E
                                                                                                                                                                                                                                                                                                                   138 AlaLysThrThrProProProValTyrProLeuValProGlySerLeu 153
                                                                                                                                                                                                                                                                                                                                 422 GCCAAAAACAACCCAACCGTTTATCCCCTGGCCCCTGGAAGCTTG 469

    1. 1553
/organism='Artificial sequences'
    1553

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                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                      CDNA encoding H-chain of anti-TMV-antibody. E08434
JP 199431936-A/7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAME TO SAME PLANT
PATENT FOR TO SAME PLANT
PATENT: JP 1994319396-A 7 22-NOV-1994;
JAPAN TOBACCO INC, KURARAY CO LTD
OS ARTIficial sequences.
PN JP 1994319396-A/7
PP 22-NOV-1994
PF O7-MAY-1993 JP 1993131208
PI SAITO YASUTO, KOGIKU TOSHIHIKO, KAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAKAMI MASAAKI, FUMINO MASAYASU A0145/00,C12N15/13,C12P21/08; strandedness: Double; topology: Linear; hypothetical: No; anti-sense: No;

    1553 / Organism="unidentified" / Mol_type="genomic DNA"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified unclassified.
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  19
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Riausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetcow, R.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haish, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bondldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstan, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunarathe, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wuzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, W., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (pickson, Mark) modepaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 8 Row: a Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (31-JAN-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Mammary tumor metastatized to lung. Tu
arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMTV."
/clone_lib="NOI_CGAP_Lu29"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNa"
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/db_xref="taxon:10090"
/clone="MGC:6628 IMAGE:3491766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: IgG1"
/db_xref="LocusID:16017"
/db_xref="MGI:96446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Igh-4 protein"
/protein_id="AAH02121.1"
/db_xref="G1:12805309"
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1. .1542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Igh-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
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2 (bases 1 to 1542)
Strausberg, R.
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BC002121 GI:12805308
MGC.
                                                                                                                                                                                                                                                                        /translation-"MEMTWVILELLSVTEGVHSQVQLQQSGAELVRPGSSVKISCKAS
GYAFSGYWINWVKQRPGQGLEWIGQIYPGDGDTDYNGKFKGKATLTADKSSSTAYMQL
SSLTSEDSAVYFCARGYDEVDYYFAMDYWGGGTSVTVSSAKTTPPSVYPLAPVGGDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 118
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                               /product-"anti-glycoprotein-B of human Cytomegalovirus
immunoglobulin Nh chain"
/protein_id="AABA2652.1"
/db_xref="GI:1680667"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="monoclonal antibody 27-156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
1. .483
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                           /mol_type="genomic DNA"
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                                                                                           /db_xref~"taxon:10090"
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                                                                                                                                    1. .>483
/codon_start=1
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609.00
85.068
75.978
74.638
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                      117
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VERSION
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SOURCE
ORGANISM
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No.:
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                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                      CDS
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/translation-"MERHMIFLELESYTAGYHSQYQLQQSGAELAKPGASYKMSCKAS
GYTFTAYWHHWVKQRPGQGLEWIGYINPNTGYTEYNQNFKDKATLTADKSSSTAYMQL
SSLTSEDSAVYYCTRSYYNYEGAMDYWGQGTSVTVSSAKTTAPSVYPLAPVCGDTTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 ATGGAAAGGCACTGGATCTTTCTCTTCCTGTTTTCAGTTACTGCAGGTGTCCACTCCCCAG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3149944
On Nov 28, 1994 this sequence version replaced gi:342018.
Original source text: Mus musculus (strain BALB/c, sub_species
domesticus) hybridoma cDNA to mRNA.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49. .105
/gene="Igg"
/John="Igg"
/gene="Igg"
/product="immunoglobulin gamma-2a chain"
- 142 c 119 g 120 t
                                                                                                                                                                                                                                                                                                           /product="immunoglobulin gamma-2a chain"
/protein_id="AAA53291.1"
/db_xref="G1:576598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525
116
9
22
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 protein I
                                                                                                                                                                           /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="MAb 6A4"
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1. .525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-836-455-4 (1-153) x MUSIGHALPA (1-525)
 aeruginosa outer membrane p
Gene 74 (2), 335-345 (1988)
89232725
                                                                                                                                                                                                                                                                            /gene="Igg"
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602.00
82.24%
76.32%
73.77%
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49. .>525
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Best Local Similarity:
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9
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          /translation="MEWIWIFLFILSGTASVHSQVQLQQSGAELARPGASVKMSCKAS
GYSFTSYGISWVKQKTRQGLEWIGEIYPGSGNYYNEKFKGKATLADKSSSTAYWQL
SZIJEBDSAVYFCARWGEPWDVWQGQCTTITVSSAKTPFPSVYPLAPGSAAQTNSMV
TLGCLVKGYPFPEPVYWWNGSSLSGVHTFPPNUGSDLYTLSSSVYVPSSTWFSGTVY
CNVAHPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPREDVLTITLTPKVTCV
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CRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDIT
VEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHH
VEKLSLSHSPGK"
325 t
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                                                                                                                                                                                                                                                                                                                                                                                            21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
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mammalla; Eutherla; Rodentla; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 525)
Marget,M., Eckhardt,A., Ehret,W., von Specht,B.U., Duchene,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and characterization of cDNAs coding for the heavy and light chains of a monoclonal antibody specific for Pseudomonas
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114
13
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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/db_xref="LocusID:16017"
                                                                                                                                                                                                                                                                                                        US-08-836-455-4 (1-153) x BC002121 (1-1542)
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603.00
83.55%
75.00%
73.90%
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Best Local Similarity:
Query Match:
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/product="ant1-human CD19 monoclonal antibody 4G7
immunoglobulin gammal heavy chain"
/protein_id="cAD88275.1"
/db_xref="G1:297868275.1"
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/db_xref="G1:29787
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Submitted (09-APR-2003) Grosse-Hovest L., Immunology, University of
Tuebingen, Auf der Morgenstelle 15, 72076 Tuebingen, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                        MUS musculus mRNA 11near ROD 09-APR-2003 Mus musculus mRNA for anti-human CD19 monoclonal antibody 467 AJ555622
     119 AsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAla 138
                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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anti-human CD19 monoclonal antibody 4G7 immunoglobulin gamma heavy chain; IGHG1 gene.
Mus musculus (house mouse)
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                                                                                                                              484 AAAACAACAGCCCCATCGGTCTATCCACTGGCCCCT 519
                                                                                                    139 LysThrThrProProProValTyrProLeuValPro 150
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/organism="Mus musculus"
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/clone="4G7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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/gene="IGHG1"
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/gene="IGHG1"
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60. .1404
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/gene="IGHG1"
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/gene="IGHG1"
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2 (bases 1 to 1526)
Grosse-Hovest, L.
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                                                                                                    540 bp DNA linear PAT 03-JAN-1994 variable region of a monoclonal antibody which cross reacts with 19 Al3735.1 GI:491743
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SSLTSEDESAVYTCASYTVEGAMDYMGGGTSVTVSSAKTTAPSVYPLAPVCGDTTG"
144 c 130 g 121 t
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                                                                                                                                                                                                                                                                                        synthetic construct
synthetic construct
synthetic construct
synthetic synthetic
synthetic construct
synthyll sequences.
1 (bases 1 to 540)
Domdey, H., Marget, M. and von Specht, B.U.
Monoclonal antibodies to Pseudomonas aeruginosa, their production
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139 LysThrThrProProProValTyrProLeuValPro 150
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           and use
Patent: EP 0338395-A 3 25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEHRINGWERKE Aktiengesellschaft
Location/Qualifiers
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Best Local Similarity:
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Translation-"MEWSGVETFLLSVTAGVHSQVQLQQSGAELVRPGTSVKMSCKAA
GYTFTNYWIGWVKQREGHGLEWIGDIYPGGGTYNYNIEKFKGKATLTADTSSSTAYNOL
SSLTSEDSATYCCARLGGGYYAMDYWGQGTSVTVSSATTAPSVYPLVPGSSTAYNOL
SSLTSEDSATYCCALKGYFPEPEYTVKMNYGALSSGVFRTVSSATTAPSVYPLYPGSSTAYNOL
TVICNVAHPASKTELIKRIEPRIPKPSTPPGSSCPPGNILGGPSVFIFPPRFXDALMI
STLPKYTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQYNSTFRVYSALPIQHQ
DWMRGKEFKCKVNNKALLPATIERTISKPKGRAQTPQVYTIPPPREQMSKKKVSLTCLV
TNFFSERISVSPREFKCYNNTPFILDSBGTYFLYSKLTVDTDSWLQGELFTCSV
YHEALHNHHTQKNLSRSPGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 GTCCAACTGCAGCAGTCTGGAGCTGAGGCTGGTAAGGCCTGGGACTTCAGTGAAGATGTCC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nose,M.
Direct Submission
Direct Submission
Submitted (10 MAR-1993) Masato Nose, Tohoku University School of Medicine, Dept.
Miyaqi 980, Japan (F-mail:d22181@cctu.cc.tohoku.ac.jp,
Tel:81-22-273-9042, Fax:81-22-234-1986)
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                            /product="immunoglobulin gamma-3 heavy chain precursor"
/protein_id="BAA03476.1"
/db_xref="G1:1304160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453. .1442
/product-"immunoglobulin gamma-3 secreted C-region"
1466. .1544
                                                                                                                                                                                                                                                                                                   /note="precursor of C and V-D-J regions from 7B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33. .89
90. .1442
/product-"immunoglobulin gamma-3 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90. .452
/product="immunoglobulin V-D-J region"
/note="7B6.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1544
116
14
21
3
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Mismatches:
Indels:
                                                                                                                                                                                                                             /clone="pBHH1"
/clone_lib="pBluescript KS(+)"
/dv_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326
                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="MRL/MpJ-lpr/lpr"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368
                                                                                                                                                                                                                /chromosome="14"
                                                                                                                                                                                                                                                                                                                    /codon_start=1
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599.50
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75.32%
                          (bases 1 to 1544)
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mat_peptide
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DB:
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Mus musculus mRNA for immunoglobulin gamma-3 heavy chain precursor,
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Takahashi, S., Itoh, J., Nose, M., Ono, M., Yamamoto, T. and Kyogoku, M. Cloning and cDNA sequence analysis of nephritogenic monoclonal antibodies derived from an MRL/Ipr lupus mouse 93156722
8429833
                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 GAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCTCCAGCACAGCCTACATG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACTACGGTAGTAGGGTATTTGACTACTGGGGCCAAGGCACCACTCTCACAGTACGGTATTTGACTACTGGGGCCAAGGCAACGCACACTCTCACAGTACTCTCA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
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                                                                                                                                                                                                                                                                                                   21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                                                                                                                                                                                                                                                                             CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ono,M., Yamamoto,T., Kyogoku,M. and Nose,M.
Sequence analysis of the germ:line VH gene corresponding to
nephritogenic antibody in MRL/lpr lupus mice
Clin. Exp. Immunol. 100 (2), 284-290 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaLysThrThrProProProValTyrProLeuValProGlySer 152
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115
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Matches:
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Mus musculus
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1475. .1480
/gene="IGHG1"
1510
                                      /gene="IGHG1"
                                                                                                              2.5e-52
601.50
82.58%
74.19%
73.71%
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 polyA_signal
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                             polyA_site
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MUSIGB1H1
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449 pp DNA linear ROD 22-NOV-1996 immunoglobulin Vh chain gene, partial cds.
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GYTFSGSWMMWWQRPGQGLEWIGRIYPGDGDTNYSGKFKGKATLTADKSSSTAYLQL
SSLTSVDSAVYFCARDDGYYVAFDYYAMDYWGQGTSVTVSSAKTTPPSVYPLVPVCGG
                                                                                                                                                                                                                                                                        140
                                                                                                                                                 100
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                                                                                                                                                                101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
                                                                                                                                                                                                                                          364
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GTGCAACTGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCC 127
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies specific for the antigenic domain 1 of glycoprotein B (gpUL5) of human cytomegalovirus bind to different substructures Virology 216 (1), 133-145 (1996) 96187797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 489)
Schoppel, K., Hassfurther, E., Britt, W., Ohlin, M., Borrebaeck, C.A. and Mach, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-NOV-1995) Michael Mach, Institute of Virology,
University Erlangen-Nuernberg, Schlossgarten 4., 91054 Erlangen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="anti-glycoprotein-B of human Cytomegalovirus immunoglobulum Vh chain"
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/db_xref="GI:1680669"
                                                                                                                                                                                                                                                                       121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr
                          GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="monoclonal antibody 27-287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="Balb/C"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                 141 ,ThrProProProValTyrProLeu 148
                                                                                                                                                                                                                                                                                                                                                 425 ACACCCCCATCTGTCTATCCACTG 448
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Schoppel, K.
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TITLE
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MMU39900
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/db_xref="G1:27763666"
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/translation="MGWSCIMFPLVATATGVHSLVOLOQPGAELVKPGASVKMSCKAS
GYTFTSYNHHWVKQTPGGGLEWIGVIYPGNGDTSYSQKFKGKATLTADKSSTAYMQL
SSLTSEDSAVYYCGGAGIANHWGGTSVTVSSAKTTPPSVYPLAKD"
119 c 122 g 102 t
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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            GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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/product="antiporphyrin immunoglobulin G heavy chain
variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 457)
Sari,M.-A., Quilez,R. and Mahy,J.-P.
Antiortho-carboxy-substituted tetraarylporphyrin antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Call (12-NOV-2002) UMR8601-CNRS, Universite Rene Saints-Peres, Paris 75006, France Location/Qualifiers
                                                                                                                                                                                                            AlaLysThrThrProProProValTyrProLeuValProGly 151
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115
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Mismatches:
Indels:
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2 (bases 1 to 457)
Sari,M.-A., Quilez,R. and Mahy,J.-P.
Direct Submission
Submitted (12-NOV-2002) UMR8601-CNRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRRN"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="13G10"
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/translation="MKCSWVILLFCQVTSGVYSQVOLQQSGAELARPGASVKLSCKAS
GYTFSSHWIHGKQRPGQGLEWTGAIPPGDGDSRYNKFFKGKASLTADKSSSTAYIQLS
SLASEDSAVYYCHONFDPFPZWGQGTLVTVSAAKTTPPPVYPLAPGSL"
115 c 123 q 120 t
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Mus musculus immunoglobulin heavy chain 4 (serum IgG1), mRNA (cDNA
clone MGC:6486 IMAGE:2646928), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLysThrThrProProProValTyrProLeuValProGlySerLeu 153
                                                                                                                                /codon_start=1
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/protein_id="BAB87183.1"
/db_xref="G1:19909917"
                                                                                                                                                                                                                                                                          469
113
17
20
6
                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                            Length:
Matches:
                                    /db_xref="taxon:10090"
/cell_line="hybridoma 6G9"
/cell_type="B cell"
1. 469
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                            Gaps:
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                                                                                          /gene="VH6G9"
9. .>467
                                                                                                                     /gene="VH6G9"
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Mus musculus VH6G9 mRNA for anti-dsRNA (RDV-RNA) antibody, partial
                                                                                                                                                                                                                                                                                                                              GInIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
                                                                                                                                                                                                                                                                                                                                                                                                           354
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (17-ocr-2000) Yoshichika Kitagawa, Akita Prefectural
Submitted (17-ocr-2000) Yoshichika Kitagawa, Akita Directity, Botechhoology Institute; minami 2-2, Ogata, Akita
010-0444, Japan (E-mail:kitagawa@agri.akita-pu.ac.jp,
URL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
Fax:81-185-45-2678)
                                                                                                                      MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                               1 ATGGAATGCAGCTGGGTCTTTCTCTTCCTCTGTCAATAACTGCAGGTGTCCATTGCCAG
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  489
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119
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                              Conservative:
Mismatches:
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Published Only in Database (2002)
3 (bases 1 to 469)
    Length:
Matches:
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Mus musculus
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  3.22e-52
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81.65%
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                         Percent Similarity:
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: i Column: 17.
Location/Qualifiers
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Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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Submitted (20-FEB-2001) National Institutes of Health, Mammalian
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_llb="NCI_GGAP_Mam1" /lab_host="BH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BOX-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/db_xref="LocusID:16017"
/db_xref="MGI:96446"
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/strain="FVB/N"
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HHTEKSLSHSPGK"
456 c 374 g 337 t
/translation="MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKAS
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ORIGIN
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OM protein - nucleic search, using frame_plus_p2n model

August 30, 2003, 22:10:01 ; Search time 230.013 Seconds Run on:

(without alignments)
1795.608 Million cell updates/sec

US-08-836-455-4

816

1. MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

2552756 segs, 1349719017 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:
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-WODEXTO_UNITS-b1ts.-GFNRT-1-END-1-MATRIX-b10sum62 -TRANS-human40.cd1
-LIST-465 -DOCALEGN-200 -THR_SCORE-pct -THR_ANX-100 -THR_MIN-0 -ALIGN-15
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-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPPLOCK-100 -LONGLOG
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 ${\bf Pred.}$ No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

escription		Murine monoclonal	Antibody Ilbio nea	Mouse IIDIU antibo	Cobacco mosa	Mones DNA speeding	Mouse DNA encouring	4040	dva naratrak akon Moratrak danam) (Monoo oot 1 bod: 2017	2	heavy chain v	SP 2H7	Mouse 2H7 antibody	Mouse 2H7 antibody	2H7 antibody heavy	Coding sequence fo	3F4 (Chimeric) hum	Murine anti-porcin	Monoclonal antibod	human			Antibody C2B8 CH2	DNA encoding a dim	Human C2B8 antibod	Antibody C2B8 heav	Vector contg. TCAE	TCAE8 expression v	Traget plasmid Mol	Anti-Fas MAD HFE/A	CDNA encoding mous		Mouse numanised an	Aumanised anti-ras	Times costes been	nullan penton base	Д.	Human penton base	encoding mo	eavy ch	VEGF		Nucleotide sequenc				
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AAT85150 standard; cDNA; 461 BP. AAT85150;

(updated)
(first entry) 25-MAR-2003 04-JAN-1998 Murine monoclonal anti-idiotype antibody 11D10 VH cDNA.

Monoclonal antibody 11D10; anti-idiotype antibody; mucin; human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.

Mus musculus

Key

Location/Qualifiers

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Page

140

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Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11010 heavy chain variable region. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HMFG) associated tumnour in an individual having low tumnour burden. The antibody 11010 is used to prevent the recurrence of HMFG-associated tumnours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for treating breast tumnours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
//product= "antibody 11D10 heavy chain variable region"
/note= "no stop codon is given at the 3' end of the
sequence"
                                                                                                                     241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG
                                                     101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp
                                                                                                      GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delaying development of, or treating, HMFG-associated tumours using anti-idiotype antibody 11D10 raised against antibodies thuman milk fat globule protein
                                                                                                                                                                                                                                                                                                                                                                      Antibody 11D10 heavy chain variable region coding sequence
                                                                                                                                                                                    421 ACACCCCCACCCGTCTATCCACTGGTCCCTGGAAGCTTG 459
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                                                                                                                                                                    141 ThrProProProValTyrProLeuValProGlySerLeu 153
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P-PSDB; AAW87594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA sequence encodes the heavy chain variable region VH (AAM85150) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are and/or 11D10 polypeptides and/or 11D10 polypurcleotides, including methods of treating HMFG-associated thousand are and/or 11D10 polypurcleotides, including methods of treating HMFG-associated.
                                                                                                                                                                                                                                                                                                                                                                         response
                                                                                                                                                                                                                                                                                                                                                                   Monoclonal anti-idiotype antibody 11D10 - elicits immune ragainst human milk fat globule disease associated tumours,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 94; 130pp; English.
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/product= "Mouse 11D10 anti-idiotype antibody heavy chain
variable region"
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                                                                                                        CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro·60
                                                       MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                  1 ATGGAATGCAGCTGGTCTTTCTCTTTCTCTGTCAATAACTACAGGTGTCCACTCCCAG
                                                                                                                               Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA; 11D10; 3H1; HWFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
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Mismatches:
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                                                                                                                                                                                                                                                                                      The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for TEA (e.g. 3H1). The method is useful for anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for present DNA sequence encodes the heavy chain variable region of the mouss 11D10 anti-idiotype antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGGGTCTGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGTGCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLySMetSer
                                                                                                                                                              Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA) associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g. breast tumor) in humans
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 461 BP; 112 A; 121 C; 119
                                                                                                                                                                                                                                                       Disclosure; Fig 2; 98pp; English
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816.00
100.00%
100.00%
17-MAY-2001; 2001US-0861294
                                                                       ΚĄ;
                                  (KENT ) UNIV KENTUCKY
                                                                       Chatterjee M, Foon
                                                                                                          2003-129216/12.
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Best Local Similarity:
Query Match:
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GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
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               GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet
                                                                                                        Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
                                                                                                                                                                                                                             SerAlaLysThrThrProProProValTyrProLeuValProGlySer 152
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116
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Matches:
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602.00
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(updated)
(first entry)
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31-OCT-2002
15-MAR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transformed plant producing animal-derived anti-virus antibody esp. tobacco plants producing anti-tobacco mosaic virus monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light chains of an animal derived anti-tobacco mosacic virus (TMV) monoclonal antibody. The cDNAs were incorporated into a Ti plasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform tobacco plants, making them TMV resistant, the plants could also be biofarmed for the prodn. of anti-virus antibodies.
                                                                               Anti-tobacco mosaic virus monoclonal Ab heavy chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 386 Å; 450 C; 372 G; 345 T; 0 other;
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.118
.15
.19
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                                                                                                         lc virus; TMV; monoclonal antibody;
virus-resistant plants; biofarming;
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Matches:
Conservative:
Mismatches:
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  AAQ79930 standard; cDNA to mRNA; 1553 BP
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                                                                                                                                                                          Location/Qualifiers
56..1453
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56..112
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113..1450
/*tag= c
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85.26%
75.64%
76.10%
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P-PSDB; AAR66758.
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                                                                                                           mosaic
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                                                                                                                       heavy chain;
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                                                     01-SEP-1995
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                                                                                                                                                                                                                 sig_peptide
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                                                                                                                                                Synthetic
                           AAQ79930,
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DB:
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                                                                                                                                                                                                                                                                        ds; T-cell receptor; gene; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; FSMA; tumour; 3D8; 4D4; 3E11; prostate-specific membrane antigen; zeta signalling chain; CD881pha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouse.
                                                                                           GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGly----- 11:8
                                                                                                                                                                                                                                                                                                                        AsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAla 138
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                                                                              1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                      CysLysalaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                                                                                                                                                            84 IGCAAGGCTICTGGCTACACCTTTACTGCCTACTGGATGCACTGGGTAAAACAGAGGCCT
                                                                                                                                                                                                               GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn
                                                                                                                          21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse DNA encoding antibody 4D4 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "4D4 heavy chain variable region""
/partial
  1 25
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 Conservative:
             Mismatches:
Indels:
Gaps:
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                                                        US-08-836-455-4 (1-153) x AAN91645 (1-540)
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14..430
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30-NOV-2000;
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The invention relates to a chimaeric molecule comprising the GD3 (ganglioside antigen) binding domain of antibody MB3.6, with any of 3 variable gene sequences, or the PSMA (prostate-specific membrane antigen) binding domain of antibody 3D8, 4D4 and 3B11, with variable gene sequences, the zeta signalling chain of the T cell receptor and an intervening CD812pha hinge in which cysteine residues have been mutated. The chimaeric molecules expressed in T cells or NK cells or other effector cells are useful in treating patients with cancers expressing the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3B11 constructs to engage additional stimulatory and functional properties of the effector cells to enhance the antitumour therapeutic efficacy (claimed). They are particularly useful in disorders including
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                                                                                                        as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody -
                                                                                          New chimeric molecule useful in treating patients with disorders,
                                                                                                                                                                                                                                                                                                                                                  neuroendocrine tumours and prostate and small cell lung
the present sequence encodes the mouse antibody 4D4 heavy
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 736 BP; 170 A; 210 C; 186 G; 170 T; 0 other;
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Mismatches:
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Matches:
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86.67%
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                                                   WPI; 2003-208946/20.
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                                                                  P-PSDB; ABG74245.
(JUNG/) JUNGHANS
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                          Junghans RP;
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100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed sequence tag; EST; probe; chemotactic; proliferative; inmunomodulatory; haematopoletic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatopoletic; choostatic; antibacterial; antiinflammatory; cytostatic; antibacterial; antiingal; antiiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiliore; osteopathic; neuroprotective; notropic; antipaoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (SESTs), isolated from human, mouse, chicken and rat
                                                                             GGACAGGGTCTGGAATGGATAGATAATCCTAGCCGTGGTTATACTAATACAAT
GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn
                                                                                                                             GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet
                                                                                                                                                insulin, dependent diabeters; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheiner's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse; chicken; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse secreted expressed sequence tag SEQ ID NO:396.
                                                                                                                                                                                                                                                                                                                                                  ThrThrProProProValTyrProLeuValPro 150
                                                                                                                                                                                                                                                                                                                                                                     461 ACAACAGCCCCATCGGTCTATCCACTGGCCCCT 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 306; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA43821 standard; cDNA; 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US24206.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-317938/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-0CT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The OK3T heavy chain sequence was isolated from a cDNA library prepared from OK3T producing cells. The library was screened with a probe complementary to a sequence in the mouse IgG2a constant CH1 domain region. The OK3T sequence was used in CDR-grafting experiments to prepare humanised antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis
                                                                                                                                                                                                                    OK3T; heavy chain; humanised antibodies; CDR-grafting; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1570 BP; 447 A; 443 C; 356 G; 324 T; 0 other;
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113
8
29
                                                                                                                                                                                    Monoclonal antibody OK3T heavy chain coding sequence.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                             /*tag= a
98..1447
/*tag= b
/product= OK3T heavy chain
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Gaps:
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                                                                                                                                                                                                                                                                                             Location/Qualifiers 41..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2a; 91pp; English.
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                                                     AAQ12637 standard; DNA; 1570 BP.
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574.50
80.13%
74.83%
70.40%
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89GB-0028874.
                                                                                                                                                  (first entry)
                                                                                                                               (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adair JR, Athwal DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CLLT ) CELLTECH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-222915/30.
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                                                                                                                           25-MAR-2003.
03-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1990;
21-DEC-1989;
                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                              sig_peptide
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                                                                                         AAQ12637;
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DB:
                   RESULT 7
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ò g ò immunoglobulin E; IgE; allergy; transgenic animal;

Mouse;

Mouse immunoglobulin E heavy chain encoding DNA

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disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                            (multiple sciences, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
                                                                                         chemokinetic; analgesic; haemostatic; thrombolytic; antilifiammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antibathmatic; vulnerary; antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibolies. They may be useful for treatment of autoimmune disorders
tissue sources. The SESTs can have a range of activities depending the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic;
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Sequence 725 BP; 163 A; 222 C; 172 G; 168 T; 0 other;

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114 GTTCAGCTGCAGCTGGAGCTGAGCTGATGAAGCCTGGGGGCCTCAGTGAAGCTTTCC 173
                                                                                                                                                                                                                                                                                                                               GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
                                                                                                                                                                                                                                                    CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
                                                                                                     1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20
                                                                                                                                                                                                                                GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn
                                                                                                                                               21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLySMetSer
                                                                                                                                                                                                     725
106
19
21
                             Conservative:
Mismatches:
Indels:
         Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCCCCATCGGTCTATCCACTGGCCCCT 491
                                                                                  (1-725)
                                                                                  US-08-836-455-4 (1-153) x AAA43821
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        2.15e-46
570.00
83.33%
70.67%
69.85%
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                            Percent Similarity:
Best Local Similarity:
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Alignment Scores:
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121 TGCAAGAGTTCTGGATATACATTCACAAGCTACGGTATAAACTGGGTGAAGCAGAGGCCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is useful as a model for evaluating the activity and the ability of substances i.e. with antiallergic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present sequence encodes the mouse immunoglobulin E (IGE) heavy chain, given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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109
14
27
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Mismatches:
Indels:
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(TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
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Matches:
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                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Taya C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 19-24; 42pp; English
                                                                                                  1..1683
/*tag= a
/note= "no stop c
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568.00
82.00%
72.67%
69.61%
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/*tag= b
58..1683
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
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P-PSDB; AAY17415.
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Best Local Similarity:
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                                                                                                                                                                                                            3P921189-A1
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---GlyAsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSer 136
                                                                                                                   21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse antibody 2H7 heavy chain variable region encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pelB pectate lyase; secretion signal; chimeric antibody, heavy chain; B-cell antigen; antibody 2H7; ss.
              458
112
6
18
                         Matches:
Conservative:
Mismatches:
Indels:
                Length:
                                                                        Gaps:
                                                                                              US-08-836-455-4 (1-153) x AAN91146 (1-458)
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/note= "partial CDS"
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40..459
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90US-0501092.
93US-0020671.
94US-0357234.
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86WO-US02269.
87US-0077528.
88US-0142039.
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(first entry)
                        565.00
84.29%
80.00%
69.24%
                                    Percent Similarity:
Best Local Similarity:
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29-MAR-1990;
22-FEB-1993;
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30-MAR-1999
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24-JUL-1987;
11-JAN-1988;
   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV82357;
                                                                                                                                                                                                                                                                                                                                                                                                      118
                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
              Pred. No.:
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                                                                                                                            101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
                                                                                              GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence carries 2H7 VH region of the chimeric immunoglobulin sequence. The antibodies are useful in passive immunisation avoiding negative immune reactions. They are also useful in assaying and in vitro imaging (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide(s) encoding Immunoglobulin molecules - used for efficient prodn. of chimeric human or non-human or class switched antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 458 BP; 113 A; 120 C; 112 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note="Sequence homologous to DSP.2"
360..406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Better
                                                                                                                                                                                                                                                                                                                                                      Antibodies; passive immunisation; pH3-6a; ss.
                                                                                                                                                                           Robinson RR, Liu AY, Horwitz AH, Wall R,
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ('ITGE-) INT GENETIC ENG INC. (INGE-) INGENE INT GENETIC ENG INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/note="JH1 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page ?; 7pp; English.
                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                              AAN91146 standard; DNA; 458
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                                                                                                                                                                                                                                                                                             (updated)
(first entry)
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/*tag= a
398..408
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                                                                                                                                                                                                                                                                                                                               2H7 Vh sequence.
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25-MAR-2003 06-JUL-1990

AAN91146;

RESULT 10

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AAN91146

misc_feature

WO8900999-A 09-FEB-1989 24-JUL-1987;

chimeric immunoglobulin; chimeric antibody

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Human; mouse;
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                                                                                                                                            The present sequence encodes the mouse antibody 2H7 heavy chain variable region. Antibody 2H7 is specific for human B-cell antigen. The antibody sequence was used to construct a chimeric human-mouse antibody. In the course of the invention. The chimeric antibody is expressed in a secretion vector comprising a pelB pectate lyase secretion signal peptide. The pelB pectate lyase secretion sequence is useful for producing a protein such as a chimeric antibody in a bacterial host. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                                                                                                                                                                                                                                                                 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpVallysGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 ---GlyAsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pelB pectate lyase signal sequence - and vector for expression of secreted proteins in Gram-negative bacteria
                             Robinson RR;
                                                                                                                                                                                                                                          Sequence 459 BP; 113 A; 121 C; 112 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                         459
112
6
                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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                             Liu AY,
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                                                                                                                         Example 4; Fig 21; 98pp; English.
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                             Lei
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                            Horowitz AH,
                                                           WPI; 1999-059072/05.
                                       Wilcox GL
        (XOMA ) XOMA CORP.
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                                                                     P-PSDB; AAW89540
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                                       Wall R,
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The present invention describes a method for preparing an immunoglobulin that is capable of binding antigen involves modular assembly of that is capable of binding antigen involves modular assembly of cantibodies through gene cloning and expression of light and heavy chains. The cloned immunoglobulin gene can be produced by expression in genetically engineered organisms. The method comprises: (a) expression in genetically engineered organisms. The method comprises: (a) expression, consider that cloned involves the second nucleic acid that encodes a bacterial signal sequence operably linked to either the light chain or light chain confirmation of fragment, and obtaining the immunoglobulin from the periplasmic space or culture medium; or (b) operably linking a nucleic acid encoding a bacterial signal sequence to a nucleic acid encoding the heavy chain or the light chain variable region or the light chain variable region or the heavy chain or the light chain variable region or both of the cransport of the heavy chain or heavy chain fragment, or the variable regions through the cytoplasmic or light chain fragment, or the variable regions through the cytoplasmic contains or heavy chain fragment, and a light chain or heavy chain fragment, and the light chain fragment or heavy chain fragment, and a light chain or heavy chain fragment or heavy chain fragment and a light chain or heavy chain fragment.

The method is useful for producing genetically engineered antibodies of method is also useful large scale production of human antibodies.

Continue the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparing immunoglobulins or genetically engineered antibodies for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    large scale production of antibodies involves modular assembly of
antibodies through cloning and expression of light and heavy chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Fig 21; 100pp; English.
genetic engineering; primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0501092.
92US-0987555.
95US-0450731.
85US-0793980.
86WO-US02269.
87US-0077528.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-289514/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Robinson RR,
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08-DEC-1992;
25-MAY-1995;
                                                                     Homo sapiens
                                                                                                                                                                       US6204023-B1
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27-OCT-1986
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(XOMA ) XOMA CORP
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              Better M,
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                                                                       CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                     GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg-----
                   AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                                                                        ---GlyAsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSer
                                                                                                                                                                                                                                                         Antibody engineering; heavy chain; light chain; chimaeric antibody; passive immunisation; diagnosis; hybridoma; monoclonal antibody; 2H7; B-cell antigen; Bp35; ss.
                                                                                                                                                                                                                                                                                                                                                                     element"
                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "JH1 sequence element"
129..439
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/note= "primer JHBstEII"
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'note= "DSP.2 sequence
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72..128
                                                                                                                                                                                                                                             2H7 heavy chain variable sequence.
                                                                                                                                                                                               AAT70868 standard; cDNA; 491
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88US-0142039.
92US-0870404.
94US-0235225.
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(first entry)
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129..491
/*tag= b
393..439
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01-NOV-1985;
27-OCT-1986;
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11-JAN-1988;
17-APR-1992;
29-APR-1994;
                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                       misc_feature
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04-SEP-1997
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                                                                                                        Secretable immunoglobulin heavy and light chain fragments - capable of assembling into chimeric antibodies, useful for e.g. passive immunisation, diagnosis, etc
                                                                                                                                                                                                            A cDNA clone (AAT70868) codes for the heavy chain variable region (AAW16343) of the 2H7 mouse monoclonal antibody, which recognises human B-cell surface antigen Bp35. The sequence was isolated from a 2H7 cell line cDNA library by PCR amplification. The 2H7 light chain variable sequence (AAT60869) has also been isolated. The antibody with specificity for the human-mouse chimaeric updated on 25-MAR-2003 to correct PF field.)
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112
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 Robinson RR;
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Matches:
Conservative:
Mismatches:
 Liu AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-836-455-4 (1-153) x AAT70868 (1-491)
                                                                                                                                                                              Example 4; Fig 21; 96pp; English.
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565.00
84.298
80.008
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Horwitz AH, Wilcox GL;
                                                    WPI; 1997-225473/20.
P-PSDB; AAW16343.
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Best Local Similarity:
Query Match:
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Gaps:

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The present sequence was used in the development of a novel method for the production of an immunoglobulin (1g) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the 1g fragment, under conditions so that the 1g fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences and secreted. The nucleic acid molecule comprises DNA sequences and secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of an 1g light chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable region of an 1g light chain, where (a) and (b) are operably linked to a plant chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic transcription unit. The method is used to produce chimeric Fab molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a gainst human B-cell surface antigen. The invention provides a properties. The cloned Ig gene products can be produced by chemical gene synthesis, recombinant DNA cloning and production of chemical gene synthesis, recombinant DNA cloning an effective compliant of the efficient large scale producing a solution of human maniform when the efficient large scale producing a solution of human maniform when the efficient large scale producing a solution of properties.
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Mouse; murine; heavy chain; variable region;
immunoglobulin fragment production; Ig fragment production;
monoclonal antibody 2H7; human B-cell surface antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;
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                                                                                                        Location/Qualifiers
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/*tag= a
129..491
/*tag= b
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87US-0077528.
88US-0142039.
92US-0987555.
94US-0299085.
95US-0467140.
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P-PSDB; AAW47513.
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18-AUG-1994;
06-JUN-1995;
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Conservative: Mismatches: Indels:

Length: Matches:

.13e-46

Pred.

565.00 84.29% 80.00% 69.24%

> Percent Similarity: Best Local Similarity:

Query Match:

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311
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                              61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn
                                                                                                                                                                                             Gln11eSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg-----
                                                                                                                                                                                                                                                                            1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                          21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; murine; heavy chain; variable region;
immunoglobulin fragment production; Ig fragment production;
monoclonal antibody 2H7; human B-cell surface antigen; ss.
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US-08-836-455-4 (1-153) x AAV18557 (1-491)
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94US-0299085.
95US-0450731.
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88US-0142039
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Wall R, Wilcox GL;
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25-MAY-1995;
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us-08-836-455-4.p2n.rng

NPI; 1998-031749/03.

Production of chimeric antibody fragments - by culturing E. coli transformed with dicistronic expression cassette

Example IV; Fig 21; 98pp; English.

The present sequence was used in the development of a novel method for the production of an immunoglobulin (1g) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the that has been transformed with a nucleic acid molecule encoding the and secreted. The nucleic acid molecule encoding the sequences and secreted. The nucleic acid molecule comprises DNA sequences conditions so that the Ig fragment is produced and secreted. The nucleic acid molecule comprises DNA sequence encoding at least the variable region of an Ig Hight chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a bingle profaction promoter to form a dicistronic transcription unit. The method is used to produce chimeric Fab molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a novel approach for producing genetically engineered antibody 2H7 raised castred variable region specificity and constant region production of chemical gene synthesis, recombinant DNA cloning and production of chemical gene synthesis, recombinant DNA cloning and production of specific Ig chains in various organisms provides a solution to the problem of class switching antibody molecules.

Sequence 491 BP; 113 A; 152 C; 113 G; 113 T; 0 other;

Alignment Scores:
Pred. No.: 565.00 Matches: 112
Score: 565.00 Matches: 112
Percent Similarity: 84.29% Conservative: 6
Best Local Similarity: 80.00% Mismatches: 18
Query Match: 19.24% Indels: 4
DB:

US-08-836-455-4 (1-153) x AAV03926 (1-491)

81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg----- 117 40 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20 41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 101 g g ð ò ద ò ò ò 셤 셤 ð

Search completed: August 30, 2003, 22:20:13 Job time : 232.013 secs

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Scoring table:

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Sequence 8, Sequence 5, Sequence 7, Sequence 7, Sequence 87, Sequence 87, Sequence 11, Sequence 11, Sequence 11, Sequence 11, Sequence 21, Sequence 
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REPERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/09/861,294
CURRENT FILING DATE: 2001-05.17
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 09/096,244
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOSS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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2 US-10-367-506-3

3 US-10-367-506-3

1 US-09-911-692-3

1 US-09-911-692-3

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1 US-09-911-692-3

1 US-09-911-703-3

1 US-10-216-484-8

1 US-10-216-484-8

1 US-10-216-484-8

2 US-10-216-484-8

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1 US-09-991-75-1

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2 US-10-269-921-75-1

1 US-09-908-97-1

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Patent No. US20020098190A1
GENERAL INFORMATION:
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NAME/KEY: CDS
LOCATION: (1)...(461)
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-WODEL-frame+p2n.model.PEW-xlh
-WODEL-frame+p2n.model.PEW-xlh
-WODEL-frame+p2n.model.PEW-xlh
-WOSTO_SPOOL/US08836455/runat_29082003_132902_22302/app_query.fasta_1.654
-US-Cgn2_1/USPTO_spool/US08836455/runat_29082003_132902_22302/app_query.fasta_1.654
-USOPEL-0 -LOOPEXT-0 -UNITS-bits -STRAT-1 -END--1 -NATRIN-blosum62
-LOOPEXT-0 -UNITS-bits -STRAT-1 -END--1 -NATRIN-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MNN-0 -ALIGN-15 -MODE-LOCAL -OUTPMT-ptc -NORM-ext -HEARSIZE=500 -MINLEN-0
-MAXEN-200000000 -USER-US08836455, @CGN_1_1_271_@runat_29082003_132902_22302
-NORD-6 -ICPU-3 -NO_MAAP -LARGEQUERY -NG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEY_TIMEOUT-120 -WARN_TIMEOUT-30 -THRRADS-1 -KGAPOP=10 -KGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     816
1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153
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/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                   - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence:
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Database

Score

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Appli

911, App 2, Appli 3, Appli 75, Appl 97, Appl 75, Appl 75, Appl 5, Appli 5, Appli

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FEATURE:
NAME/KEY: CDS
LOCATION: (14)..(430)
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Best Local Similarity:
Query Match:
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ORGANISM: Mus
                                                                                                                     Alignment Scores:
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                                                                                                                                                                                            1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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Matches:
Conservative:
Mismatches:
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Fublication No. US20030152575A1
GENERAL INFORMATION:
APPLICANT: Malaya CHTTERJEE
APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
CURRENT APPLICATION NUMBER: US/10/367,506
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/09/861,294
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                    US-08-836-455-4 (1-153) x US-09-861-294-3 (1-461)
                                                                                                                                Indels:
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                                                                                5.23e-93
816.00
100.00%
100.00%
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-09-861-294-3
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ORGANISM: Mus musculus
                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                      Alignment Scores:
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US-10-367-506-3
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Receptors Against Tumor A
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Publication No. US20020132983A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Rece

FILE REFERENCE: 003

CURRENT APPLICATION NUMBER: US/10/006,773

CURRENT FILING DATE: 2001-12-10

PRIOR FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin version 3.1

SEQ ID NO 12

LENGTH: 736
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153
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Indels:
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Matches:
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100.00%
100.00%
; NAME/KEY: CDS
; LOCATION: (1)...(461)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-10-367-506-3
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RESULT 5
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                 LeuThrSerGluAspSerAlaValTyrPheCysAlaArg---GlyAsnTrpGluGly--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                         123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
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                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                         GlufrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsnGlnLySPheLys
; "OTHER INFORMATION: 4D4 Heavy chain V region, plus leader US-10-006-773-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                             US-08-836-455-4 (1-153) x US-10-006-773-12 (1-736)
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APPLICANT: Athwal, Diljet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOOGCOCK Washburn Kurtz Mach
                                                                                                         Gaps:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                              1.49e-65
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
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MEDIUM TYPE: Floppy
                                                                    Percent Similarity:
Best Local Similarity:
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                                  Alignment Scores:
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101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArg---GlyAsn 119
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Mismatches:
Indels:
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Matches:
FILING DATE: U1-w...
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35.719
REFERENCE/DOCKET NUMBER: CARP-0057
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1570 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
"DOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09911692; Publication No. US20030095963A1; GENERAL INFORMATION: APPLICANT: ANDERSON, Darrell; HANNA, Nabil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEONARD, John E.
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565.50
79.47%
74.17%
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| LOCATION: 98.1444
| US-09-795-515-6
                                                                                                                                                                                                                                                                                                                                    LOCATION: 41..1444 FEATURE:
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Query Match:
                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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2751 TACGGGGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA 2810
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         81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
                                                                                                101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
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                                   121 GluGlyAla------LeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer
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COUNTRY: United States
ZIP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TEM SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNET/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION UMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/911,703
FILING DATE: 25-Jul-2001
CLASSIFICATION: CURNOWN>
PRIOCLASSIFICATION DATA:

APPLICATION DATA:

RILING DATE: <UNKNOWN>
FILING DATE: <UNKNOWN>
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Matches:
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09911703
Publication No. US20020197255A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEONARD, John E.
NEWMAN, Roland A.
REFF, Mitchell E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HANNA, Nabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYMPHOMA
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Pred. No.:
Score:
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US-09-911-703-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20
NEWMAN, Roland A.
REFF, Mitchell B.
RASTETTER, WILLIAM H.
THERAPEDTIC APPLICATION OF CHIMERIC AND
RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2451 GTACAACTGCAGCAGCCTGGGGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCC
                                                                                                                                                                                                                                                                        STATE: VIGINIA
STATE: VIGINIA
CONTRY: United States
ZIP: 22313-1404
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/911,692
FILING DATE: 25-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CIT: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/149,099C
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGGY: circular
MOLECULE_TYPE: DNA (genomic)
ANTI-CENNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 836-6620
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561.50
80.00%
70.32%
68.81%
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                                                                                                                                                                NUMBER OF SEQUENCES: 9
                                                                                                                                           LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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DB:
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2401 ATGGGTTGGAGCCTCATCTTGCTTGTCGCTGTTGCTAGCGGTTGCTGCTGTTCCTAG 2460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2701 CAGCTCAGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-836-455-4 (1-153) x US-09-905-928-2 (1-9209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO POSITION IN GENOME: CHROMOSOME/SEGMENT: anti-CD20 in TCAE
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                               012712-158
                                                                                                                                                                                                                             NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10238681 Publication No. US20030147885A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 9209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               561.50
80.00%
70.32%
68.81%
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STRANDEDNESS: single
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Best Local Similarity:
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DB:
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APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Restetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell Lymphoma
TITLE OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                   2461 GTACAACTGCAGCAGCCTGGGGCTGAAGCTGGAAGCCTGGGGCCTCAGTGAAGATGTCC 2520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GluGlyAla-----LeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
                                                                                                                                                                                                  1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn 80
                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                            21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
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13
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        Conservative:
Mismatches:
Indels:
                                                                                                                                            US-08-836-455-4 (1-153) x US-09-911-703-3 (1-9209)
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07-JUN-1995
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APPLICATION NUMBER: US/09/905,928
FILING DATE: 17-JUL-2001
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
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; Publication No. US20030021781A1
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
80.00%
70.32%
68.81%
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     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                           Query Match:
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us-08-836-455-4.p2n.rnpb

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               APPLICANT: Anderson, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
Publication No. US20030082172A1 GENERAL INFORMATION:
                                                                                                                                                                               NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                Hanna, Nabi
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80.00%
70.32%
68.81%
                                                                                                                                                                                                                                                                                USA
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ANTI-SENSE: NO
                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 22314
                                                                                                                                                                                                                                                                  STATE: VA
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
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                                       APPLICANT: LEONARD, JOHN E.
APPLICANT: NEWANN, ROLAND A.
APPLICANT: REFF, WITCHELLE H.
APPLICANT: REFF, WILLIAM H.
APPLICANT: REFF, WILLIAM H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND RADIOLABELED
TITLE OF INVENTION: LYMPHONA B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: LYMPHONA B LYMPHONA B LING OF B CELL
TITLE OF INVENTION: LYMPHONA B LYMPHONA B LING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1997-08-29
PRIOR FILING DATE: 1993-11-03
PRIOR FILING DATE: 1993-11-03
PRIOR PILING DATE: 1992-11-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2520
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-836-455-4 (1-153) x US-10-238-681-3 (1-9209)
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Matches:
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US-10-096-964-2
; Sequence 2, Application US/10096964
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80.00%
70.32%
68.81%
                                  HANNA, NABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Murine US-10-238-681-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 9209
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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Leonard, John E.
Newman, Roland A.
Reff, Mitchell E.
Rastetter, William H.
OF INVENTION: Therapeutic Application of Chimeric and
Badiolabeled Antibodies to Human B Lymphocyte Restricted
Differentiation Antigen for the Treatment of B-Cell Lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/096,964
FILING DATE: 14-Mar-2002
CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9209
109
15
28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR PAPLICATION DATA:

PRIOR APPLICATION NUMBER: US/08/475,813

PILING DATE: 07-UNN-1995

APPLICATION NUMBER: US 08/149,099

FILING DATE: 03-NOV-1993

APPLICATION NUMBER: US 07/978,891

FILING DATE: 13-NOV-1992

ATTORNEY/AGATION NUMBER: 35,030

REGISTRATION NUMBER: 35,030

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012/12-158

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEPHONE: 703-836-6620

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 9209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOSOME/SEGMENT: anti-CD20 in TCAE;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-096-964-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-836-455-4 (1-153) x US-10-096-964-2 (1-9209)
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9433 ATGGGTTGGAGCCTCATCTTGCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAG 9492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                                                                                                                     9493 GTACAACTGCAGCAGCCTGGGCTGAAGCTGGGGCCTCACTGAAGATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer
                                                                                                                                                                                                                                                                            1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
                                                                                                                                                                                                                                                                                                                                                                21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 AlaLysThrThrProProProValTyrProLeuValProGlySer 152
                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Serizawa, No. US20030103976Alufusa APPLICANT: Baruyama, Hideyuki APPLICANT: Nakahara, Kaori APPLICANT: Nakahara, Kaori APPLICANT: Tamaki, Tkuko APPLICANT: Takahashi, Tohru TITLE OF INVENTION: AATI-Fas Antibodies FILE REFERENCE: 980126CIP/HG CURRENT APPLICATION NUMBER: US/99/499,662 PRIOR FILING DATE: 2000-02-09 PRIOR PLICATION NUMBER: US/99/499,662 PRIOR PLICATION NUMBER: US/99/499,662 PRIOR PLILING DATE: 1999-04-01
                                                                                                                                                                                                                            US-08-836-455-4 (1-153) x US-10-109-853-2 (1-18986)
                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
                                                                                        561.50
80.00%
70.32%
68.81%
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ORGANISM: Mus.musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat peptide
LOCATION: (58)..(1392)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)..(1392)
                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1392
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US-10-109-853-2
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                                                                                        Score:
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Publication No. US20020192820A1
GENERAL INFORMATION:
BARNETT, Richard Spence
MCLACHIAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT
SPECIFIC STEES IN MAMMALIAN CELLS VIA HOMOLOGOUS
RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE SAME
                                                                                                         111 :::|||||||:::
2761 TACGGCGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA 2820
                                             2641 CAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTACATG 2700
                                                                                                                                                                                                                                                                                                                       81 GInLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerThrAlaTyrMet 100
                                                                                                                                                                                                                                                                                             GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
                                                                                                                                                                                                                                                                                                                                                                                   121 GluGlyAla------LeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137
                     9
                   CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2821 GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCC 2865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/109,853
FILING DATE: 01-APPL-2002
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/023,715
FILING DATE: CURNOWN>
APPLICATION NUMBER: US/09/023,715
APPLICATION NUMBER: US/09/023,715
ATORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 31,030
TELEPHONE: (703) 836-6520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AlaLysThrThrProProProValTyrProLeuValProGlySer 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18986 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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Sequence 1, Application US/0903327A

Sequence 1, Application US/0903327A

Batent No. US20020164333A1

GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erquang

TITLE OF INVENTION: BEFORE

TITLE OF INVENTION: DELIVERY

FILE REFERENCE: 22008-1228

CURRENT APPLICATION NUMBER: US/09/903,327A

CURRENT APPLICATION NUMBER: US/013,017

PRIOR FILING DATE: 2000-07-10

NUMBER: OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 ------ATTGCTTACTGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGAAACG 405
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; LOCATION: (28)...(1395)
; OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 ACACCCCCATCTGTCTATCCACTGGCCCCTGGATCT 441
                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                         US-08-836-455-4 (1-153) x US-09-903-327A-5 (1-1314)
                                                                                                            Indels:
                                         1.22e-59
554.50
80.26%
69.74%
67.95%
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                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
                                Alignment Scores:
US-09-903-327A-5
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APPLICANT: Li, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT PILLING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                          -----GlyAsnTrpGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrVal 135
                                                                                                                                                                                                                                                                                                                     GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet 100
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LOCATION: (0)...(1314)
OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
OTHER INFORMATION: bifunctional antibody
                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                           Gaps:
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                                                                                         2.34e-60
560.50
77.718
71.348
68.698
           ; NAME/KEY: sig peptide
; LOCATION: (1)..(57)
US-10-216-484-8
                                                                                                                        Percent Similarity:
Best Local Similarity:
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                                                                          Alignment Scores:
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US-10-244-821-85
                  NAME/KEY: sig_peptide
LOCATION: (1)..(57)
                                          ) NAME/KEY: mat_peptide
) LOCATION: (58)..(408)
US-10-160-232-7
  LOCATION: (1)..(408)
                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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LENGTH: 406
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NAME/KEY:
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                                                                           GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn
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106
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        Conservative:
Mismatches:
                                                US-08-836-455-4 (1-153) x US-09-903-327A-1 (1-1516)
Matches:
                        Indels:
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554.50
80.26%
69.74%
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       Percent Similarity:
Best Local Similarity:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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Fublication No. US2003014323341
GENERAL INFORMATION:
APPLICANT: GOSHORN, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Schultz, Joanne Elaine
APPLICANT: And Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
TITLE OF INVENTION: STREFTAVIDIN EXPRESSED GENE
TITLE OF INVENTION: STREFTAVIDIN
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: STREFTAVIDIN
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE REFERENCE: 69022.547C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
COFTWARRE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                          US-08-836-455-4 (1-153) x US-10-160-232-7 (1-409)
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		20	09	40	120	09	180	80	240	100	300	120	357		
406 104 ve: 8 : 23 . 1		MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln	ATGGAAAGGCACTGGATCTTTCTTTTTTTCAGTAACTGCAGGTGTCCCACTCCCAG	AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer	GTCCAGCTTCAGCAGTCTGGGGCTGAACTGGGGAAAACCTGGGGGCCTCAGTGAAGATGTCC	nMetHisTrpValLysGlnThrPro.	TGCAAGGCTTCTGGCTACACCTTTACTAGCTACAGGATGCACTGGGTAAAACAGAGGCCT 18	GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn	AGCACTGGGTATACTGAA9	GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerThrAlaTyrMet	CAGAAGTICAAGGACAAGGCCACATIGACTGCAGACAAATCCTCCAGCACAGCCTACATG	GInIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp	CTATTACTGTGCAAGAGGGGGG	GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer 137	358GGGGTCTTTGACTACTGGGCCAAGGAACCACTCTCACAGTCTCTCA 405
Length: Matches: Conservative: Mismatches: Indels: Gaps:	US-08-836-455-4 (1-153) x US-10-244-821-85 (1-406)	eLeuPheLeuLeuSe	TCTCTTCCTGTTTTC	yAlaGluLeuValAre		rLeuThrSerTyrAsi	CTTTACTAGCTACAG	ilyGlnGlyLeuGluTrpIleGlyAsnIlePhePro	TGGATATATTAATCC	aSerLeuThrAlaAs	CACATTGACTGCAGA	rGluAspSerAlaVa	TGAGGACTCTGCAGT	AspTyrTrpGlyGlnGlyThrSerValThrValSerSe	GGGCCAAGGAACCAC
1.64e-58 540.00 81.75* 75.91* 66.18*	3) x US-10-24	/sSerTrpValPh	GCACTGGATCTT	euGlnGlnSerGl	TTCAGCAGTCTGG	laSerGlyTyrTh	CTTCTGGCTACAC	lyLeuGluTrpIl	STCTGGAATGGAT	heLysGlyLysAl	TCAAGGACAAGGC	erSerLeuThrSe	SCAGCCTGACATT	laLeuAspTyrTr	CTTTGACTACTG
larity: imilarity	6-4 (1-15)	1 MetGluCy	1 ATGGAAA	AlaTyrLe				-						GluGlyA	36666
Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	08-836-455	П	1	21	61	41	121	61	181	81	241	101	301	121	358
Pred. Score: Percen Best I Query DB:	-SD	Qy	q	οy	q	QY	a a	ογ	q	οy	q	οy	QQ	Qy	qa

Search completed: August 31, 2003, 01:08:53 Job time : 209.802 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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August 30, 2003, 22:11:21; Search time 1841.13 Seconds (without alignments) 2019.725 Million ceil updates/sec
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1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYFLVPGSL 153
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OM protein - nucleic search, using frame_plus_p2n model
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext ;
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Maximum DB seq length: 200000000
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                                                                                                                        Title:
Perfect score:
Sequence:
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Command line parameters:
-WODEL-framet_pDn.model.-DEV-xlh
-WODEL-framet_pDn.model.-DEV-xlh
-WODEL-framet_pDn.model.-DEV-xlh
-DB-EST -QFMT-fastap -SUFFIX-pDn.rst -MINNATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -QFMT-fastap -SUFFIX-pDn.rst -MINNATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -QFMT-fastap -SUFFIX-blosum62 -TRANS-human40.cdi -LIST-45
-UNCALIGN-DO -THE_SCORE-pct -THR_MAX=100 -TRR_MAX:DN-0 -ALIGN-15 -MODE-LOCAL
-UNCALIGN-DO -THR_SCORE-pct -THR_MAX=100 -TRR_MAX:DN-200000000
-USER-USONBS455_GCGN_11_3596_G-NT-29082003 132902_22290 -NCPU-6 -ICPU-3
-NO.MAAP -LARGEQUERY -NEG_SCORES-0 -WAT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FCAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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em_gss_phg:*
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gb_gssl:*
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Database :
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID Description																																																
# SUMMARIES Query Query 2		cription	34158 601	24721 BY	31961 601	37918 Mus	55456 601	18664 603	38189 601	50371 603	10551 60	76389 KO	76594 KO	24012 AG	55486 601	36295 601	24790 BY	52852 601	79750 KO	15548 uy	36093 601	30087 KO7	77954 KO	38460 601	36397 601	23796 AGE	10088 603	78968 K07	10035 601	52137 602	74907 KO	70382 KU	70000	100 60067	36104 601	58025 601	79143 KO7	78534 KO7	36612 AGE	79084 KO7	58514 603	13757 601	19320 603	29209 AGI	14014 601	78116 KO7		
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Coore Match Score Match 603 73.9 5600 73.5 5600 73.		Leng	73	က	64	57	9	σ	4	Φ	7	2	4	σ	4	Н	9	8	4	0	9	ч	2	9	4	S	0	m	0	2	9 6	•	* 5	4 6	ď	Ó	2	~	0	Н	a	æ	6	m	a	9		
SCORE SC		ch	6		•	•	•	•	•	•	•	•	٠			•	٠		•	•				•	٠	•	•	•	•			•		٠	•													
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		cor	- 09	0	59	89.	88.	28	78.	77.	57	70.	70.	^	26	62.	61.	LO.	54	48.	48.	54	47.	47.	54	44.	54	43	5.0		42.	♂ •	* *	, 6	3.7	53	36.	36.	36.	35.	53	34.	34.	31.	30.	28.		
			•	7	m	4	Ω	9	7	8	σ	10	11	12	13	14	15	16	17	18	, 19	20	21	22	23	24	25	26	27	28	20.0	30	100	9 6	34	35	36	37	38	39	. 40	41	42	43	44	45		

RESULT 1 BE284158 LOCUS DEFINITION ACCESSION VERSION	BE284158 739 bp mRNA linear EST 13-JUL-2000 601099428F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5', BE284158 BE284158 GI:9160900
KEYWORDS SOURCE ORGANISM	EST. Mus musculus (house mouse) **Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 739)

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DEFINITION
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PUBMED
                                                                                                 ACCESSION
                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                             AUTHORS
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                    RESULT 2
BY724721
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                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib-"NCI_CGAP_Lu29"
//clone_lib-"NCI_CGAP_Lu29"
//note-"Organ: lung; Vector: pCMV-SPORT6; Site_l: Sall;
Site_2: NotI; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
10 c 184 g 161 t
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/db_xare="laxan:10090"
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/tissue_type="spontaneous tumor, metastatic to mammary.
/tab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/TLNL at:
http://mage.llnl.gov. h column: 07
High quality sequence stop: 535.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Matches:
Conservative:
Mismatches:
Indels:
                                                Contact: Robert Strausberg, Ph.D.
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Mammalia Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus Ammmalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mammalia; Eutheria; Rasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Casterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchis, L., McRacierski, R.M., Nagashima, T., Numata, K., Okido, T., Pee, Y., Lenhard, B., Lyons, P.A., Majott, D.R., Maltais, L., Marchis, J.U., Qi, D., Ranachadran, S., Ravasi, T., Rede, D.J., Reid, J., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Sctou, M., Shimada, K., Sultana, R., Taylor, M.S., Teasdale, K.D., Yang, L., Yang, L., Yang, C., Wynshaw, Boris, A., Yang, L., Yang, C., Wynshaw, Boris, A., Yang, L., Yang, C., Wynshaw, Boris, A., Yang, L., Yang, C., Mynshaw, Boris, A., Yang, C., Yangawa, K., Sakai, K., Sakai, D., Kawa, J., Indaya, M., Markawa, T., Romo, H., Nakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishi, Y., Shibata, K., Shinagawa, A., Kagawa, I., Myaza, M., Malayashi, R., Sakai, K., Sakai, D., Sakai, K., Sakai, K., Shinagawa, A., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, Sakai, K., Sakai, S
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URL:http://genome_gsc.riken.go.jp,
Adachl.J., Aizawa,K., Akimura,T., Araawa,T., Carninci,P., Fukuda
Adachl.J., Aizawa,K., Akimura,T., Hirozane,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Ragawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
EST 17-DEC-2002
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
BY724721
BY724721 RIKEN full-length enriched, adult male aorta and vein Mus
musculus cDNA clone A530011123 5', mRNA sequence.
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 ATGGAATGGAGCAGAGTCTTTATCTTTCTCCTATCAGTAACTGCAGGTGTTCACTCCCAG 111
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cDNA library was prepared and sequenced in Mouse Genome broyclopedia project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                           /tissue_type="aorta and vein"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANGSIJ row: c column: 05
High quality sequence stop: 561.
1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
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further details.
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Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810060009 product:immunoglobulin heavy chain 6 (heavy chain of IgM), full insert sequence.
                                                              101 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp
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---GGATCCATCTATGGTTACGGCCTCTACTACTTTGACTACTGGGGCCCAAGGCACC
                                       61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrTyrAsn
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/clone_lib="NCI_CGAP_LU29"
//clone_lib="NCI_CGAP_LU29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_l: Sall;
/site_lib="Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
214 c 190 g 177 t
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAM9270 row: m column: 12
High quality sequence stop: 695.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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/note="unnamed protein p
6 (heavy chain of IgM) (
evidence: BLASTN, 100%,
putative"
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                                                   /codon_start=1
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BF165456
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/strain="CzECH II"
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Investigator providing samples: Gilbert Smith, NIH"
32 a 266 c 248 g 195 t
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                       pGluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysTh 140
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
10 266 c 211 g 198 t
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: gapbs.remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: capbs.remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM4855 row: h column: 07
High quality sequence stop: 771.
Location/qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:3491766"
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/lab_host="DH108"
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BG518664 892 bp mRNP
602578528F1 NCI_CGAP_Lu29 Mus musculus
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Mus musculus
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BG518664
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COUNT 185 a 229 c 200 g 180 t N	Alignment Scores: 3.87e-50 Length: 794 Score: 577.50 Matches: 113 Bercent Similarity: 83.55% Conservative: 14 Best Local Similarity: 74.34% Mismatches: 22 Query Match: 12 Gaps: 2 DB:	1 MetGlucysSerTrpValPheLeup 1 MetGlucysSerTrpValPheLeup 1 ATGGGATGGATGGATGTGATTCTCTCT 2 AlaTyrLeuGlnGlnSerGlyAlaG 1 (1)	
BASE COUNT ORIGIN	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	US-08-836- QY Db CQY Db CQY Db CQY Db CQY Db CQY COMENT COMMENT COMMENT	
:::	26 SerGlyAlaGluLeuValArgSerGlyAlaSerValLySMetSerCysLysAlaSerGly 45	66 TrpliedlyAanliePheProGlyAanGlyAspfhrTyTyTAsnGlnLySPheLySGly 85 203 TGONTGGACCATTATACTGGAGACATCACATCACAACACACCAGGC 262 80 LySAAbserLeuthNAABSPTRASTESSTHANATORYTACAATCACAACCAGGC 262 81 CHARACTGACACTGCACACAATCCTCCACACACCACACCAGGC 232 82 AAGGCACATGACTGCACACAATCCTCCACACACACCAGACCTG 322 82 AAGGCACATGACTGCACACAAATCCTCCACACACACACAC	

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1.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/Chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/Chloroform and Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Luo, A., Carter, M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute on Aging/National Institutes of Health 313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: KO644 row: A column: 12 Seq primer: M13 Reverse High quality sequence stop: 529 POLYA-No.
        Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Cai
Taub, D., Longo, D.L., Keller, J. and Ko, M.S. H.
Systematic Analyses of NIA. Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)
                                                                                                                                                                                                                                                                                                                                         /db_xref="niaEST:K0644A12-5N"
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/lab_host="DH10B"
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                       Other ESTs: K0644A12-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_l: NotI;
Site_2: Sall; transgenic model WNT-1, expression driven by
MMYV-LIR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
79 a 215 c 195 g 182 t
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Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)"
(Ince="Vector: pSPORTI (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 546)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin, C-KIt-/Sca-1+) cDNA Library (Long)
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7. Organism="Mus musculus"

/mol_type="muscr: k0647B06-5N"

/db_xref="miaEST: k0647B06-5N"

/db_xref="taxon:10090"

/clone="NiA: k0647B06 IMAGE:30073265"

/tissue_type="Hematopoletic Stem Cell (Lin-/c-Kit-/Sca-1+
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CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
and Casell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plater: K0647 row: B column: 06
Seg primer: M13 Reverse
High quality sequence stop: 546
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11: 1553-1558 (2001). [PMID: 11544199]). Total RNAS
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1. .847
//organism="Musm musculus"
//mol_type="mRNA"
//strain="CzECH II"
//db_xref="taxon:10090"
//clone="InARE:4019039"
//issue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
//ab_host="bh108"
//clone_lib="NoI_GGAP_Lu29"
//note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NoI; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
223 c 242 g 203 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
i column: 24
High quality sequence stop: 760.
     GCAGAGCCTGCAAGAGCCCACCATCTACCCACTG 488
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Site_2: Sal1; Cloned unidirectionally. Primer: Ollgo dT.
Site_2: Note: this is a NCI_CGAP_Library."

253 c 226 g 212 t 2 others
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                         Craniata; Vertebrata; Euteleostómi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                      Email: cgapbs-remail.nih.gov.
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arraped by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov.p column: 14
High quality sequence stop: 592.
Location/Qualifiers

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 896)
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AUTHORS
TITLE
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COMMENT
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114 GAGCTCAGGAGCTCAGCCTCTGCAGGAGGACTGGGAGGAGACTAC 370 126 GAGCTCAGGAGCCTCAGCACCTCTGCAGGAGGAGACTAC 370 127 GAGGAGCTGAGGACCTCTGCAGGACTCTCCCCGAGGTTGCC 430 128 GAGGAGCTGAGGACCACTCTCCCCGAGGTTGCC 430 129 AGGAGGACCAGGACCACTCTCCCCGAGGTTGCC 430 121 GAGGATGCTTGCTGCACACTCCCCACGAGGTTGCC 430 121 TAPPCAGCCCACCACTACCACCACTCCCCACGAGGTTGC 472 127 GAGGATTGCTTGCTGCACACTCCCACGAGGTTGC 472 128 F156295 128 F156295 129 F156295 120 F156295		GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp ::::::	QΩ	69
113 GUINALAGUASPYTTTGGYGLIGYTTTGGYGLIANTHVAISSTEERALALISTTH 140 1111:::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!		GAGCTCAGCAGCCTGACCTCTGAGGACTCTGCCGTCTATTACTGTGCAAGGGACTAC	Qy	41
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111 ThrProportovalTypFockeuvalProGitySertem 153 411 AGAANTCCACCACCACCACCACCACCACCACCACCACCACCACCA		AGTGGTAGCCTTGACTACTGGGGCCAAGGCACCACTATCACAGTCTCCTCAGAGTCTGCG	Qy	61
### AGANTCCCACCACCACCACCACCACCACCACCACCACCACCACC			qa	189
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The pages The pick	HOT NUONO	musculus Mryota; Metazoa; Chordata; Malia: Eutheria: Rodentia:	δy	•
National Institutes of Health, Mammalian Gene Collection (MGC) Context: Robert Strausberg, Ph.D. Email: capbs refamil: nih gov Tissue procurement: dilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies Clone distribution: NGT-CGAP CLONE distribution information can be found through the I.M.A.G. E. Consortium/LiML at: Clone distribution: NGT-CGAP CLONE High quality sequence stop: 613. Location/Qualifiers Location/Qualifiers Location/Qualifiers Ab_Laref-Texan.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Taxon.10090 Aptered-Toxon.10090 Ap	REFERENCE	1 (bases 1 to 616) NHH-MGC http://mgc nci nih gow/	qa	4
Unitact: Gapbs-remail.nh.gov Tissue Procurement: Gibert Saith, Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by:Indyte Genomics, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by:Indyte Genomics, Inc. Clone distribution: NCI-CCAP Colone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lange.llnl.gov Plate: LLMA0245 for cov: j column: 04 High quality sequence stop: 613. Location/Qualifiers ree 'Arraylan-"CabcH II" // Arraylan-"CabcH II" // Arraylan-"CabpcH II" // Arraylan-"CabcH II" // Arr	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	RESULT BY7247	15 90
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Close distribution: NCI-CGAP close distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov Plate: LLAM2545 row: 1 column: 04 High quality sequence stop: 613. Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Amble Transmary and	Origina	Contact: Nobel Strusberg, Fn.D. Email: cgapbs-r@mail.nih.emi++ bb.D.	DEFINI	TION
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LANL at: http://image.llnl.gov Plate: LLAM9245 row: j column: 04 High quality sequence stop: 613. Location/Qualifiers ree l.6ation/Qualifiers i.616 /organism="Mus musculus" /mol_type="manA" /db_xref="taxon:10090" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone="IMAGE:400943" /clone=lib="NCI_CGAP_Lu30" /clone=li		construction of the second of	ACCESS VERSIC	NOI
High quality sequence stop: 613. Location/Qualifiers Location/Qualifiers 1. 616 /organism="Mus musculus" //organism="Mus musculus" //db_xref="taxon:10090" //db_xref="taxon:10090" //db_xref="taxon:10090" //tissue_type="tundry musculus" //tissue_type="tundry musculus" //issue_type="tundry musculus" //issue_type="tundry musculus" //issue_type="tundry musculus" //issue_type="tundry musculus" //issue_type="tundry constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" t Scores: t Scores: 1.02e-48		information	SOURCE	NISM
Location/Qualifiers I. 616 / Organism="Wus musculus" // Organism="Wus musculus" // Altain="C2ECH II" // Ab_xref="tax.on:10090" // Cione="ImAGE:4009443" // Lissue_type="tumor, metastatic to mammary" // Lissue_type="tumor, metastatic to metastatic to m		nttp://image.iin.gov Plate: LiAm9245 row; j column: 04 High quality sequence stop: 613	88.688	Z.
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Alab_host="NoI_GGAP_Lu30" Alab_host="NoI_GGAP_Lu30" Anote="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driven by MTV-LTR enhancer: Cloned unidirectionally. Primer: Oligo MTV-LTR enhancer: Cloned unidirectionally. Primer: Oligo MTV-LTR enhancer: Oligo Investigator providing samples: Gilbert Smith, NIH" 1.02e-48		/clouerance.tupog443/ /tissue_type="tumor, metastatic to mammary"		
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dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 170 c 160 g 148 t		<pre>/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo</pre>		
1.02e-48 Length: 616 562.50 Matches: 113 83.12% Conservative: 15 73.38% Mismatches: 22 68.93% Indels: 4 10 Gaps: 1	SASE COUNT	σ		
1.02e-48 Length: 616 562.50 Matches: 113 83.12% Conservative: 15 73.38% Mismatches: 22 68.93% Indens: 4 10 Gaps: 1	ORIGIN			
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	JS-08-836-4	(1-153) x BF136295 (1-616)	TIL	гā

1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20

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Solvazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schrimi, L.M., Kanaphi, A., Matsuda, H., Batalov, S., Quackenbush, J., Schrimi, L.M., Kanaphi, A., Matsuda, H., Batalov, S., Baise, J.A., Bradt, D., Brusic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehhard, B., Lyons, F.R., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Magashima, T., Numatca, K., Okido, T., Pavan, W.J., Pertea, G., P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Magashima, T., Numatca, K., Okido, T., Pavan, W.J., Pertea, G., Perrovsky, N., Villai, R., Pontius, J. U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Raid, J., Sandelin, A., Schneider, C., Semple, C.A., Satole, G., Petrovsky, W., Shimada, K., Sullana, R., Yandina, Y., Taylor, M.S., Tasadale, R.D., Tomita, M., Varardo, R., Wanner, L., Wahlestedt, C., Wataner, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, K., Arakwa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Sakai, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Anakwa, T., Konno, H., Wadawa, T., Anakwa, T., Koshino, R., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Loch, M., Habistaki, Y., Anakwa, T., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Loch, M., Maltor, Chan, M., Washa, M., Sakai, M., Sakai, D., Shinagawa, A., Washinayasa, A., Was
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BY724790. GI:27137917
BSY24790. GI:27137917
BSY24790. Gi:27137917
BSY ansculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Lyfaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Butheria; Rodentia; Sciurognathi; Murinae; Mus. 1 (bases 1 to 667)
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                                                                                                                                                                                                                                                                 1 CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
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GlnLysPheLysGlyLysAlaSerLeuThrAlaAspThrSerSerSerSerThrAlaTyrMet 100 GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120 :::::: GluGlyalaLeu------AspTyrTrpGlyGlnGlyrhrServalrhrValSer 136 :::||| ||| ||| 372 CAGGGATGGTTACTACGTAGGAGCTACTACTGGGGCCAAGGCACCACTCTCACACGTCTCC 431 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln 20 21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer 40 61 GlyGlnGlyLeuGluTrpIleGlyAsnIlePheProGlyAsnGlyAspThrTyrAsn 80 SerAlaLysThrThrProProProValTyrProLeuValProGlySer 152 327 GAGCTCCGCAGCCTGACCATCTGAGGACTCTGCCGTCTATTACTGT--3 6 7 Mismatches: [ndels: Gaps: US-08-836-455-4 (1-153) x BY724790 (1-667) 72.44% 68.81% Best Local Similarity:

Search completed: August 31, 2003, 01:02:03 Job time : 1843,13 secs

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August 31, 2003, 00:02:06; Search time 3130.85 Seconds (without alignments) 1999.191 Million cell updates/sec
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153
1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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Chatterjee, M. and Foon, K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11D10
anti-idiotype antibody 11D10
L. Patent: JP 2001523269-A2 20-NOV-2001,
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
OS Unidentified
PN JP 2001523269-A/2
PD 20-NOV-2001
PF 12-UN-1999 UP 1999503252
PR 13-JUN-1997 US 60/049540,11-JUN-1998 US 09/096244 PI WALAYA CHATTERJEE, KENNETH A FOON
PC AGIX39/395, AGIK39/39//CO7K16/42
CC Strandedness: Single;
CC TOPOLOGY: Linear;
CC Methods of delaying development of HMFG-associated tumors CC
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                                                                                                                                                                        (bases 1 to 461)
Chatterjee,M. and Foon,K.A.
Chatterjee,M. and Foon,K.A.
Methods of delaying development of HMFG-associated tumors using anti-idiotype antibody 11b10
Patent: US 6274143-A 3 14-AUG-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
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Matches:
Conservative:
Mismatches:
Indels:
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3 6274143.
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                                                                                                                                                                                                                                                                                                            /organism="unknown"
121 c 119 g
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BD085738.1 G1:22631348

JP 200152369-A/2.

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Sequence 3 from patent (
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AR164506.1 GI:16237556
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a 126 c 121 g 110 t
                                                                                                                                                     ROD 02-APR-2002
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The separation of three antibody populations from anti-poly(A) poly(U) antibodies elicited in mice or rabbits and antigenic features of poly(A), poly(U), MOL. Immunol. 19 (2), 257-266 (1982) 82245325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; Minami 2-2, Ogata, Akita
010-0444, Japan (E-mail:Kitagawa@agri.akita-pu.ac.jp,
URL:www.akita-pu.ac.jp/, Tel:81-185-45-2056(ex.400),
Fax:81-185-45-2678)
                                                                                                                                                   AB050080 471 bp mRNA linear ROD 02
Mus musculus VH9H8 mRNA for anti-A/U antibody, partial cds
                                                                     123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSer
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Mismatches:
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Published Only in Database (2002)
3 (bases 1 to 471)
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/cell_line="hybridoma 9
1. .471
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Mus musculus
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                                                                                                                                                                                    AB050080
AB050080.1 GI:19909935
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11. .>469
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Query Match:
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SYTLTSYNHWWVROPGQGLEWIGNIFPGRODTYYNOKFKGKASLTADTSSSTAYMQI
SSLTSBSAVYFCKWWEGALDYWGGGTSYTVSS"
101 c 107 g 101 t
     22-MAY-2001
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Tripathi, P. K., Oln, H., Bhattacharya-Chatterjee, M., Ceriani, R. L., Foon, K. A. and Chatterjee, S. K.
Construction and characterization of a chimeric fusion protein consisting of an anti-idiotype antibody mimicking a breast Hybridoma 18 (2), 193-202 (1999)
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Chatterjee_S.K. and Tripathi,P.K.
Chatterjee_S.K. and Tripathi,P.K.
Subirect Submission
Submitted (29-JAN-1999) Internal Medicine, University of Kentucky,
800 Rose Street, Lexington, KY 40536, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 SerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrpGluGly 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSerCysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"anti-idiotype antibody 11D10; mimics a breast cancer-associated antigen, human fat globule (HMFG)"
 24720 411 bp mRNA linear ROD 23 musculus immunoglobulin heavy chain mRNA, partial cds
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/mol_type="mRNA"
/strain="BALB/c"
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                                                                                 Mus musculus (house mouse)
                                                  AF124720.1 GI:14164544
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PAT 10-APR-2003

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AF303872 294 bp mRNA linear ROD 25-SEP-2001 Mus musculus clone J558.41 immunoglobulin heavy chain variable region mRNA, partial cds.
AF303872.1 GI:11612050
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                                                                                                                                                                                         Unknown.
Unknown.
Unclassified.
I (bases 1 to 458)
Chatterjee,N., Foon,K.A. and Chatterjee,S.K.
Chatterjee,M., Foon,R.A. and chatterjee,S.K.
Monoclonal antibody 1A7 and use for the treatment of melanoma and small cell carcinoma
Patent: US 6509016-A 3 21-JAN-2003;
Location/Qualifiers
- "ARR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 294)
Haines, B.B., Angeles, C.V., Parmelee, A.P., McLean, P.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brodeur, P. H. Gernillon diversity of the expressed BALB/C VhJ558 gene family Mod. Immunol. 38 (1), 9-18 (2001) 21376477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 294)
Haines, B.B., Angeles, C.V., Parmelee, A.P., McLean, P.A.
Brodeur, P.H.
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Submitted (08-SEP-2000) Pathology, Tufts University &
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
1. .294
                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                     AR275320 458 bp
Sequence 3 from patent US-6509016.
AR275320. GI:29708411
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
1 (bases 1 to 458)
Foon, K.A. and Chatterjee, M.
Methods and compositions for the treatment of psoriasis
Patent: US 6355244-A 3 12-MAR-2002;
                                                                                linear
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Chatterjee, M., Foon, K.A. and Chatterjee, S.K.
Monoclonal antibody 1A7 and related polypeptides
Patent: US 5977316-A 3 02-NOV-1999;
Location/Qualifiers
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                                                                           Sequence 3 from patent US 5977316.
AR083801
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Sequence 3 from patent US 6355244.
AR198720. GI:20248794
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                                                                                                                                                                                                                                                           /organism-"unknown"
131 c 114 g
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Mouse hybridoma 12s18 mRNA for immunoglobuin heavy chain V region. X58580 Y00794 X58580.1 GI:51591
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LEWIGYIYPRDGDTNYNQKFKGKATLTADTSSSTAYMQISSLTSEDSAVYFCTRSRDA
YYVGAMDFWGQGTSVTVSSGGGGGGGGGGGGGGGSDIVWTQSQKFMSTSVGDRVSVTC
                                                                                                                                                                                                                                                  KASQNVGTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISNVQSE
DLAEYFCQQYNSYPYTFGGGTNLELKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 357)
Meek, K., Haseman, C., Pollok, B., Alkan, S.S., Brait, M., Slaoui, M., Urbain, J. and Capra, J.D.
Structural characterization. of antiidiotypic antibodies. Evidence J. Exp. Med. 169 (2), 519-533 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 LeuThrAlaAspThrSerSerSerThrAlaTyrMetGlnIleSerSerLeuThrSerGlu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 TIGACIGCAGACACATCCICCAGCACACGCTACAIGCAGAICAGCAGGCCTGACATCIGAA 267
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Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern
Medical School, 5323 Harry Hines Blud. Microbiology, Dallas Texas
75235, USA
                                                                                                                                                                                                                                                                                                                /#2...411 / note="(Gly4Ser)3 linker sequence" / note="(Gly4Ser)3 linker sequence" / 412...735 / product="lmmunoglobulin light chain variable region" / 206 q 165 t
                                                                                                                                                                                                                                                                                                     'product="immunoglobulin heavy chain variable region"
                                                                                                                                          /product="anti-guinea pig C5 ScFv antibody"
/protein_id="CAB60133.1"
/db_xref="G1:6272273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X58580.1 GI:51591
Ig heavy chain; Ig variable region; immunoglobulin. Mus musculus (house mouse)
Mus musculus
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                       musculus,
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/organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                           /transl_table=11
                     /organism="Mus
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                                                                                                                                                                                                           /product-"immunoglobulin heavy chain variable region"
/protein_id-"AAG39153.1"
/protein_id-"aAG39153.1"
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LEWIGYIYPGNGGTNYNOKPKRKATLTADTSSSTAYMGISSLTSEDSAVYFCAR"
69 c
77 g
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Selection of phage-displayed anti-guinea pig C5 or C5a antibodies and their application in xenotransplantation
Mol. Immunol. 38, 1235-1247 (1999)
2. [bases 1 to 735)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ250760.1 GI:6272272 antibody; heavy chain; immunoglobulin superfamily; light chain; ScFv; variable region. Synthetic construct synthetic construct
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1. .735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 AspSerAlaValTyrPheCysAlaArg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GACTCTGCGGTCTATTTCTGTGCAAGA 294

    .366
    /organism="Mus musculus"
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    /db_xref="taxon:10090"

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                                                                                                                                                                            /note="VhJ558 family"
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Mus musculus immunoglobulin heavy chain precursor (IgH) mRNA, partial cds.

M54977.

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C.region; V-region; immunoglobulin heavy chain.

Mus musculus (house mouse)
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                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Original source text: Mouse anti-idiotypic hybridome cell line 4C11, cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                     6 others
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/cell_line="4cl1"
/tissue_type="anti-idiotypic hybridoma"
1. 486
/gene="IgH"
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22
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Matches:
Conservative:
Mismatches:
Indels:
/db_xref="taxon:10090"
/cell_line="Hybridoma 12S28-G"
1. .357
                                                                                                                                                                                                                                                                                                                                                     80 t
                                                                                                                                                                                                                                                                                      <1. .>357
/gene="IG heavy chain"
/product-"IG heavy chain"
/note="variable region"
a 86 c 96 g 80 t
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/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                            <1. .>357
/gene="IG heavy chain"
/note="variable region"
                                                                          /gene="IG heavy chain"
/note="variable region"
/evidence=experimental
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                                         /gene="IG heavy chain" <1. .>357
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277 GTCTAT 282
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Best Local Similarity:
Query Match:
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AUTHORS
TITLE
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MEDLINE
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                                    gene
                                                                mRNA
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Ig heavy chain; Ig variable region; immunoglobulin. Mus musculus (house mouse)
                                                                                                                                                                         /codon_start=1
/product=1G heavy chain"
/prototein_id="CAA41456.1"
/db_xref="G1:930150"
/translation="OYOLQEPGAEVYRPGASYKMSCKASGYTFTNYWHWVKQXPGQG-LEWKGNIPPESSYFAYWQISSLTSEDSAVYYCARNEGY-AWYFDVWGXGTTVAXSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 357)
Meek, K., Hasemann, C., Pollok, B., Alkan, S.S., Brait, M., Slaoui, M., Urbain, J. and Capra, J.D.
Structural characterization of antidiotypic antibodies. Evidence that Abzs are derived from the germline differently than Abis 99092248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern
Medical School, 5323 Harry Hines Blud. Microbiology, Dallas Texas
75235, USA
                                                                                                                                                                                                                                                                                                                                                     9 others
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Matches:
Conservative:
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Indels:
/db_xref-"taxon:10090"
/cell_line="Hybridoma 12S18-G"
1. .357
                                                                                                                                                                                                                                                                                                                                                   78 t
                                                                                                                                                                                                                                                                                    <1. .>357
/gene="IG heavy chain"
/product="IG heavy chain"
/note="variable region"
a 87 c 95 g 78 t
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1. 357
/organia="Mus musculus"
/mol_type="mRNA"
/strain="A,J"
                                            /gene="IG heavy chain"
<1. .>357
<gne="IG heavy chain"
/note="warlable region"
/evidence=experimental
                                                                                                                            <1. .>357
/gene="IG heavy chain"
/note="variable region"
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277 GTCTAT 282
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Best Local Similarity:
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AUTHORS
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AUTHORS
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/note="complementarity determining region"
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Best Local Similarity:
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Pred. No.:
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DEFINITION
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ORIGIN
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                                            /codon_start=1
/product="immunoglobulin heavy chain precursor"
/product="immunoglobulin heavy chain precursor"
/product="immunoglobulin" |
/db_xref="G1:553945"
/db_xref="G1:5539
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Cheng, H.L., Sood, A.K., Ward, R.E., Kleber-Emmons, T. and Kohler, H. Structural basis of stimulatory anti-idiotypic antibodies Mol. Immunol. 25 (1), 33-40 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Original source text: Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-region; V-region; anti-idiotypic antibody; complementarity determining region; immunoglobulin heavy chain. Mus musculus (house mouse) Mus musculus
                                                                                                                                                                                                                               37. .93
/gene="IgH"
94. .2484
/gene="IgH"
/product-"immunoglobulin heavy chain"
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="BALB/c"
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/gene="CDR1"
184. .198
/gene="CDR1"
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/gene="IgH"
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/gene="4C11"
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/gene="4C11"
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457 CCCCCA 462
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DEFINITION
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TITLE
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PUBMED
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Mus musculus monoclonal antibody K1-11 heavy chain variable region mRNA, partial cds.
AF433159
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Ho, M. and Segre, M.
Mimicry of cocaine by anti-idiotypic antibodies
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                                                                                                                                                   /note-"complementarity determining region"
                                                                                                                                                                                                                                                                   388. 411
/gene="CDR3"
/note="complementarity determining region"
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/tissue_type="hyperimmunized spleen"
/dev_stage="adult"
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Matches:
Conservative:
Mismatches:
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/db_xref="G1:17016946"
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/sex="female"
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241. .291
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241. .291
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/gene="4C11"
a 134 c
                                                                         241. .291
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                                                                                                                                                                                             388. .411
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22.00
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100.008
14.388
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MUSL77IGHV 390 bp mRNA · linear ROD 29-OCT-1994
Mouse hybridoma Ig rearranged H-chain mRNA V-region, partial cds.
M97876
/translation="EVOLOQSGPGLVKPSQTMSLTCTVTGISITTGNYRWNNTRQFPG
KLEWIGYIYYSGTITYNSLTSRTTTRDTSRNQFFLEMNSLIAEDTATYYCARDPI
GLYYALDYWGGTSVTYSSARTPPSSV"
113 c 78 9 91 t
                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 390)
Lohman, K.L., Buck, D.W., Carrillo, M.A. and Kennedy, R.C. Characterization of murine monoclonal anti-CD4; epitope recognition, idiotope expression, and variable gene sequence Unpublished (1992)
Original source text: Mus musculus (strain BALB/c, sub_species domesticus) SP20-BALB/c fusion hybridoma cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name="L77; monoclonal antibody (CD4 antigen specificity)"

100 c 102 g 90 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                           M97876.1 GI:198678
V-region; immunoglobulin heavy chain; processed gene.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sub_species="domesticus"
/db_xref="taxon:10090"
/map="chromosome 12"
/tissue_type="SP20-BALB/c fusion hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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/gene="IgH"
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MUSL771GHV
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TITLE
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Search completed: August 31, 2003, 03:58:14 Job time : 3132.85 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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August 30, 2003, 22:12:36; Search time 230.013 Seconds (without alignments) 1795.608 Million cell updates/sec US-08-836-455-4 153 1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153 OM protein - nucleic search, using frame_plus_p2n model 2552756 seqs, 1349719017 residues) , Xgapext 60.0) , Ygapext 60.0) , Fgapext 7.0) , Delext 7.0 60.0 60.0 6.0 6.0 OLIGO Xgapop Ygapop Fgapop Delop Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Total number of hits satisfying chosen parameters: Word size:

Post-processing: Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution

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Description	Murine monoclonal	ibody 110	antib	Anti-idiotype mono	MAD 1A7 heavy chal	Monoclonal antibod	Anti-STX1 heavy ch	SFV anti-rev seque Single chain sFV a	່ ຜ	encoding	a [DNA encoding a CD-	for 1g'h	Anti-carcinoembryo	DNA encoding anti-	Sequence encoding	DNA encoding anti-	Anti-Cal25 bifunct	Anti-HCV Ser/Thr p	2H7 Vh sequence.	Mouse antibody 2H/ 2H7 heary chair ya	Mouse VLA-4 antibo	Alpha-4 integrin m	Mouse anti-idiotyp	Mouse anti-idiotyp	nonocl	2H7 heavy chain va	Mouse 2H7 antibody	2H7	ntibo	ng seguen	-chain V-reg	rec	ntibody 7G12	otor a								11D10 VH CDNA.	antibody; mucin; ast cancer; vaccine; ss.		
SOMMAKIES	AAT85150	AAV83773	AAL51274	AAT31333	AAZ31366 AAX80553	AAX60630	AAX82028	AAQ81500 AAT45347	AAC86590	AAC86591	AAC86563	AAA15019	AAT96345	AAQ71395 AAQ71396	AA090425	AAQ37471	AAQ90426	AAF81910	AAX57786	AAN91146	AAV82357	AA099892	AAT74760	AAT70808	AAT / 0810 AAT 70806	AAT59339	AAT70868	AAV18557 AAV03926	AAV18593	AAT36316	AAT51042	AAQ43385	ACC44927	AAT87815	ACC44914 ACC44915		ALIGNMENTS		BP.				type antibody	nti-idiotype; tumour; bre		lifiers
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ore	ı G	153	2	31	3.1 3.1	30	27	22	20	20	200	70 70	19	91.0	16	19	13	10	19	19	6 T F	19	119	19	, o	13.	19	110	13	19	19	L9	10	19	19 19				85150	T85150;	000	-MAK-2003 -JAN-1998	Murine monocl	Monoclonal human milk	s musculus	>-
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241 CAGAAGTTTAAGGGCAAGGCCTCATTGACTGCAGACACATCCTCCAGCACAGCCTACATG 300
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13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysLysAlaSerGlyTyrThrLeuThrSerTyrAsnMetHisTrpValLysGlnThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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                                                                                                                                                                                                                                                                                                                                                                  This cDNA sequence encodes the heavy chain variable region VH (AAW85150) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ATCC 12020. 11D10 was obtained by immunishing naive mice with MC-10 anti-HMFG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10 polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are and diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or 11D10 polynucleotides, including methods of treating HMFG-
                                                                                                                                                                                                                                                                                             response
                                                                                                                                                                                                                                                                                            immune retumours,
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153
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against human milk fat globule disease associated
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 94; 130pp; English.
                                                                                                                                                                                                                          Chatterjee M, Chatterjee SK,
                                                                                                                                            95US-0575762.
96US-0591965.
96US-0766350.
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Best Local Similarity:
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                                                                WO9722699-A2
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13-DEC-1996;
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 sig_peptide
                           mat_peptide
                                                                                          26-JUN-1997
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GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
                                                                                                                                                   Murine; mouse; antibody; light chain; variable region; anti-idiotype; ss; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "antibody 11D10 heavy chain variable region"
/note= "no stop codon is given at the 3' end of the
sequence"
Delaying development of, or treating, HWFG-associated tumours using anti-idiotype antibody 11D10 raised against antibodies thuman milk fat globule protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibody 11D10 heavy chain variable region coding sequence.
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17-MAY-2002; 2002WO-US15840
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Query Match:
                                     Chatterjee M,
             17-MAY-2001;
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                                                                              21 AlaTyrLeuGlnGlnSerGlyAlaGluLeuValArgSerGlyAlaSerValLysMetSer
                                                                                                                                                                                                                                                                                                                      Mouse; murine; gene; ss; vaccine; tumour; human milk fat globules; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                                                                                           Mouse 11D10 antibody heavy chain variable region coding sequence.
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                                           US-08-836-455-4 (1-153) x AAV83773 (1-461)
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The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for anti-idiotypic antibody for treating HMFG/CEA-associated tumours. The present DMA sequence encodes the heavy chain variable region of the mouse 11D10 anti-idiotype antibody.
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                                                                                                                                            Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                            T; 0 other;
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100.00%
2001US-0861294
                                                                                                                                                                                               breast tumor) in humans
                              (KENT ) UNIV KENTUCKY
                                                                                             WPI; 2003-129216/12.
P-PSDB; AA016293.
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The present sequence encodes the murine anti-idiotype monoclonal antibody (MAb) 1A7 variable heavy chain. Wab 1A7 was raised against the anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2. As the glycosphingolipid GD2 is expressed at high density by human neuroecodermal tumours, e.g. malignant melanoma, neuroblastoma, glioma, soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its colms can be used in a vaccine to treat or palliate such diseases. They can also be used to reduce the risk of recurrence of a clinically detectable tumour, and detect an arti-GD2 Ab bound to a tumour cell.

MAb 1A7 overcomes immune tolerance and induces an immune response against GD2, which comprises anti-GD2 Ab (humoral response) and coll-specific cells (cellular response). It can be used to purify anti-GD2, anti-GD2 (Ab1') or 14G2a (Ab1), detect anti-1A7 or anti-GD2 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA, and amplify desired polynucleotides for use in gene therapy.
(Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                  Anti-idiotype monoclonal antibody 1A7 variable heavy chain, cDNA.
                                                                                                                                               Murine; mouse; anti-idiotype; monoclonal antibody; MAb; 1A7; variable heavy chain; ganglioside 2; GD2; 14G2a; neuroblastoma; ylycosphingolipid; human; neuroectodermal; tumour; glioma; lung; malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine; treatment; palliate; detection; diagnosis; recombinant production; purification; probe; primer; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s) - useful to treat or palliate a GD2-associated disease, e.g. melanoma and glioma
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                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                     amplification; gene therapy; ss.
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 standard; cDNA; 458
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96US-0591196.
95US-0372676.
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16-JAN-1996;
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26-FEB-1997
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AAT31333
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Sequence 458 BP; 106 A; 131 C; 114 G; 107 T; 0 other;

458

Length:

Alignment Scores: Pred. No.:

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elicits an anti-GDZ (tumor-associated antigen) immunological response in humans. MAb 1A7 has defined light and heavy chain variable region sequences. The MAD 1A7 and polypeptides can be used for eliciting an anti-GDZ immune response. The polypeptides can also be used for detecting or purifying anti-GDZ antibody. The products can be used for treating GDZ -associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue carcinoma, and small cell carcinoma. They can be used for palliating the disease or for reducing the risk of recurrence. The present sequence represents the CDNA encoding the heavy chain variable region of MAD 1A7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides a monoclonal antibody (MAb) designated 1A7, which
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                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma; neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma; tumor-associated antigen; ss.
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                                                                               US-08-836-455-4 (1-153) x AAT31333 (1-458)
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Conservative: Mismatches: Indels:

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Gaps: (1-458)

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US-08-836-455-4 (1-153) x AAX89553
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                                       AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
                                                  The sequence is the variable heavy chain region of monoclonal anti-idiotype antibody 1A7. The polypeptide encoded by this sequence has three CDRs (complementarity determining regions). When administered to an individual the 1A7 antibody induces an immune response against ganglioside GD2. The light chain variable region of the 1A7 antibody hoth the heavy and light chain variable regions of the 1A7 antibody produce anti-GD2 real and antibody responses. The peptides and antibodies may be useful for the modulation of ganglioside GD2, and particularly for the treatment of GD2-associated tumours (e.g. melanoma, neuroblastoma, glioma, soft tissue sarcoma, and small cell carcinoma (including small cell lung cancer).
                                                                                                                                                                                                                             heavy chain variable region; antibody 1A7; T cell response; melanoma; ganglioside GD2; CDR; complementarity determining region; carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anti-GD2 immunological peptides useful for the treatment of tumours especially melanomas and small cell carcinomas
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                                                                              Location/Qualifiers
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//ttobare
//product= "Vh chain MAb 1A7
//note= "No stop codon given"
Gaps:
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                 US-08-836-455-4 (1-153) x AAZ31366 (1-458)
                                                                                                                                           AAX89553 standard; cDNA; 458 BP
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95US-0372676.
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The invention provides a method of treating of psoriasis by administering an antigen which has similar immunogenic properties to an antigen expressed on cells of psoriatic tissue so that an immunological response is elicited in the individual. The antigen stimulates the generation of anti-idiotype antibodies that neutralize the aberrant immune response causing the psoriasis. The method is used to treat psoriasis, especially chronic plaque, gulttate, pustular, plaque-type psoriasis or psoriatic arthritis. The compositions allow the individual's own immune system to act against psoriatic tissue. The present sequence represents a cDNA encoding the heavy chain variable region of monoclonal antibody 1A7.
123 AlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrPro 142
                            Psoriasis; immunological response; anti-idiotype antibody; gluttate; chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis; monoclonal antibody; 1A7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody 1A7 heavy chain variable region encoding cDNA.
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97US-0065774.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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17-NOV-1997;
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The invention relates to humanised monoclonal antibodies (MAb) against Shiga toxins. The humanised MAb that binds to Shiga toxin comprises a constant and a variable region, where: (a) the constant region contains at least part of a human immunoglobulin (Ig) constant region; and (b) the variable region contains at least part of a non-human Ig variable region. Host cells transformed with vectors encoding a humanised MAb against shiga toxin type 2 is useful for treating a patient with an infection caused by enterchemorrhagic Escherichia coli (EHEC) or other Shiga toxin producing bacteria. The humanised MAb can also be used to reduce illness caused by EHEC or other Shiga toxin producing bacteria. EHEC are
                                                                      Humanised; monoclonal antibody; MAb; Shiga toxin; immunoglobulin;
Iq constant region; enterohemorrhagic Escherichia coll; EHEC; uremia;
edema; bloody diarrhoea; hemorrhagic collitis; hemolytic uremic syndrome;
thrombocytopenia; EHEC-mediated disease; anti-STX1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/transl_except= (pos;67..60, aa:Asp)
/note= "the start and stop codons are not indicated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanized monoclonal antibodies against Shiga toxins, useful for
protection against enterohemorrhagic Escherichia coli or other Shiga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmitt CK, Stinson JL;
                                                                                                                                                                                                                                                                                                         Anti-STX1 heavy chain variable region encoding DNA.
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                                                                                                                                143 ProProValTyrProLeuValProGlySer 152
                                                                                                                                               Indels:
               Gaps:
                                            US-08-836-455-4 (1-153) x AAX60630 (1-458)
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1..366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig 3; 75pp; English.
                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melton-Celsa A, O'Brien AD,
                                                                                                                                                                                                                   AAX82028 standard; DNA; 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0215163.
97US-0068635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US27267
                                                                                                                                                                                                                                                                            10-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MELTON-CELSA A.) O'BRIEN A D.
SCHMITT C K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxin producing bacteria
                                                                                                                                                                                                                                                                                                                                                                                                            Shigella dysenteriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-418935/35
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23-DEC-1997;
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                                                                                                                                                                                                                                                AAX82028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MELT/) (OBRI/) (SCHM/) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MONG/)
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Query Match:
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associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic colitis) and the hemolytic uremic syndrome. In particular, the humanised MAbs ameliorate edema, thrombocytopenia and uremia associated with EHEC-mediated disease. The present sequence represents a DNA encoding an anti-STX1 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1; human immunodeficiency virus type 1; AIDS; Rev protein; intracellular immunization; gene therapy; single chain antibody; Fv; sFv; antibody engineering; resistance; cell immunity; HeLa; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence given in AAQ81500 encodes an sFv anti-rev antibody consisting of the variable domains of the heavy and light chains of a mouse MAA against HIV-1 IIIB rev. The sFv specifically binds a highly conserved Rev domain. Hela T4 cells expressing the sFv were resistant to all HIV-1 clinical isolates tested. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Method for conducting gene therapy - comprises using recombinant gene encoding antibody binding antigen associated with a disease; useful for providing cell immunity.
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                                                                                       Sequence 366 BP; 94 A; 92 C; 92 G; 88 T; 0 other;
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                   US-08-836-455-4 (1-153) x AAX82028 (1-366)
                                                                                                                                                                                                                                                                                                                                     268 GACTCTGCGGTCTATTTCTGT 288
                                                                                                                                                                                                                                                                                                                        109 AspSerAlaValTyrPheCys 115
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                                                                                                                                                                                                                                                                                                                                                                                                            BP
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                                                                                                                                                                                                                                                                                                                                                                                                            AAQ81500 standard; cDNA; 861
                                                                                                                                  3.42e-16
27.00
100.008
100.008
17.658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sFv anti-rev sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duan L, Pomerantz R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-082039/11.
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                      Alignment Scores:
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30-AUG-1995
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Conservative: Mismatches:

Indels:

Length: Matches:

3.53e-11 22.00

Alignment Scores:

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Score:

100.00% 100.00% 14.38%

Percent Similarity: Best Local Similarity:

Query Match:

us-08-836-455-4.p2noli.rng

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The present sequence encodes a single chain sFV anti-rev antibody
constructed using variable domains of the heavy and light chains of a
murine monoclonal antibody against (HIV-IIIIB) rev (the parent
antibody). This is incorporated into a viral vector where
expression of the anti-rev gene causes inhibition of the rev function
and so affects replication of the other viral (HIV). Rev is one of the
essential requiatory proteins of HIV, it binds to rev responsive element
(RRE) and promotes the nuclear export, stabilisation and utilisation of
the viral mRNA's containing RRE. A novel gene therapy method has been
produced, where a recombinant (rec) gene is introduced into the cells of
a mammal. The method is improved by using a rec gene encoding an
antigen associated with a disease. The method is used to prevent or
antigen associated with a disease. The method is used to prevent or
halt the progress of a disease by IC immunisation. Specifically, the Ab
can be used to inhibit the replication of a virus, such as human T-cell
can be used to inhibit the replication of a virus, such as human T-cell
benkamia virus or especially HIV-i. or of other pathogens, e.g.
development of the disease and can be used to control the severity of
                                                                                                                                                   Improved gene therapy using recombinant gene coding for an antibody - for intracellular immunisation against pathogens recognised by the antibody, esp. human immunodeficiency virus HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene therapy; antibody; immunisation; human immunodeficiency virus; HIV; human T-cell leukaemia virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 861 BP; 199 A; 234 C; 230 G; 198 T; 0 other;
861
22
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                                   Conservative:
Mismatches:
                     datches:
   Length:
                                                                    Indels:
                                                                                    Gaps:
                                                                                                                    US-08-836-455-4 (1-153) x AAQ81500 (1-861)
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                                                                                                                                                                                                                                                                                                                     AAT45347 standard; cDNA; 861 BP.
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100.00%
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14.38%
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                                                                                                                                                                                                                                         854 TATCCT 859
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                               Percent Similarity:
Best Local Similarity:
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The present sequence encodes a fusion of an anti-CD20.single chain antibody and streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs to expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence are intended in a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular,
                                                                                                                                                      126 TyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrProProProVal 145
                                                                                                                                                                          Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a fusion of a single chain antibody and streptavidin.
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861
222
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                                                                                      Gaps:
                                                                                                                         (1-861)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 95; 100pp; English.
                                                                                                                                                                                                                                                                                                                                   AAC86590 standard; DNA; 765 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, e.g. adenocarcinomas -
                                                                                                                         US-08-836-455-4 (1-153) x AAT45347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptavidin; tumour cell; ca
hematological malignancy; ss.
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99US-0168976.
                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces avidinii.
Unidentified.
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                                                                                                                                                                                                                            146 TyrPro 147
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The present sequence encodes a fusion of an anti-CD20 single chain antibody and streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.

Cells, particularly tumour cells associated with cancer.
                                                                                                                                                                                                                                                 these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, target site within a mammallan host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a fusion of a single chain antibody and streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanderson JA,
                                                            Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;
                                                                                                         765
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                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 95; 100pp; English.
                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                         2.33e-09
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                                                                                                                                                                       13.078
22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces avidinii. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-091213/10.
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                                                                                                                                                        Best Local Similarity:
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                                                                                                                                         Percent Similarity:
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                                                                                              Aliqnment Scores:
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The present sequence encodes a fusion of an anti-CD20 single chain antibody (B9E9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a clound site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour
is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding a fusion of anti-CD20 single chain antibody/streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanderson JA,
                                                                              Sequence 765 BP; 170 A; 201 C; 231 G; 163 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour cell; cancer; adenocarcinoma;
                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                       US-08-836-455-4 (1-153) x AAC86591 (1-765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schultz JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 11A; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                    AAC86563 standard; DNA; 1239 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hematological malignancy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer, e.g. adenocarcinomas
                                                                                                                           2.33e-09
20.00
100.00%
100.00%
13.07%
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99US-0168976.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avidinii.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-091213/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEOR-) NEORX CORP.
                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB30694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200075333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goshorn SC,
                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                   AAC86563;
                                                                                                                                                                                                                                                                         49
                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                       AAC86563
                                                                                                                                                  Score:
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8888888

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e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a
nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells particularly tumour cells associated with cancer,
                                                                                                                                                                                                              target site within a mammalian host.
                                                                                                                                                                                               purposes, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA15019;
                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                 ..
No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA15019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a fusion of an anti-CD20 single chain antibody (1989) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second
                   e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-CD20 single chain antibody/streptavidin fusion protein cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product- "anti-CD20 scFv and streptavidin fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sanderson JA,
   particularly tumour cells associated with cancer,
                                                                                                                         Sequence 1239 BP; 270 A; 392 C; 356 G; 221 T; 0 other;
                                                                                                                                                                          1239
20
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour cell; cancer; adenocarcinoma
                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                               US-08-836-455-4 (1-153) x AAC86563 (1-1239)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
3..1274
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC86564 standard; DNA; 1280
                                                                                                                                                                 3.64e-09
20.00
100.00%
100.00%
13.07%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0137900.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avidinii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEOR-) NEORX CORP.
                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin;
                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1999;
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   cells,
                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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CD20+ malignancy; non-Hodgkin's lymphoma; myeoablative chemotherapy; stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetically engineered CD20-specific redirected T cells useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, and autoimmune disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor; CD-20 speciifc redirected T cell; leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a synthetic CD20-specific chimeric
Sequence 1280 BP; 267 A; 397 C; 388 G; 228 T; 0 other;
                                                      1280
20
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                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a CD-20 specific chimeric receptor.
                                                                                                                                     Indels:
                                                                                                                                                       Gaps:
                                                                                                                                                                                          US-08-836-455-,4 (1-153) x AAC86564 (1-1280)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 50-53; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
27..1928
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu AM;
                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                  AAA15019 standard; DNA; 1925
                                                      3.75e-09
20.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MC,
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raubitschek A, Jensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CITY ) CITY OF HOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-339676/29.
P-PSDB; AAY84965.
                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W0200023573-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD20-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1998;
                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                              21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-APR-2000
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cc receptor. The specification describes CD-20 specific redirected T cells which express and bear on the cell surface membrane a CD20-chimeric receptor comprising an intracellular signalling domain, a transmembrane domain and an extracellular domain, the extracellular domain comprising a CD20-specific receptor. The genetically engineered CD20-specific credirected T cells are useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a chaman patient having previously undergone myeoablative chemotherapy and stem cell rescue. The genetically engineered CD20-specific redirected crem cell rescue. The genetically engineered CD20-specific redirected crem cell rescue. The genetically engineered CD20-specific redirected cas autoimmune disease (lupus or rheumatoid arthritis) in a patient.
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other;	1925 20 0 0 0
359 T; 0	Length: Matches: Conservative: Mismatches: Indels: Gaps:
C; 541 G;	Lengt Match Conse Misma Indel Gaps:
471 A; 554	5.48e-09 20.00 100.00% 100.00% 13.07%
SQ Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;	Alignment Scores: Pred. No.: Score: Percent Similarity: Guery Match: DB:
S	Alignme Pred. N Score: Percent Best Lo Query M DB:

US-08-836-455-4 (1-153) x AAA15019 (1-1925)

Search completed: August 31, 2003, 01:16:26 Job time : 232.013 secs

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Sequence 4
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Sequence 5
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Sequence 3
Sequence 3
Sequence 3
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Sequence 1
Sequence 3
Sequence 9
Sequence 1
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Sequence
Sequence
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APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
FILE REFERENCE: 304142000620
CURRENT APPLICATION NUMBER: US/09/861,294
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 6/2049,540
2 US-10-367-506-3

0 US-09-990-205-3

4 US-10-153-401-3

2 US-10-244-821-44

4 US-10-131-173-44

4 US-10-013-173-44

4 US-10-013-173-44

4 US-10-150-762-45

4 US-10-150-762-45

4 US-10-150-762-5

4 US-10-150-762-5

5 US-10-244-821-5

6 US-10-150-762-5

6 US-10-150-762-5

6 US-10-150-762-5

6 US-10-150-762-5

6 US-10-150-762-37

6 US-10-225-784-10

6 US-10-225-184-10

6 US-10-225-184-10

6 US-10-232-408-4
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PRIOR APPLICATION NUMBER: 09/096,244
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 38
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO.3
LENGTH: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09861294
Patent.No. US20020098190A1
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408
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LOCATION: (1)...(461)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-861-294-3
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                                                                                                                                                                                 -MODEL-frame+_pln.model -DEV-xlh
-Q-/cgn2_1/USPTO_spool/USO8836455/runat_29082003_132954_23062/app_query.fasta_1.654
-DB-Published_Applications_NA -OFMT-fastap -SUFFIX-P2Rol1.rnpb -MINNATCH-0.1
-LOOPEL-0 -LOOPEXT-0 -UNITS-blt. -START=1 -END-1 - MATRIX-011go
-TRANS-human40.cd1 -LIST-45 -DCCALIGN-200 -THR_SCORE-quality -THR_NIN-1
-ALIGN-15 -MODB-LOCAL -OUTEMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN-0
-MAXLEN-200000000 -USER-US08836455_GCGN_1_1_271_@runat_29082003_132954_23062
-MORD-6 -ICPU-3 -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_INMOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -VGAPEXT=60 -DELEXT=7
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                                                                                                                                                                                                                             (without alignments)
1730.853 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                             US-08-836-455-4
153
1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153
                                                                                                                                                                                                   August 31, 2003, 01:02:06; Search time 202.802 Seconds
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/cgn2_6/ptodata/2/pubpna/DCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                   version 5.1.6
- 2003 Compugen Ltd.
                                                                                                                                                nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted score greater than or equal to the score of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1533700 seqs, 1147125425 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 US-09-861-294-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xgapop 60.0 , Xgapext 60.0 Ygapop 60.0 , Ygapext 60.0 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
                                   GenCore
Copyright (c) 1993
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Maximum DB seq length: 200000000
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ORGANISM: Mus Musculus
           (1)...(461)
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US-09-990-205-3
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          LOCATION:
FEATURE:
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                                            LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10367506; Publication No US20030152575a1; GENERAL INFORMATION:
    APPLICANT: Malaya CHATTERJEE
    APPLICANT: Malaya CHATTERJEE
    APPLICANT: Kenneth A. FOON
    TITLE OF INVENTION: TUMORS BEARING HAFG AND CEA ANTIGENS
    TITLE OF INVENTION: TUMORS BEARING HAFG AND CEA ANTIGENS
    FILE REFERENCE: 304142006620
    CURRENT APPLICATION NUMBER: US/10/367,506
    CURRENT PILING DATE: 2003-02-13
    PRIOR PILING DATE: 2001-05-17
    PRIOR PILING DATE: 1997-06-13
    PRIOR FILING DATE: 1997-06-13
    PRIOR FILING DATE: 1998-06-11
                                                                           461
153
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Mismatches:
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                                                                           Length:
Matches:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                          6.85e-146
                                                                                     153.00
100.00%
100.00%
100.00%
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ORGANISM: Mus musculùs
FEATURE:
         ; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-09-861-294-3
NAME/KEY: sig_peptide
                                                                                              Percent Similarity:
Best Local Similarity:
                                                                Alignment Scores:
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US-10-367-506-3
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Sequence 3. Application US/09990205
Patent No. US20020150572A1
General INFORMATION:
APPLICANT: FOON, Kenneth A.
APPLICANT: CHATTERJEE. Malaya
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
FILE REFERENCE: 304142000501
CURRENT APPLICATION NUMBER: US/09/990,205
CURRENT FILING DATE: 2001-11-20
PRIOR PELLING DATE: 1998-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnIleSerSerLeuThrSerGluAspSerAlaValTyrPheCysAlaArgGlyAsnTrp 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GluGlyAlaLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThr 140
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                                                                                                                                                                                                                                                                                                 1 MetGluCysSerTrpValPheLeuPheLeuLeuSerIleThrThrGlyValHisSerGln
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153
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Matches:
Conservative:
Mismatches:
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PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                               Gaps:
                                                                                                                                                      153.00
100.00%
100.00%
                               FEATURE:

'NAME/KEY: mat_peptide

'LOCATION: (58)...(461)

US-10-367-506-3
NAME/KEY: sig_peptide
                  (1) \dots (57)
                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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MOLECULE TYPE: DNA (genomic)
                                                                                           NAME/KEY:
                                        NAME/KEY:
                                                           LOCATION:
                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                               LOCATION:
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Best Local Similarity:
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                      FEATURE
                                                                        FEATURE
                                                                                                                                               US-10-153-401-3
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US-10-153-401-3
US-10-153-401-3
Sequence 3, Application US/10153401
Sequence 3, Application No. US20030114398A1
SERERAL INFORMATION:
Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.
TITLE OF INVENTION: MONCLONAL ANTIBODY 1A7 AND USE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTARING SYSTEM: PC-DOS/MS-DOS
SOFTARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27-002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALON APPLICATION NUMBER: US 09/293,533
FILING DATE: 1999-04-15
APPLICATION NUMBER: US 08/372,676
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/591,196
FILING DATE: 1996-01-16
ATTORNEY AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 304142000202
                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           2.46e-22
31.00
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                                 ; LOCATION: (1)..(456)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(456)
US-09-990-205-3
                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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FEATURE:
NAME/KEY: (
LOCATION:
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OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin OTHER INFORMATION: fusion construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goshorn, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Renc, John M.
APPLICANT: Renc, John M.
APPLICANT: REPERSON: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERBUE: 69022. 54763
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT PILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
Indels:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                          424 CCACCCGTCTATCCATTGGTCCCTGGAAGCTTG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-836-455-4 (1-153) x US-10-244-821-44 (1-765)
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Matches:
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                                         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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; Sequence 45, Application US/10244821
mat_peptide
58
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49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/10150762

Publication No. US20030103948A1

GENERAL INFORMATION:

APPLICANT: Goshorn, Stephen C.

APPLICANT: Schultz, Joanne E.

APPLICANT: Lin, Yukang

APPLICANT: Reno, James A.

APPLICANT: Reno, John M.

APPLICANT: Market Streep A.

TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 690022.54762
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Goshorn, Stephen C.
APPLICANT: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Lin, Yukang
APPLICANT: Lin, Yukang
APPLICANT: Reno, James A.
APPLICANT: Reno, John M.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
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Mismatches:
Indels:
Gaps:
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                    US-08-836-455-4 (1-153) x US-10-013-173-44 (1-765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/150,762 CURRENT FILING DATE: 2002-05-17
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                    US-10-013-173-45; Sequence 45, Application US/10013173; Publication No. US20030095977A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity:
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LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: B9E9 single chain antibody-genomic Streptavidin; OTHER INFORMATION: fusion construct
US-10-013-173-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Goshorn, Stephen C.
APPLICANT: Goshorn, Stephen C.
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Sanderson, James A.
APPLICANT: Sanderson, James A.
APPLICANT: Sanderson, James A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 69022.547C1
CURRENT RAPLICATION NUMBER: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 765
                                                                                                                                                    APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.347C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
SUFRENT SEQ ID NOS: 92
SOFTWARE: FASTERO for Windows Version 4.0
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Publication No. US20030095977A1
GENERAL INFORMATION:
                                     : Goshorn, Stephen Charles : Graves, Scott Stoll
                                                                          APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
US20030143233A1
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LENGTH: 765
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Query Match:

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FILE REFERENCE: 690022.547C3
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LENGTH: 1239
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; Sequence 5, Application US/10244821
; Publication No. US20030143233A1
; GRBERAL INFORMATION:
   APPLICANT: Graves, Scott Stoll
; APPLICANT: Graves, Scott Stoll
; APPLICANT: Lin, Yukang
; APPLICANT: Sanderson, James Allen
; APPLICANT: Reno, John M.
; APPLICANT: Reno, John M.
; APPLICANT: Reno, John M.
; TITLE OF INVENTION: STREFTAVILIN EXPRESSED GENE FUSIONS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                   RESULT 10
US-10-150-762-45

Sequence 45, Application US/10150762

Sequence 45, Application US/10150762

Publication No. US20030103948A1

GENERAL INFORMATION:
APPLICANT: Goshorn, Stephen C.
APPLICANT: Schultz, Joane E.
TAPLICANT: Reno, Joanh M.
APPLICANT: Bearstyne, Erica A.
TITLE OF INVENTION: STREPTANIDIN EXPRESSED GENE:
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C2

CURRENT APPLICATION NUMBER: US/10/150.762

CURRENT APPLICATION NUMBER: 2002-05-17

NUMBER OF SOD ID NOS: 90

SOSTWARE FRASESED for Windows Version 4.0
                                                                         Length:
Matches:
; OTHER INFORMATION: fusion construct US-10-150-762-44
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LENGTH: 765
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; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion US-10-013-173-5
                                                                                                                                                                                              OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10013173
Sequence 5, Application US/10013173
Sequence 5, Application No. US2030095977A1
Sepulcation No. US2030095977A1
Sepulcant: Graves, Scott Stoll
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Heno, John M.
TITLE OF INVENTION: STREETAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                               Indels:
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1239
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                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion constru 0S/10/013, 173-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goshorn, Stephen C.
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Reno, Jonh M.
TITLE OF INVENTION: STREPTANIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEC ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 7
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                                                                                                       ; Sequence 7, Application US/10013173; Publication No. US20030095977A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: B9E9 single chain antibody-genomic streptavidin fusion
US-10-150-762-5
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APPLICANT: GOSDOON, Stephen Charles
APPLICANT: Graves, Scott Stoll

APPLICANT: Graves, Scott Stoll

APPLICANT: Schultz, Joanne Elaine
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Sanderson, James Allen
APPLICANT: Renco, John M.

APPLICANT: Renco, John M.

APPLICANT: REFERENCE: 690022.547C3

CURRENT APPLICATION: METHODS OF USE THEREOF

FILE REFERENCE: 690022.547C3

CURRENT APPLICATION NUMBER: US/10/244,821

CURRENT FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 92

SOFTWARE: FASISEQ for Windows Version 4.0

SEQ ID NO 7
                                                          APPLICANT: Sanderson, James A. APPLICANT: Sanderson, James A. APPLICANT: Reno, Jonh M. APPLICANT: Reno, Jonh M. TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 690022.5470.
CURRENT APPLICATION NUMBER: US./10/150,762
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ. ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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Publication No. US20030143233A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                    Schultz, Joanne E.
Lin, Yukang
                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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à g 49 ThrSerTyrAsnMetHisTrpValLysGlnThrProGlyGlnGlyLeuGluTrpIleGly 68

Gaps:

100.00% 100.00% 13.07%

Best Local Similarity: Query Match: Percent Similarity:

US-08-836-455-4 (1-153) x US/10/244 (1-1280)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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August 30, 2003, 22:20:21; Search time 1841.13 Seconds (without alignments) 2019.725 Million cell updates/sec
  nucleic search, using frame_plus_p2n model
OM protein
                                              Run on:
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.....TVSSAKTTPPPVYPLVPGSL 153 45562604 22781392 seqs, 12152238056 residues hits satisfying chosen parameters: 60.0 60.0 7.0 7.0 US-08-836-455-4 153 1 MECSWVFLFLLSITTGVHSQ. , Ygapext (
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, Fgapext ,
, Delext 0.00 OLIGO Xgapop Ygapop Fgapop Delop Total number of score: Scoring table: Word size: Searched: Sequence: Title: Perfect :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Command line parameters:

MODEL-frame+_p2n.model -DEV-x1h
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-0-7cgn2_170FPQ_spool/US0836455/runat_29082003_132953_23055/app_query.fasta_1.654
-0B=EST -0FWT=fastap -SUFFIX=p2noli.rst -MINMATCH=0.1 -LOOPCL=0 -LIOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=0.1190 -TRANS=hunan40.cdi -LIST=45
-DCCALIGN=200 -TRR_SCORE=quality -THR_MIN-1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM-ext -HEAPSIZE=500 -MMINLEN=0.00000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	871607 60279009	99697 6028845	59087 6012217	53063 6028280	3213/ 6028269 37216 6017844	55668 6031738	13948 6017864	51077 6029170	53883 6017723	42302 6017918	95410 mac28d12 96916 mg56b01	77954 K0716F08	71136 60121862	44014 60179127	52366 60282717	78874 60209543	38/90 MK1-HTT0	13088 QVI	54985 MR4-SN00	38776 uf57d02.	5192 UI-R-C2p-	77519 K0710F01	78969 K0731A0	76938 K0702C06	78347 K0722D09	49725 6028485	9014 AV259014	36295 6017814	24721 BY724721	81961 6010995	07163 Mus	36279 6017809	84158 6010994	36397 6017839	50371 6029152	46353 AGENCOU	49876 6029959	38460 6017829	18664 6025785	49320 6028488
DB ID	2 BG871607	2 BI09969	0 BE36908	2 BG96306	Z BG96213	2 BI45566	0 BF14394	2 BI15107	0 BF16388	0 BF14230	0 BG09541	4 CA57795	0 BE37113	0 BF14401	2 BG96236	0 BF57887	5 BQ358/9	DEFESSES 0 BF82283	3 BQ36498	0 AW90877	AI555192	4 CA57751	4 CA57896	4 CA57693	4 CA5/834	DED451	AV259014	0 BF13629	4 BY72472	0 BE28196	1 AK0071	0 BF13627	0 BE28415	0 BF13639	2 BII5037	3 BU94635	2 BI24987	0 BF13846	0 BG51866	2 BI14932
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RESULT 1 BG871607 LOCUS	BG871607 T45 bp mRNA linear EST 29-MAY-2001
ACCESSION	oor/Jocopt Mcl_Conf_Joor Mus muscuius comm cione immos: #3#1#39 5 , mRNA sequence. MRNA sequence.
VERSION KEYWORDS	BG871607.1 GI:14222147 EST.
SOURCE ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 745)

em_gss_vrl: gb_gssl:*

ALIGNMENTS

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 958)
                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Hitp://mage.llnl.gov
Plate: LLAM10839 row: c column: 24

High quality sequence stop: 582.
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Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
33 a 285 c 231 g 208 t lothers
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602884553F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:5040084
5., mRNA sequence.
BI099697
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Contact: Capbb.remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLone distribution: McC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1110 row: i column: 13

High quality sequence stop: 741.

Location/Qualifiers

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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/site_2: NotI: Cloned unidirectionally.
/site_2: NotI: Cloned unidirectionally.
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IIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average Insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | " 214 c 185 g 167 t
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8758 row: b column: 17
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602826902F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4981585 5', BG962137
                                                                                                                  602828076F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982827 5', BG963063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10986 row: g column: 20

High quality sequence stop: 875.

High quality Sequence stop: 875.
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                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                         125 ASPTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLySThrThrProPro 143
                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 903)
NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_CO24"
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Matches:
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/organism="Mus musculus"
/organism="mus musculus"
/organism="rwb"
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BASE COUNT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Email: cgapbs-rement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MG Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
LOAD Sequencing Dy: Column: MG Clone distribution information can be http://image.llnl.gov column: 02
High quality sequence stop: 713.
Location/Qualifiers
I. 734
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/clone="Ibbeat-"DH10B (TI phage-resistant)"
/clone="Ibbeat-"DH10B (TI phage-resistant)"
/clone="Ibbeat-"DH10B (TI phage-resistant)"
/clone="lbeat-"Organ: colon; Vector: pCWV-SPORT6; Site_I: NotI;
/site_I: Salti. cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
IB3 a 199 c 180 g 162 t
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 724)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDM Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                          Mus musculus (house mouse)
  GI:14349774
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/clone_lib="NCI_CGAP_Lu30"
/clone_lib="NCI_C
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603173862F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:5253279 5',
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnln.gov
Plate: LLAM9253 row: column: 17
High quality sequence stop: 697.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11639 row: 1 column: 16
High quality sequence stop: 780.
Location/Qualifiers
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/dev_stage="7, months"
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Matches:
Conservative:
Mismatches:
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/strain="CZECH II"
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Mus musculus
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B1455668.1 GI:15246324
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Best Local Similarity:
Query Match:
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Mismatches: Indels:

Gaps:

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US-08-836-455-4 (1-153) x BF143948 (1-862)
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Mus musculus
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                Query Match:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9258 row: 1 column: 23 **
High quality sequence stop: 671.
High quality Sequence stop: 671.

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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pcmodel WMT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

236 c 236 g 176 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF143948 862 bp mRNA linear EST 24-OCT-2000 601786493F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014430 5',
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/note="Organ: mammary; Vector: pCWV-SPORT6; Site_l: Sall;
Site_2: Noti; Cloned undirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 862)
NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tlssue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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Matches:
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/mol_type="mRNA"
/strain="CZECH II"
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                                                                                                                   211 g
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Mus musculus
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BF143948
BF143948.1 GI:10982988
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Percent Similarity:
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BF143948
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BF163883 914 bp mRNA linear EST 30-OCT-2000 601772396F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991558 5',
                                                                                                                                                            BI151077 883 bp mRNA linear EST 05-JUL-2001 602917012F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:5067314 5',
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//site_1: Not1: Cloned unidInfectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"
268 c 217 g 187 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Gistribution: MGC clone distribution information can be found through the I.N.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAMINISI row: h column: 03
High quality sequence stop: 719.
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                         125 AspTyrTrpGlyGlnGlyThrSerValThrValSerSerAlaLysThrThr 141
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Matches:
Conservative:
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/strain="CZECH II"
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Tissue Procurement: Gilbert Smith, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
228 c 265 g 201 t
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                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla; Eutheria; Rodentia, Sciurognathi; Muridae, Murinae; Mus. I to 914 ol 140 l l Haber Marinae, Mus. INTH-MGC http://mgc.nol.nih.gov/.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9204 row: p column: 23
High quality sequence stop: 679.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Conservative:
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Mus musculus
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Mus musculus
                                  BF163883.1 GI:11044161
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Best Local Similarity:
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CDNA Library Proparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genemics. Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9279 row: h column: 12
High quality sequence stop: 711.
Location/Qualifiers
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393 bp mRNA linear EST 26-JAN-200 SMDS Muschlus cDNA clone IMAGE: 4000967 5' similar to SW.DTCM_MOUSE P01882 IG DELTA CHAIN C REGION MEMBRANE-BOUND FORM: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mumania; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (20 393)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: agapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1012
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High quality sequence stop: 334.
Location/Qualifiers
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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KEYWORDS
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                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                       EST 21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE136816 439 bp mRNA linear EST 21-JUN-2000 ug56b01.y1 Barstead bowel MPLRB9 Mus musculus cDNA clone landE:1546345 5' similar to gb:M12376 Mouse immunoglobulin H-chain V-region pseudogene mRNA, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 439)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,Watterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine, 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                     Indels:
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                                                                                                                                                                                                                                                                                                                                                                                US-08-836-455-4 (1-153) x BG095410 (1-393)
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Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 439
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Mus musculus
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COMMENT
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529 bp mRNA linear EST 19-NOV-2002 CDNA Library (Long) Mus musculus CDNA Library (Long) Mus musculus CDNA clone NIA:K0716F08 (LONG) CAS77954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-) cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2:
Not1: Mouse cDNA project by the Laboratory of Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Nus. I (bases 1 to 529)
Plao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H. (in-/c.fit-/carl) con N. Mouse Hematopoietic Stem Cell (Lin-/c.fit-/Sca-1-) con Library (Long)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        other_ESTS: K0716F08-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: Cdna@lgsun.grc.nia.nih.gov
Plate: K0716 row: F column: 08
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/lab_host="DH10B"
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Mismatches:
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High quality sequence stop: 529
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Alignment Scores: Pred. No.:

Score:

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 16.00 100.00% 100.00% 10.46% Percent Similarity: Best Local Similarity:

US-08-836-455-4 (1-153) x CA577954 (1-529)

Query Match:

δ g

Search completed: August 31, 2003, 02:16:28 Job time : 1845.13 secs

2H7 heavy chain va

us-08-836-455-4.rag

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August 30, 2003, 19:50:30 ; Search time 36.453 Seconds (without alignments) 666.204 Million cell updates/sec
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1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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			Description		Murine monoclonal	Antibody 11D10 hea	Mouse 11D10 antibo	Anti-tobacco mosai	Heavy chain of mon	Monoclonal antibod	Mouse immunoglobul	2 H7 VH gene. Svn	2H7 antibody heavy
SUMMARIES			ID		AAW27120	AAW87594	AA016293	AAR66758	AAP93079	AAR13061	AAY17415	AAP94780	AAW10588
			DB	: :	87	20	24	16	10	12	20	10	18
			Match Length DB ID	1 1 1	LS3	153	153	465	159	468	561	140	140
	æ	Ouery	Match		100.0	100.0	100.0	76.1	73.8	70.4	9.69	69.5	69.2
			Score	1 1	918	816	816	621	602	574.5	568	565	565
		Result	SO.		-	7	m	4	S	9	7	8	6

Heavy chain variab	2H7	Mouse 2H7 antibody	2H7 heavy chain va	3F4 (Chimeric) hum 3F4 (Chimeric) hum	3F4 Human 1964 exp	Murine anti-porcin Monoclonal antibod	Human CH2 domain d Antibody C288 CH2	A dimeric anti-CD2	Human C2B8 antibod Antibody C2B8 heav	Sequence encoded b	MOUSE anti-Fas ant	Murine anti-Fas an	Humanised anti-Fas		20 2	Mouse DAV-1 neavy MAP 55.1 heavy cha	N-termina	Human N-terminal D	DAV-1 heavy	Human N-terminal D Mouse DAV-1 heavy	an N-te se DAV-	N					11D10 VH region.	antibody; mucin; east cancer; vaccine.					1.	determining region 1"		
AAW10242	AAW47513	AAW47520	AAB98092	AAW14939 AAW14940	AAW14941	AAR40384	AAE27924 ABB82833	AAB08026	ABE27923 ABB82832	AAP70627	AAB14747	AAW90897	ABB74912	ABG76347	AAE18370	ABG/6343 AAR76088	AAE18379	ABG/0334 AAE18378	ABG76353	ABG76352	AAE18380 ABG76355	ALIGNMENT		153 AA.			ype antibody	nti-idiotype; tumour; br		/Qualifiers	peptide	protein	FR1 framework region	CDR1 complementarity	•	ework region
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Murine; mouse; antibody; heavy chain; variable region; anti-idiotype; human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
                                                                           Antibody 11D10 heavy chain variable region.
           AAW87594 standard; Protein; 153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KENT ) UNIV KENTUCKY RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chatterjee M, Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-060029/05.
N-PSDB; AAV83773.
                                                                                                                                                                                                                                                                                                                                                                                                        WO9856419-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1997;
                                                      16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                 AAW87594;
                                                                                                                                                               Peptide
                                                                                                                                                                                      Protein
                                                                                                                                 Mus sp
                                                                                                                                                                                                          Region
                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                Region
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AAW87594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide sequence comprises the heavy chain variable region (VH) of monoclonal anti-idiotype antibody 11D10 produced by hybridoma cell line ArCC 12020. I1D10 was obtained by immunising naive mice with MC-10 anti-HWG antibody to obtain an anti-idiotype response. It elicits an immune response against a specific epitope of a high mol.wt. mucin of human milk fat globule (HMFG). It induces an immunological response to HMFG in mice, rabbits, monkeys and patients with advanced HMFG-associated tumours. Pharmaceutical compositions and vaccines comprising IlD10, IlD10 polypeptides and/or IlD10 polypuclectides (see also ART85149-50) are claimed. Also claimed are diagnostic kits and methods of using IlD10, IlD10 polypeptides and/or IlD10 polynuclectides; including methods of polypeptides and/or IlD10 polynuclectides; including methods of method of palliating HWFG-associated disease and in claimed kits to detect or quantify anti-HWFG antibody.

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MECSWVFLFLLSITTGVHSQAXLQQSGAELVRSGASVKMSCRASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                            Monoclonal anti-idiotype antibody 11D10 - elicits immune response against human milk fat globule disease associated tumours,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                     /label- CDR3
/note- complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 153;
 'note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 816; DB 18;
100.0%; Pred. No. 3.7e-55;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127...137
/label= FR1
/note= "framework region 4"
138..153
                               "framework region 3"
                                                                                                                                                                                                                                                                         Foon KA;
                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 94-95; 130pp; English.
                                                                                                         138..153
/label= Constant
                                                                                                                                                                                                                                                                         Chatterjee M, Chatterjee SK,
                                                                                                                                                                                                         95US-0575762.
                                                                                                                                                                                                                   960S-0591965.
960S-0766350.
          86..117
/label- FR3
                                                                                                                                                                                   96WO-US20757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 153; Conservative
                                           .126
                                                                                                                                                                                                                                                                                                                                                   especially breast cancer
                                   'note-
                                                                                                                                                                                                                                                   (KENT ) UNIV KENTUCKY
                                                                                                                                                                                                                                                                                              WPI; 1997-341690/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 AA;
                                                                                                                                                                                                                                                                                                         N-PSDB; AAT85150
                                                                                                                                          WO9722699-A2
                                                                                                                                                                                     19-DEC-1996;
                                                                                                                                                                                                                  26-JAN-1996;
13-DEC-1996;
                                                                                                                                                                                                         20-DEC-1995;
                                                                                                                                                               26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                            Region
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118..126 /label- CDR3 /note- "complementarity determining region 3"

127..137 /label= framework_4

98WO-US12250.

97US-0049540 98US-0096244

"complementarity determining region 2"

6..117 label= framework_3

"complementarity determining region 1"

'label= framework_2

69..85 /label= CDR2

"mature protein" 'note= "signal peptide" Location/Qualifiers

20..153

(first entry)

'label framework_1

/label - CDR1

/note=

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                                                                                                                                                                                 This sequence represents the heavy chain variable region of the murine antibody 11D10. This anti-idiotype antibody is used to delay the development of, or treat, a human milk fat globule (HWFG) associated tumour in an individual having low tumour burden. The antibody 11D10 is used to prevent the recurrence of HMFG-associated tumours e.g. ovarian, non-small cell lung and pancreatic carcinoma, especially for treating breast tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Delaying development of, or treating, HMFG-associated tumours - using anti-idiotype antibody 11D10 raised against antibodies to human milk fat globule protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 816; DB 20;
100.0%; Pred. No. 3.7e-55;
ive 0; Mismatches 0;
                                                                                                                                Disclosure; Fig 2; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AA;
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RESULT 2

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1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP06319396-A
                                                                                                                                                                                                                                                        01-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                      61
                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
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                                                                                                                                                                                       AAR66758
                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                         1..19
/label= signal_peptide
20..153
/note= "Mature murine 11D10 antibody heavy chain variable
region"
                                                                The invention comprises a method for delaying the development of, or treating a tumour that is associated with human milk fat globules (HMFG) or carcinoembryonic antigen (CEA). The method of the invention involves administering an anti-idiotypic antibody for HMFG (e.g. 11D10), and an anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for delaying the development, of or treating HMFG/CEA-associated tumours. The present amino acid sequence represents the heavy chain variable region of
                                                   GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
               Use of anti-idiotypic antibodies for human milk fat globules (HMFG)-carcinoembryonic antigen (CEA)-associated tumor for delaying the development of, or treating a HMFG- or CEA-associated tumor (e.g.
                                                                                                                                                                                                                                                                                                        Mouse; murine; vaccine; tumour; human milk fat globules; HMFG; carcinoembryonic antigen; CEA; 11D10; 3H1; HMFG-associated tumour; CEA-associated tumour; anti-idiotype antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 816; DB 24;
100.0%; Pred. No. 3.7e-55;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             Mouse 11D10 antibody heavy chain variable region.
                                                                                                    the mouse 11D10 anti-idiotype antibody
                                                                                                                                                                                                AA016293 standard; Protein; 153 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KENT ) UNIV KENTUCKY RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Fig 2; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2002; 2002WO-US15840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001; 2001US-0861294.
                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor) in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chatterjee M, Foon KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-129216/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAL51274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200292012-A2
                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                    20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-2002
                                                                                                                                                                                                                           AA016293;
                                                                           61
                                                                                                       121
                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
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                                                                                                                                                                                                                                                                                                                                                                                            Key
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Gaps

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Indels

Conservative

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5
                                                                      GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                                                                                                61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transformed plant producing animal-derived anti-virus antibody esp. tobacco plants producing anti-tobacco mosaic virus monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 621; DB 16; Length 465;
; Pred. No. 1e-39;
15; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monoclonal antibody. The CDNAs were incorporated into a Tiplasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants, making them TMV resistant, the plants could biofarmed for the prodn. of anti-virus antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chains of an animal derived anti-tobacco mosaic virus (TMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-tobacco mosaic virus monoclonal Ab heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco mosaic virus; TMV; monoclonal antibody; heavy chain; virus-resistant plants; biofarming.
                                                                                                                                                                          EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
                                                                                                                                                                                                      /note= "variable heavy domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "constant heavy domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "J heavy 4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Pages 14-15; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20..465
/label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 AAR66758 standard; Protein; 465 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..19
/label= leader
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75.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NISB ) JAPAN TOBACCO INC. (KURS ) KURARAY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.19
Best Local Similarity 75.69
Matches 118; Conservative
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1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.4%; Score 574.5; DB 12; Length Best Local Similarity 74.8%; Pred. No. 3.7e-36; Matches 113; Conservative 8; Mismatches 29; Indels
                                                                                                                                                                                                                     OK3T; light chain; humanised antibodies; CDR-grafting.
120 WEGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 DHYCLDYWGQGTTLTVSSAKTTAPSVYPLAP 151
                                                                                                                                                                                                                                                                                                         /label- signal peptide
20..468
/label- light chain
                                                                                                                                                                                          Monoclonal antibody OK3T heavy chain.
                                                                                                                                                                                                                                                                              Socation/Qualifiers
                                                                                      A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 2b; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emtage JS;
                                                                                      AAR13061 standard; Protein; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                         90WO-GB02017.89GB-0028874.
                                                                                                                                                                                                                                                                                                                                                                                                                              90WO-GB02017
                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adair JR, Athwal DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CLLT ) CELLTECH LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-222915/30.
N-PSDB; AAQ12637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 AA;
                                                                                                                                             25-MAR-2003
03-OCT-1991
                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1990;
21-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                     WO9109967-A
                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1991
                                                                                                                   AAR13061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                           Protein
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                                                        RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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            as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The peptide is encoded by the heavy chain of monoclonal antibody 6A4. 6A4 reacts with the OMP-1 protein of all 19 known serotypes of P. aeruginosa. It is used for therapy and diagnosis of infection, and a carrier for drugs. The antibody is 19G2a subclass. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody 6A4; heavy chain; Pseudomonas aeruginosa; OMP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                               119 -NW-EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGS 152
                                                                                                                                               Score 602; DB 10;
Pred. No. 9.4e-39;
9; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWEGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                                                                                                                                                                     Heavy chain of monoclonal antibody 6A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vonspecht B;
                                                                                                                                                                                                                                   AAP93079 standard; peptide; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; page 6; 7pp; german.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.8%;
76.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89EP-0106463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88DE-3813023
                                                                                                                                                                                                                                                                                            (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variable antibody regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 76.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domdey H, Marget M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-310861/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN91645
                                                                                                                                                                                                                                                                                         25-MAR-2003
31-OCT-2002
15-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                           EP338395-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                               AAP93079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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us-08-836-455-4.rag

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Polynucleotide(s) encoding Immunoglobulin molecules - used for efficient prodn. of chimeric human or non-human or class switched antibodies.
                                                                                  Antibodies; passive immunisation; pH3-12a; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horwitz AH, Wall R,
                                                                                                                                        ..19
label≃Leader peptide
                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            (ITGE-) INT GENETIC ENG INC.
(INGE-) INGENE INT GENETIC ENG INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page -; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.2%;
80.0%;
                                                                                                                                                                                                                         69..85
/label=CDR2
                                                                                                                                                                                                                                                                            label=CDR3
                                                                                                                                                                                                                                                                                                                                                                                    88WO-US02514
                                                                                                                                                                                                                                                                                                                                                                                                       87US-0077528
                                                                                                                                                                                                                                                                                      131..140
/label=FR4.
108..123
/label=JK2
                                                                                                                                                                                  50..54
/label=CDR1
                                                                                                                                                                                                                                             86..117
/label=FR3.
                                                                                                                                                             20..49
/label=FR1.
                                                                                                                                                                                                      55..68
/label=FR2
                                (updated)
(first entry)
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                                                                                                                                                                                                                                                                  118..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robinson RR, Liu AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-061144/08.
N-PSDB; AAN91146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 AA;
                                                            H7 VH gene
                                                                                                                                                                                                                                                                                                                                                                                   25-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-1987;
                             25-MAR-2003
06-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                              19-FEB-1989
                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
           AAP94780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          imaging
                                                                                                                                      Peptide
                                                                                                                                                             Domain
                                                                                                                                                                                  Domain
                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                         Jomain
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                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is substances i.e. with antiallergic activity and the ability of substances i.e. with antiallergic activity, to affect any allergic reaction caused in the animal by the administration of the antigen to the animal, and applying the substance to be evaluated. The present sequence is the mouse immunoglobulin E (IGE) heavy chain, given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MELIWVFLFLLSVTAGVHSEVQLQQSGAELVRPGSSVKMSCKSSGYTFTSYGINWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%; Score 568; DB 20; Length 5 72.7%; Pred. No. 1.4e-35; ive 14; Mismatches 27; Indels
                                                                                            Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
                                                                                                                                                                    20..561
/label= immunoglobulin_E_heavy_chain
                                                                                                                                                                                                                                                                                                                     Taya C, Yonemawa
                                                                                                                                                                                                                                                                                     (SANY ) SANKYO CO LTD.
(TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                                                                                                                                                                                        Transgenic non-human animal allergy models
                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; Page 24-27; 42pp; English.
                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP94780 standard; protein; 140 AA.
                                                                       Mouse immunoglobulin E heavy chain.
         AAY17415 standard; Protein; 561 AA.
                                                                                                                                               1..19
/label= signal
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                                                                                                                                                                                                                                                                                                                     (arasuyama H, Matsuoka K,
                                                    (first entry)
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Best Local Similarity 72.79
Watches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                                                                                                                                                                                         WPI; 1999-315404/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 AA;
                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX61084.
                                                  86-JUL-1999
                                                                                                                                                                                                                                                                 14-NOV-1997;
                                                                                                                                                                                                    EP921189-A1
                                                                                                                                                                                                                        19-JUN-1999
                              AAY17415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                        Key
Peptide
                                                                                                                                                                     Protein
                                                                                                                   us sp
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ID AAP9
AAY17415
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GOGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--- 117
Sequence carries the variable region of the chimeric immunoglobulin sequence. The antibodies are useful in passive immunisation avoiding negative immune reactions. They are also useful in assaying and in vitro
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                        1 MGFSRIFLELLSVTTGVHSQAYLQQSGAELVRPGASVKMSCRASGYTFTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                           1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                 Length 140;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                           Score 565; DB 10;
Pred. No. 5.6e-36;
6; Mismatches 18;
                                                                                                                (Updated on 25-MAR-2003 to correct PA field.)
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61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the 2H7 antibody. The 2H7 cDNA was used in the preparation of a novel polynucleotide molecule encoding an Ig fragment. The DNA molecule compities 2 DNA sequences encoding 2 pectate lyase excretion signal sequences respectively linked to a DNA sequence encoding an Ig Fd molecule or Ig light chain, operably linked to a single prokaryotic promoter so as to form a dicistronic transcription unit, provided that the Ig fragment can bind an antigen and is producted and secreted by an E. coli host cell when the nucleic acid molecule is expressed in the host cell. The nucleic acid molecule is used for the production of recombinant antibodies, which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging caequents, in complement mediated lysis and for therapeutic agent. Cupdated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibody engineering; heavy chain; light chain; chimaeric antibody; passive immunisation; diagnosis; hybridoma; monoclonal antibody; 2H7; B-cell antigen; Bp35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 565; DB 18; Length 140;
Pred. No. 5.6e-36;
6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /...c. comptementativy determined the second second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "framework region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "framework region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW16343 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2H7 heavy chain variable sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YSNSYWYFDVWGTGTTVTVS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 -GNWEGALDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.2%;
80.0%;
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/label= FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69..85
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50..54
/label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20..49
/label= FR1
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 69.2
Best Local Similarity 80.0
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                       140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
04-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
AAW16343
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          SSSSSSSSSSSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin G; IgG; heavy chain; recombinant production; artibody; passive immunisation; serum sickness; anaphylactic shock; immunoassay; imaging; reagent; complement mediated lysis; therapy; variable; region; complementarity determining; CDR; framework.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encodinding immunoglobulin fragment - comprising discistronic transcription unit with pectate lyase signal sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is the heavy chain variable region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69..85
/label- CDR_2
86..117
/label- framework_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00.140
label- mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20..49
/label- framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55..68
/label= framework_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131..140
/label= framework_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                         AAW10588 standard; Protein; 140 AA
                                                      121 YSNSYWYFDVWGTGTTVTVS 140
                               -GNWEGALDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 21; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50..54
/label= CDR_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18..130
label- CDR_3
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85US-0793980.
86WO-US02269.
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88US-0142039.
92US-0987555.
94US-0299085.
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                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-107579/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT36316.
                                                                                                                                                                                                                                                                                                                                                                                2H7 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
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                                                                                                                                                                                                                                                                                                       25-MAR-2003
21-OCT-1997
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                                                                                                                                                                                                                                                        AAW10588;
                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus spp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                   A polypeptide (AAW16343) comprises the heavy chain variable region of mouse monoclonal antibody 2H7, which recognises human B-cell surface antigen Bp35. It is encoded by a cDNA clone (AAM70868) obtd. from a 2H7 CDNA library by PCR amplification. The 2H7 light chain variable sequence (AAW16344) is also provided. A novel human-mouse chimaeric antibody with specificity for the human B-cell antigen has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                        Secretable immunoglobulin heavy and light chain fragments - capable of assembling into chimeric antibodies, useful for e.g. passive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
/note= "complementarity determining region 3"
131..1de
/label= FR4
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.2%; Score 565; DB 18; Length 140; 80.0%; Pred. No. 5.6e-36; ive 6; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                  Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heavy chain variable sequence of 2H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW10242 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 -GNWEGALDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 YSNSYWYFDVWGTGTTVTVS 140
                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 21; 96pp; English.
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                                                                                                                                                                                                                                                                                                                                                                   immunisation, diagnosis, etc
                                                                                                                                    900S-0501092.
85US-0793980.
86WO-US02269.
87US-0077528.
88US-0142039.
92US-0870404.
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                                                                                                             94US-0235225
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(first entry)
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Best Local Similarity 80.0'
Matches 112; Conservative
                                                                                                                                                                                                                                                                  Horwitz AH,
                                                                                                                                                                                                                                                                                                    WPI; 1997-225473/20.
                                                                                                                                                                                                                                                                            Wilcox GL;
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                                                                                                             29-APR-1994;
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06-AUG-1997
                                                                                                                                                  01-NOV-1985;
27-OCT-1986;
                                                                                                                                                                                      11-JAN-1988;
17-APR-1992;
                                                           US5618920-A
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                                                                                    08-APR-1997
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                                                                                                                                                                                                                                                                  Better M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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             Region
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This sequence represents the heavy chain variable region of the 2H7 mouse monoclonal antibody. The 2H7 antibody recognises the human B-cell surface antigen Bp35, which plays a role in B-cell activation. This sequence was used in a human-mouse chimeric antibody with human B-cell antigen specificity, that was produced using the method of the invention. The method of the invention is for the production of a protein in a Gram-negative bacterium. The method improves on current techniques, by using a vector including DNA encoding the pectate lyase signal sequence (see AAT51034), attached to the sequence encoding the protein for production. The method is especially used to make immunoglobulins (Ig), particularly those with a human constant region, suitable for passive immunisation (without risk of serum sickness or anaphylaxis) or for in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vivo/in vitro diagnosis and imaging. The Ig may also be used therapeutically, optionally coupled to toxins, etc. Alternatively the protein to be produced is the sweetener thaumatin. The presence of this signal sequence means that the protein is exported from the cytoplasm and can be recovered from the culture medium or periplasm, in active and correctly folded form. The method allows the class of any antibody to be switched, e.g. most human-human Ig are of M class, easily reduced and aggregated, and these can now be changed to G, A or E classes.
protein production; human; constant region; passive immunisation; toxin; serum sickness; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm; antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer; myeloma cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Improved prodn. of protein in Gram -ve bacteria using signal sequence - from pectate lyase to ensure transport of protein from the cytoplasm, esp. for prodn. of antibodies
                                                                                                                                                                                                                   "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 3" 131..140
                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                    "complementarity determining region
                                                                                                                                                                                                                                                                                                                     "framework region 3"
                                                                                                                                                                                                                                                                                                                                                                                      /note= "framework region 4"
                                                                                                                                                                                      "framework region 1"
                                                                                                                                                                                                                                                    /note= "framework region 2"
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                                                                                                                                                   /note= "leader peptide"
                                                                                                                      Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 21; 86pp; English.
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86WO-US02269.
87US-0077528.
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92US-0987555.
93US-0020671.
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/note=
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/note=
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N-PSDB; AAT51042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-1988;
08-DEC-1992;
22-FEB-1993;
09-DEC-1994;
                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-DEC-1994;
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27-OCT-1986;
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                                                                                                                                       Peptide
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69.2%;
80.0%;
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85US-0793980.
86WO-US02269.
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                                                                                                                                                                                              Query Match
Best Local Similarity 80.0
Matches 112; Conservative
                                                                                                                                                                                 140 AA;
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01-NOV-1985;
27-OCT-1986;
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                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                              AAW47513;
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                                                                     1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence was used in the development of a novel method the production of an immunoglobulin (19) fragment capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Production of chimeric antibody fragments - by culturing E. coli
transformed with dicistronic expression cassette
                                               4;
                               Length 140;
                                                                                                                                                                                                                                             Mouse; murine; heavy chain; variable region;
immunoglobulin fragment production; Ig fragment production;
monoclonal antibody 2H7; human B-cell surface antigen.
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robinson RR;
                                              18;
                              Score 565; DB 18;
Pred. No. 5.6e-36;
6; Mismatches 18;
                                                                                                                                                                                                                              Mouse 2H7 antibody heavy chain variable region.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu AY,
                                                                                                                                                                                                                                                                                                  1..19
/label= sig_peptide
20..140
/label= mat_peptide
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                AAW41070 standard; Protein; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example IV; Fig 21; 98pp; English.
                                                                                                                                   121 YSNSYWYFDVWGTGTTVTVS 140
                                                                                                                           118 -GNWEGALDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s,
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87US-0077528.
88US-0142039.
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94US-0299085.
95US-0450731.
                               69.2%;
80.0%;
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                                                                                                                                                                                                               01-JUN-1998 (first entry)
                                     Best Local Similarity 80.0 Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-031749/03.
N-PSDB; AAV03926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (XOMA ) XOMA CORP.
               140 AA;
                                                                                                                                                                                                                                                                                                                                                                       25-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                       02-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                      27-0CT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Better M,
                Sequence
                                                                                                                                                                                               AAW41070;
                              Query Match
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                                                                                                                                                                                                                                                                                                  Peptide
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61 RQGLEWIGAIYPGNGDTCXNQKFKGKATLTVDKSSSTAXMQLSSLTSEDSAVYFCARVVY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGFSRIFLFLLSVTTGVHSQAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTP 60
binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the gradment, under conditions so that the ig fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences encoding: (a) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a single prokaryotic promoter to form a dicistronic transcription unit. The method is used to produce chimeric Fab molecules, e.g. derived from murine monoclonal antibodies of against human B-cell surface antigen. The invention provides a novel approach for producing genetically engineered antibodies of desired variable region specificity and constant region properties. The cloned Ig gene products can be produced by expression in genetically engineered organisms. The application of chemical gene synthesis, recombinant DNA cloning and production of chemical gene synthesis, recombinant by provides an effective solution for the efficient large scale production of human monoclonal antibodies. The invention also provides a solution to the problem of class switching antibody molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; murine; heavy chain; variable region; immunoglobulin fragment production; Ig fragment production; monoclonal antibody 2H7; human B-cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 565; DB 19;
Pred. No. 5.6e-36;
6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse 2H7 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20..140
/label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW47513 standard; Protein; 140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GNWEGALDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YSNSYWYFDVWGTGTTVTVS 140
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heavy chain; variable region;

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1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
      Mouse; murine;
                                                     Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the development of a novel method for the production of an immunoglobulin (Ig) fragment capable of binding an antigen. The method comprises culturing an E. coil host that has been transformed with a nucleic acid molecule encoding the ind secreted. The nucleic acid molecule comprises DNA sequences and secreted. The nucleic acid molecule comprises DNA sequences encoding; (a) pectate lyase secretion signal sequence of inked to a DNA sequence encoding at least the variable region of in Ig A molecule; and (b) pectate lyase secretion signal sequence operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a DNA sequence encoding at least the variable region of an Ig light chain, where (a) and (b) are operably linked to a single proxaryotic promoter to form a dicistronic transcription unit. The method is used to produce chimeric Fab molecules, e.g. derived from murine monoclonal antibody 2H7 raised against human B-cell surface antigen. The invention provides a cover approach for producing genetically engineered antibodies of desired variable region specificity and constant region of chemical gene synthesis, recombinant DNA cloning and production of chemical gene synthesis, recombinant DNA choning an effective specific Ig chains in various organisms. The application of chemical constant into the efficient large scale production of human monoclonal antibodies. The invention also provides a solution to the problem of class switching antibody molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                          comprising at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 565; DB 19; Length 14
Pred. No. 5.6e-36;
6; Mismatches 18; Indels
                                                                                                  Liu AY, Robinson RR;
                                                                                                                                                                        ONA encoding secretable immunoglobulin fragments - on least the variable regions of light or heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse 2H7 antibody heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW47520 standard; Protein; 140 AA
                                                                                                                                                                                                           Example IV; F1g 21; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YSNSYWYFDVWGTGTTVTVS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GNWEGALDYWGQGTSVTVS 136
                                                                                                  Lei S,
87US-0077528.
88US-0142039.
92US-0987555.
94US-0299085.
95US-0467140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.2%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.2
Best Local Similarity 80.0
Matches 112; Conservative
                                                                                                 Horwitz AH,
                                                                                                                                    WPI; 1998-051492/05.
N-PSDB; AAV18557.
                                                                                                             Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AA;
                                                                          (XOMA ) XOMA CORP.
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                 Better M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47520;
                                                                                                             Wall R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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and section in another comparison to a control of a contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the production of an immunoglobulin (Ig) fragment capable of binding an antigen. The method comprises culturing an E. coli host that has been transformed with a nucleic acid molecule encoding the Ig fragment, under conditions so that the Ig fragment is produced and secreted. The nucleic acid molecule comprises DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Production of recombinant immunoglobulin fragment – comprising Fd molecule and light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 565; DB 19; Length 140;
Pred. No. 5.6e-36;
6; Mismatches 18; Indels
immunoglobulin fragment production; Ig fragment production; monoclonal antibody 247; human B-cell surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence was used in the development of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu AY,
                                                                                                                                                                                                                                                             1..19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example IV; Fig 21; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87US-0077528.
88US-0142039.
92US-0987555.
94US-0299085.
95US-0450731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.2%;
Best Local Similarity 80.0%;
Matches 112; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0501092
85US-0793980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86WO-US02269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0466203
                                                                                                                                                                                                                                                                                                                                   20..140
/label= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-051487/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV18593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS5698417-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -OCT-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3etter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38-DEC-
                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                 61 RQGLEWIGAIYPGNGDTCYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVYY 120
                                                         61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--- 117
The present sequence represents the mouse antibody 2H7 heavy chain variable region. Antibody 2H7 is specific for human B-cell antigen. The antibody sequence was used to construct a chimeric human-mouse antibody in the course of the Invention. The chimeric antibody is expressed in a secretion vector comprising a pelb pectate lyase secretion signal producing a protein such as a chimeric antibody in a bacterial host. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pelB pectate lyase signal sequence - and vector for expression of secreted proteins in Gram-negative bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pelB pectate lyase; secretion signal; chimeric antibody; heavy chain; B-cell antigen; antibody 247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu AY, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 565; DB 20;
Pred. No. 5.6e-36;
6; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse antibody 2H7 heavy chain variable region.
                                                                                                                                                                                                                                                                                       AAW89540 standard; Protein; 140 AA
                                                                                                                                                                   118 -GNWEGALDYWGQGTSVTVS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Fig 21; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.2%;
Best Local Similarity 80.0%;
Matches 112; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0357234.
85US-0793980.
86WO-US02269.
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88US-0142039
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93US-0020671
                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Better M, Horowitz AH,
Wall R, Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-059072/05.
N-PSDB; AAV82357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-1990;
22-FEB-1993;
09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-1987;
11-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2003
30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5846818-A.
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1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60

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Gaps

4;

18; Indels

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1 MGFSRIFLFLESVTTGVHSQAYLQQSGAELVRPGASVKMSCKASGYTFTSYNMHWVKQTP 60
                                                                                                                                                                                                           Search completed: August 30, 2003, 22:04:05 Job time: 37.453 secs
                                                                                                                                  121 YSNSYWYFDVWGTGTTVTVS 140
                                                                                                                -GNWEGALDYWGQGTSVTVS 136
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August 30, 2003, 21:57:15; Search time 24.6443 Seconds (without alignments) 849.188 Million cell updates/sec
                                                                                                                                                                                                                 US-08-836-455-4
816
1 MECSWVFLFLLSITIGVHSQ.....TVSSAKTIPPPVYPLVPGSL 153
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                           510680 seqs, 136781880 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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/cgn2_6/ptcdata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US10B_PUBCOMB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US6O_NEW_PUB.pep:*
/cgn2_6/ptcdata/2/pubpaa/US6O_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBC_DUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:* Published_Applications_AA: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	Sequence 4, Appli	_	Sequence 9, Appli	9	2,	13,	12,	11,	14,	Sequence 88, Appl		4	Sequence 105, App	Sequence 4, Appli
SUMMAKIES		ID	US-09-861-294-4	US-10-367-506-4	US-09-795-515-7	US-10-216-484-9	US-09-903-327A-6	US-09-903-327A-2	US-09-903-327A-13	US-09-903-327A-12	US-09-903-327A-11	US-09-903-327A-14	US-10-160-232-88	US-10-244-821-91	US-09-748-960-6	US-09-269-921-105	US-09-509-098-4
		DB	6	12	11	15	10	10	10	10	10	10	15	12	σ	11	11
		Query Match Length DB	. 153	153	468	464	438	456	493	510	597	613	136	135	180	139	139
	ap (Query	100.0	100.0	70.4	68.7	0.89	68.0	68.0	68.0	68.0	68.0	67.7	66.2	66.1	65.0	65.0
		Score	816	816	574.5	560.5	554.5	554.5	554.5	554.5	554.5	554.5	552.5	540	539.5	530	530
		Result No.	٦	8	m	4	S	9	7	œ	6	10	11	12	13	14	15

Sequence 105, App Sequence 126, App Sequence 13, Appl Sequence 13, Appl Sequence 105, Appl Sequence 305, Appl Sequence 305, Appl Sequence 286, Appl Sequence 286, Appl Sequence 11, Appl Sequence 18, Appl Sequence 38, Appl Sequence 32, Appl Sequence 32, Appl Sequence 36, Appl Sequence 38, Appl Sequence 386, Appl Sequence 387, Appl Sequence 387, Appl Sequence 387, Appl Sequence 387, Appl Sequence 387, Appl Sequence 337, Appl Sequence 337, Appl Sequence 337, Appl Sequence 334, Appl Sequence 334, Appl Sequence 334, Appl Sequence 334, Appl Sequence 334, Appl Sequence 334, Appl Sequence 336, Appl Seque
6 US-10-218-253-105 1 US-09-266-921-126 1 US-09-269-098-98 1 US-09-269-098-98 6 US-10-208-523-126 1 US-10-905-928-6 1 US-10-905-928-6 2 US-10-207-655-395 5 US-10-207-655-396 5 US-10-207-655-386 5 US-10-207-655-386 5 US-10-207-655-386 5 US-10-207-655-386 5 US-10-207-655-386 5 US-10-207-655-386 5 US-10-207-655-386 5 US-10-207-655-386 6 US-10-207-655-386 7 US-10-207-655-386 8 US-10-207-655-386 9 US-10-207-655-386 10 US-10-207-655-386 10 US-10-207-655-386 10 US-10-207-655-386 10 US-10-207-655-389 10 US-10-207-655-389 10 US-10-207-655-389 10 US-10-207-655-389 10 US-10-207-655-389 10 US-10-207-655-398 10 US-10-207-655-398 10 US-10-207-655-398 10 US-10-207-655-398 10 US-10-207-655-398 10 US-10-207-655-398
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\$30 65.0 \$228 64.7 \$228 64.7 \$228 64.7 \$228 64.7 \$220.5 64.0 \$221.5 64.0 \$221.5 63.9 \$221.5 63.9 \$221.5 63.9 \$231.5 63.9 \$231.5 63.9 \$231.5 63.9 \$231.5 63.9 \$231.5 63.9 \$231.5 63.1 \$231.5 63.1 \$23
01110 0110202020202020202020202020202020

US-09-861-294-4 Sequence 4, Application US/09861294 Sequence 4, Application US/09861294 Patent No. US20020098190al Patent INFORMATION: APPLICANT: Malaya CHATTERIEE APPLICANT: Kenneth A. FOON TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA CURRENT APPLICATION UNMBER: US/9/861,294 CURRENT FILING DATE: 2001-05-17 PRIOR FILING DATE: 1997-06-13 PRIOR FILING DATE: 1997-06-13 PRIOR FILING DATE: 1998-06-11 PRIOR FILING DATE: 1998-06-11 NUMBER OF SEQ ID NOS: 38 SOFTWARE: FastSEQ for Windows Version 4.0
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TREATING

ALIGNMENTS

ORGANISM: Mus musculus ; NAME/KEY: SIGNAL ; LOCATION: (1)...(19) US-09-861-294-4 LENGTH: 153

9 1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP Gaps ; 0 Length 153; Indels 100.0%; Score 816; DB 9; 100.0%; Pred. No. 2.4e-62; Live 0; Mismatches 0; Query Match Best Local Similarity 100.(Matches 153; Conservative

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61 GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120 61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLLSEDSAVYFCARGNW 120 1 MECSWVFLFLLSITTGVHSQAYLQOSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP g δ

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61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR-GN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: AALI-Fas Antibodies
FILE REPERENCE: 980126GIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 9, Application US/10216484; Publication No. US20030103976A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              : 468 amino acids
amino acid
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Best Local Similarity 71.3
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-795-515-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Mus musculus
US-10-216-484-9
                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKOTP
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                                                                                                                                                                                                                                  APPLICANT: Malaya CHATTERJEE
APPLICANT: Malaya CHATTERJEE
APPLICANT: Kenneth A. FOON
TITLE OF INVENTION: CUMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: TUMORS BEARING HMFG AND CEA ANTIGENS
CURRENT APPLICATION NUMBER: US/09/861,294
PRIOR APPLICATION NUMBER: US/09/861,294
PRIOR RELING DATE: 2003-02-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1997-06-13
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOSE: 38
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 816; DB 12; Best Local Similarity 100.0%; Pred. No. 2.4e-62; Matches 153; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGSL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09795515;
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.;
ITILE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        Sequence 4, Application US/10367506
Publication No. US20030152575A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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; LOCATION: (1)...(19)
US-10-367-506-4
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Gaps

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APPLICANT: Li, Erguang TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR TITLE OF INVENTION: BELIVERY TITLE OF INVENTION: DELIVERY
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                      ORGANISM: Mouse
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2
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                                                                                                                                                                        Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Fusion protein with N-terminal portion of OTHER INFORMATION: and EGF mature peptide
                                                                                                                                                                                                                   Indels
                                                                                                                                                                        DB 10;
                                                                                                                                                                      Query Match 68.0%; Score 554.5; DB 1
Best Local Similarity 69.7%; Pred. No. 1.6e-39;
Matches 106; Conservative 16; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGS 152
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CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-903-327A-13
Sequence 13, Application US/09903327A
Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
APPLICANT: Li, Erguang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09903327A; Patent No. US20020164333A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 69.7<sup>3</sup>
Matches 106; Conservative
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US-09-903-327A-12
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LENGTH: 493
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TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: 08/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Li, Erguang
TITLE OF INVENTION: BIPUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-11228
CURRENT APPLICATION UNDBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
                          61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGHSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , LACKATION: (0)...(0)
; OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein
; OTHER INFORMATION: bifunctional antibody
US-09-303-327A-6
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; Pred. No. 1.5e-39;
16; Mismatches 25; Indels
                                                                                                        121 YSNNW--YFDVWGTGTTVTVSSAKTTPPSVYPLAPGS 155
                                                                                  118 --GNWEGALDYWGQGTSVTVSSAKTTPPPVYPLVPGS 152
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                    Sequence 6, Application US/09903327A Patent No. US2002016433A1 GENERAL INFORMATION: APPLICANT: Nemerow, Glen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09903327A Patent No. US20020164333A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 68.0%;
Best Local Similarity 69.7%;
Matches 106; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mouse
                                                                                                                                                                                                              US-09-903-327A-6
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US-09-903-327A-2
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LENGTH: 456
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APPLICANT: L1, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
TITLE OF INVENTION: GENE
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: 05/09/903,327A
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER. OF SEC ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain OTHER INFORMATION: and SCF mature peptide
         61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
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CURRENT APPLICATION NUMBER: 2002-06-04
PRIOR PAPLICATION NUMBER: US/09/453,718
PRIOR PILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-05-20
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                                                                        121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPGS 152
                                                                                                  ---IAYWGQGTLVTVSAAKTTPPSVYPLAPGS 147
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APPLICATION NUMBER: 09/119,014
FILING DATE: 1998-07-20
APPLICATION NUMBER: PCT/JP97/04259
                                                                                                                                                                                                                              Sequence 14, Application US/09903327A; Patent No. US20020164333A1
GENERAL INFORMATION: APPLICANT: Nemerow, Glen R.
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Publication No. US20030088075A1
GENERAL INFORMATION:
APPLICANT: SHITARA, KENYA
APPLICANT: ITO, MIKITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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SHIBUYA, MASABUMI
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Matches 106; Conservative
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HANAI, NOBUO
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LENGTH: 613
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APPLICANT:
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APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erguang
TITLE OF INVENTION: BIPUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REPERBENCE: 12908-1128
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR APPLICATION NUMBER: 09/613,017
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELLYERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ. ID NOS: 33
SOFFWARE: FastSEQ for Windows Version 4.0
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69.7%; Pred. No. 1.8e-39;
tive 16; Mismatches 25;
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69.7%; Pred. No. 2.1e-39;
tive 16; Mismatches 25;
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Patent No. US20020164333A1
GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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Matches 106; Conservative
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Best Local Simi
Matches 106;
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Best Local
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Patent No. US20010046496A1
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                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein US-10-160-232-88
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APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Reno, John M.
APPLICANT: Perseyne, Erica A.
TITLE OF INVENTION: STREPPAVIDIN EXPRESSED GENE FUSIONS AND
FILE REFERENCE: 690022.547C3
                                                                                                                                                                                                              Ouery Match 67.7%; Score 552.5; DB 15; Length Best Local Similarity 78.8%; Pred. No. 6.1e-40; Matches 108; Conservative 10; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
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Publication No. US20030143233A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               121 EGALDYWGQGTSVTVSS 137
                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 88
LENGTH: 136
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Matches 104; Conservative
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; ORGANISM: Mus musculus
US-10-244-821-91
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US-09-748-960-6
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; Sequence 6, Application US/09748960

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; OTHER INFORMATION: Amino acid sequence of anti-HM 1.24 antibody H chain V region US-09-269-921-105
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                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Portion of the heavy chain of LDP-02 with a heavy OTHER INFORMATION: chain signal peptide
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APPLICANT: Ohtomo, Toshihiko
APPLICANT: Ohtomo, Toshihiko
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshihara, Yasuo
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODX
FILE REPRENCE: 350.29-20.07.00
CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1990-04-01
EARLIER RILING DATE: 1997-10-03
EARLIER FILING DATE: 1997-10-03
EARLIER APPLICATION NUMBER: DCT/JP97/03553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
          APPLICANT: Fox, Judith A. APPLICANT: Alison, David Edward TITLE OF INVENTION Method of Administering an Antibody FILE REFERENCE: 1855.2007-001 CURRENT APPLICATION NUMBER: US/09/748,960 CURRENT FILING DATE: 2000-12-27 PRIOR APPLICATION NUMBER: US 09/550,082 PRIOR FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%; Score 539.5; DB 9;
65.2%; Pred. No. 1.1e-38;
tive 18; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 '-NWEGALDYWGQGTSVTVSSAKTTPPPVYPLVPGS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 530; DB 11;
Pred. No. 5.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE

LOCATION: (19)...(20)

OTHER INFORMATION: signal peptide cleavage site
US-09-748-960-6
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105, Application US/09269921
Publication No. US20030045691A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1996-10-04 NUMBER OF SEQ ID NOS: 137
                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.0%;
71.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 66.1%.
Best Local Similarity 65.2%
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 105
APPLICANT: Brettman, Lee R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-269-921-105
                                                                                                                                                                                                                                                                                      LENGIH: 180
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61 GQGLEWIGSIFPGDGDTRYSQKFKGKATLTADKSSSTAYMQLSILAFEDSAVYYCARGLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                                                                                                                      GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MECSWVFLFFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps
  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Amino acid
FOTHER INFORMATION: Sequence of H chain V region of mouse anti-
OTHER INFORMATION: HMI.24 antibody
US-09-509-098-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.0%; Score 530; DB 11; Length 139; 71.9%; Pred. No. 5.2e-38; tive 15; Mismatches 22; Indels
  22; Indels
                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09509098
Publication No. US20030103970A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0274
CURRENT APPLICATION NUMBER: US/09/509,098
CURRENT FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: PCT/JP98/04469
PRIOR APPLICATION NUMBER: JP 9-271726
PRIOR PILING DATE: 1998-10-03
PRIOR PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIn Ver: 2.1
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RGGYYFDYWGQGTTLTVSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EGA--LDYWGQGTSVTVSS 137
                                                                                                                                                                                                     121 EGA--LDYWGQGTSVTVSS 137
  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.0%
Best Local Similarity 71.9%
Matches 100; Conservative
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Murine sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 139
                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-509-098-4
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Search completed: August 30, 2003, 22:06:57 Job time : 25.6443 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 30, 2003, 22:02:45; Search time 18.4832 Seconds (without alignments) 796.063 Million cell updates/sec Run on:

US-08-836-455-4 816 1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues

Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Length	BB	DI	Description
1	568	69	475	7	801321	Iq qamma-2b chain
7	563		469	N	S37483	gamma-2a
3	260	99	474	Н	G2MS11	
4	549		139	~	PS0024	heavy
S	548.5		151	7	PL0011	heavy chain
9	547		150	~	PN0444	heavy chain
7	537.5	65.	246	~	S38950	gamma
ω	537.5	65.	446	ď	S40295	
ტ	533	65.	178	N	S29594	qamma
10	529		137	~	н32513	heavy chain
11	527.5		140	~	PH1482	heavy chain
12	523.5		140	-	HVMSG7	heavy chain
13	523.5	64.2	166	~	PL0012	Ig heavy chain pre
14	516.5	63.3	140	7	PH1489	chain
15	512	62.7	141	~	A39276	heavy chain
16	510.5	62.6	138		E32513	Ig heavy chain pre
17	507.5	62.2	138	~	S21810	heavy chain
18	507	62.1	133		PC1155	
19	506.5	62.1	140		PH1488	heavy chain
20	502.5	61.6	135		PH1493	Ig heavy chain V r
21	502.5	61.6	140		PH1484	heavy chain V
22	502.5	61.6	140		PH1498	Ig heavy chain V r
23	501.5	61.5	135		PH1494	Ig heavy chain V r
24	499	61.2	135		PS0057	heavy chain
25	497		139		A27609	Ig heavy chain pre
26	496.5	8.09	135		PH1492	heavy chain
27	495	60.7	135		A30577	Ig heavy chain pre
28	494.5	9.09	140	7	PH1486	heavy chain
29	493	60.4	139	-	MHMS18	Iq heavy chain pre

Januar 2. Must musculus (house mouse)
C; Species: Mustulus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Accession: S37483
A; Reference number: S37483
A; Reference number: S37483
A; Status: preliminary
A; Accession: S37483
A; Status: preliminary
A; Rolecule type: mRNA
A; Residues: 1-469 < CDC>A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253

Ig gamma-2a chain - mouse

RESULT 2

537483

Ig heavy chain pre	chain		chain		al anti	chain	chain	chain	chain	Ig heavy chain v r	chain	chain	chain	chain	chain
PL0208	A36194	JL0076	PH1483	T01407	PC4202	S04575	S23623	S04576	F29380	PH1499	S03289	JL0077	G2MS43	E29380	A26405
2 PL0208	2 A36194	2 JL0076	2 PH1483	2 T01407	2 PC4202	2 S04575	2 \$23623	2 S04576	2 F29380	2 PH1499	2 \$03289	2 JL0077	1 G2MS43	2 E29380	2 A26405
2	7	~	7	7	7	7	7	7	~	140 2 PH1499	7	~	Н	2	2
136 2 P	140 2 1	141 2	140 2	140 2 7	214 2	140 2	171 2 8	136 2 8	137 2 1	7	117 2	136 2	137 1 (137 2 E	121 2 #
60.2 136 2 P	60.2 140 2 1	60.0 141 2	59.7 140 2 1	59.4 140 2	58.8 214 2 1	58.8 140 2 8	58.3 171 2 8	57.9 136 2 8	57.8 137 2 1	140 2 1	57.6 117 2 8	57.6 136 2	57.6 137 1 (57.4 137 2 E	57.3 121 2 4

ALIGNMENTS

27 121 EGAL DINGQUATIONS	,	Db 61 GQGLEWIGEIYPGSGNSYFNEKFKGKATLIYDKSSSTAYLHLSSLTSEDSAVFCAGPRQ 120	F;1-19/Domain: signal sequence #status predicted <sig>F;20-475/Product: Ig gamma-2b chain #status predicted <mat>F;159-223/Domain: immunoglobulin homology <imm></imm></mat></sig>	c; Nove: this sequence was determined from differentiated year C; Superfamily: immunoglobulin C region; immunoglobulin homology C: Keywords: immunoglobulin	A, Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781	A; Accession: S01321 A; Accession: S01321 A; A; Molecule type: mRNA	A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: S01320; MUID:88329081; PMID:3138116	R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988	C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C;Accession: S01321	Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse)	RESULT 1 S01321	
61 GQGLEWIGEIYPGSGNSYFNEKFKGKATLTVDKSSSTAYLHISSLTSEDSAVYFCAGPRQ	61 GQGLEWIGEIYPGSGNSYFNEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVFCAGPRQ		Query Match 69.6%; Score 568; DB 2; Length 475; Best Local Similarity 71.2%; Pred. No. 1.1e-37; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Qy 1 MECSWVELFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60 1 : :	<pre><mat> ength 475; Indels 2; Gaps CKASCYILTSYNMHWVKQTP 60 </mat></pre>	ne 2; Gaps 2: HurwkgTP 60	1580.1; PID:g51781 tiated gene homology <mat> ength 475; Indels 2; Gaps CKASGYTLTSYNMHWVKQTP 60 </mat>	1580.1; PID:951781 tiated gene homology <mat> ength 475; Indels 2; Gaps CKASGYTLTSYNMHWVKQTP 60 CKASGYTLTSYNMHWVKQRT 60</mat>	A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: S01320; MUID:88329081; PMID:3138116 A; Accession: S01321 A; Molecule type: mRNA A; Residues: 1-475 < DE1> A; Molecule type: mRNA A; Residues: 1-475 < DE1> A; Molecule type: mRNA A; Residues: 1-475 < DE1> A; Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A; Note: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin E; 1-19/Domain: signal sequence #status predicted < SIG> F; 10-75/Product: Ig gamma-2b chain #status predicted < MAT> F; 10-223/Domain: immunoglobulin homology < LNA> C Residues: 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Liliil	F.; Fiers, W. ombinant immunoglobulin 6 1580.1; PID:951781 tiated gene homology <mat> ength 475; Indels 2; Gaps CKASGYTLTSYNMHWVKQTP 60 </mat>	C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C; Accession: S01321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A; Fitle: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: S01320; MUD: 88329081; PMID: 3138116 A; Accession: S01321 A; Mole: mRNA A; Residues: 1-475 < CDE1> A; Cross -references: EMBL:X13188; NID: 951780; PIDN: CAA31580.1; PID: 951781 A; Mote: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Seywords: immunoglobulin C region; immunoglobulin homology C; Seywords: immunoglobulin R\$tatus predicted <sig> F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 2237/Domain: signal sequence #status predicted <mat> F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 19-2237/Domain: immunoglobulin homology <irm> Ouery Match Best Local Similarity 71.2%; Pred. No. 1.1e-37; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; H </irm></mat></mat></mat></mat></sig>	Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Accession: 30-3ep-1989 #sequence_revision 30-sep-1989 #text_change 23-Jul-1999 C;Accession: \$01321 R;de Waacle, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176; 287-295, 1988 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Reference number: \$01320; MUID:88329081; PMID:3138116 A;Reference number: \$01320; MUID:88329081; PMID:3138116 A;Redeasion: \$01321 A;Molecule type: mRNA A;Residues: 1-475 < Cap. A;Cross-references: EMB:X1188; NID:951780; PIDN:CA31580.1; PID:951781 A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin C;Superfamily: immunoglobulin F;1-19/Domain: signal sequence #status predicted <sig> F;20-475/Product: Ig gamma-2b chain #status predicted <mat> F;1-19/Domain: simma-globulin homology <c. <c.="" hom<="" homology="" immunoglobulin="" reywords:="" td=""><td>RESULT 1 501271 19 gamma-2b chain precursor - mouse C; Species: Mus musculus (house mouse) C; Accession: 501321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: 501320; MUID:88329081; PMID:3138116 A; Recession: 501320 A; Molecule type: mRNA A; Residues: 1-475 c.DEl> A; Molecule type: mRNA A; Residues: 1-475 c.DEl> A; Corsos-references: BMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A; Note: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Superfamily: immunoglobulin homology < IMM> C; Ti-19/Nomain: signal sequence *status predicted <sig>F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 159-223/Domain: immunoglobulin homology < IMM> Cquery Match Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Matchi </mat></sig></td></c.></mat></sig>	RESULT 1 501271 19 gamma-2b chain precursor - mouse C; Species: Mus musculus (house mouse) C; Accession: 501321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: 501320; MUID:88329081; PMID:3138116 A; Recession: 501320 A; Molecule type: mRNA A; Residues: 1-475 c.DEl> A; Molecule type: mRNA A; Residues: 1-475 c.DEl> A; Corsos-references: BMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A; Note: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Superfamily: immunoglobulin homology < IMM> C; Ti-19/Nomain: signal sequence *status predicted <sig>F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 159-223/Domain: immunoglobulin homology < IMM> Cquery Match Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Matchi </mat></sig>
61 GOGLEWIGNIFPGNGDTYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW	61 GOGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 	61	Ouery Match 69.6%; Score 568; DB 2; Length 475; Best Local Similarity 71.2%; Pred. No. 1.1e-37; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps Matches 1109; Mismatches 28; Indels 2; Gaps I MECSWYELFLISTTGVHSQAXLYRSGASVMSCKASGYTLTSVNMHWYKQTP 60	<pre><mat> ength 475; Indels 2; Gaps CKASGYTLTSYNMHWVKQTP 60</mat></pre>	tiated gene homology <pre> </pre> <pre> <pre> </pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> </pre> <pre> <pr< td=""><td>1580.1; PID:g51781 tiated gene homology <mat> ength 475; Indels 2; Gaps</mat></td><td>1580.1; PID:951781 tiated gene homology <mat> ength 475; Indels 2; Gaps</mat></td><td>A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: \$01320; MUID:88329081; PMID:3138116 A; Accession: \$01321 A; Molecule type: mRNA A; Residues: 1-475 CDEI. A; Rosidues: 1-475 CDEI. A; Rosidues: 1-475 CDEI. A; Rosidues: 1-475 CDEI. A; Note: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Reywords: immunoglobulin C region; immunoglobulin homology C; Reywords: immunoglobulin R; 1-19/Domain: signal sequence #status predicted <sig> F; 1-19/Domain: signal sequence #status predicted <mat> F; 1-19/Domain: immunoglobulin homology <iman> C; Reywords: immunoglobulin homology <iman> C word Match E; 1-19/Domain: immunoglobulin homology <iman> C word Match C ouery Match C ouery Match C ouery Match C onservative 14; Mismatches 28; Indels 2; Gaps 1; C ouery Matches 109; Conservative 14; Mismatches 28; Indels 2; Caps 1; C output Matches 109; Conservative 14; Mismatches 28; Indels 2; Caps 1; C output Matches 109; Conservative 14; Mismatches 28; Indels 2; Caps 1; C output Matches 109; Conservative 14; Mismatches 28; Indels 2; Caps 1; C output Matches 109; Conservative 14; Mismatches 28; Indels 2; Caps 1; C output Matches 109; Conservative 14; Mismatches 28; Indels 2; Caps 2; C output Matches 28; Indels 20; C output Matches 28; C output Matches 2</iman></iman></iman></mat></sig></td><td>R;de Wacle, P;; Feys, V; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Reference number: \$01320; MUD:88329081; PMID:3138116 A;Reference number: \$01320; MUD:88329081; PMID:3138116 A;Residues: 1-475 < DEL> A;Residues: 1-475 < DEL A;</td><td>C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C; Accession: S01321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Recerence number: S01320; MUID: 88329081; PMID: 3138116 A; Accession: S01321 A; Molecule type: mRNA A; Residues: 1475 Capi. A; Molecule type: mRNA A; Residues: 1475 Capi. A; Mote: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Reywords: immunoglobulin C region; immunoglobulin homology C; Reywords: immunoglobulin homology < IMM> F; 1-19/Domain: signal sequence #status predicted <sig> F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 159-223/Domain: immunoglobulin homology < IMM> Cuery Match Best Local Similarity 71.2%; Pred. No. 1.1e-37; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1;</mat></sig></td><td>Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C;Accession: 501321 R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Reference number: \$01320; MUID:88329081; PMID:3138116 A;Reference number: \$01320; MUID:88329081; PMID:3138116 A;Reference number: \$01320; MUID:88329081; PMID:3138116 A;Residues: 1-475 < CELS A;Residues: 1-475 < CELS A;Residues: 1-475 < CELS A;Residues: Liss sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin homology < Limbol. F;1-19/Domain: signal sequence #status predicted <sig> F;20-475/Product: Ig gamma-2b chain #status predicted <mat> F;159-223/Domain: immunoglobulin homology < LMM> Cuery Match Best Local Similarity 71.2%; Pred. 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1 MEMINITELEGIAGYOSOVOLOGIATARPGASVISCASGYTLISYGISHVKORT 61 GOLEMICNIFPONDDTYNOKFKCKASLTADTSSSTAYMOLSSLTSEDSAVYFCARGNW 61 GOLEMICNIFPONDSTYNOKFKCKASLTADTSSSTAYMOLSSLTSEDSAVYFCARGNW 61 GOLEMIGELYPGSGNSYFNEKFKCKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRO	1 MEMINITELISCHAGVOVOLÖGSABLARPGASVKLSCKASGYTLTSYGISWYKORT 61 GQCLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMOISSLTSEDSAVYFCARGNW	1 61	75; 2; Gaps	<pre><mat> ength 475; Indels 2; Gaps</mat></pre>	tiated gene homology <pre>AMAT> ength 475;</pre> Indels 2; Gaps	1580.1; PID:951781 tiated gene homology <mat> ength 475; Indels 2; Gaps</mat>	1580.1; PID:g51781 tiated gene homology <mat> ength 475; Indels 2; Gaps</mat>	A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Reference number: S01320; MUID:88329081; PMID:3138116 A;Accession: S01321 A;Recession: S01321 A;Recession: S01321 A;Residues: 1-475 < DEI> A;Residues: 1-475 < DEI> A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 C;Reywords: inmunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin F;1.19/Domain: signal sequence #status predicted <amt> F;159-223/Domain: immunoglobulin homology <imma 1.1e-37;="" 109;="" 14;="" 1;<="" 28;="" 2;="" 71.28;="" best="" conservative="" gaps="" guery="" indels="" local="" match="" matches="" mismatches="" no.="" pred.="" query="" similarity="" td=""><td>Ride Waele, Pr.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. 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No. 1.1e-37; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1;</mat></mat></td><td>C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C; Accession: S01321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Blochem. 176, 287-295, 1988 A; Fittle: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: S01320; MUD: 88329081; PMID: 3138116 A; Accession: S01321 A; Molecule type: mRNA A; Residues: 1-475 < CDE1 A; Cross-references: EMBL:X13188; NID: 951780; PIDN: CAA31580.1; PID: 951781 A; Residues: Lius sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin sequence #status predicted <sig>F; 1-19, Pomanin: signal sequence #status predicted <sig>F; 1-19, Pomanin: immunoglobulin homology <imm> Query Match G; Superfamily: 11.28; Pred. 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No. 1.1e-37; Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1;</imm></sig></sig>	Ig gamma-2b chain precursor - mouse C;Species: Nus musculus (house mouse) C;Accession: 801321 R;de Waale, P; F;Feys, V; van de Voorde, A; Molemans, F;Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Ference number: S01320; MUID:88329081; PMID:3138116 A;Reference number: S01320; MUID:88329081; PMID:3138116 A;Residues: 1-475 CDEI> A;Residues: 1-475 CDEI A;Res	RESULT 1 SQ1321 Ig gamma-2b chain precursor - mouse C; Species: Mus musculus (house mouse) C; Date: 30-sep-1889 #sequence_revision 30-sep-1989 #text_change 23-Jul-1999 C; Accession: S01321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. 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1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP	1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCRASGYTLTSYNMHWVRQTP	1 1		F;1-19/Domain: signal sequence #status predicted <sig>F;20-475/Product: Ig gamma-2b chain #status predicted <mat>F;159-223/Domain: immunoglobulin homology <imm></imm></mat></sig>	A Note: Lils sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin E;1-19/Domain: signal sequence #status predicted <sig> F;20-475/Product: Ig gamma-2b chain #status predicted <mat> F;159-223/Domain: immunoglobulin homology <imm></imm></mat></sig>	A; residues: 1-47.5 CLEI. A; residues: 1-47.5 CLEI. A; residues: 1-47.5 CLEI. 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Eur. J. Biochem. 176, 287-295, 1988 A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A.; Molemans are recombinant immunoglobulin directe A; Reference number: S01320; MuID: 88329081; PMID: 3138116 A; Accession: S01321 A; Molecule type: mRNA A; Residues: 1-475 CMEL. A; Accession: S01321 A; Molecule type: mRNA A; Residues: 1-475 CMEL. A; Coss. references: EMBL: X13188; NID: 951780; PIDN: CAA31580.1; PID: 951781 A; Note: this sequence was determined from the differentiated gene C: Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin E; 1-19/Domain: signal sequence #status predicted <sig> F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 159-223/Domain: immunoglobulin homology <imm></imm></mat></sig>	Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C;Accession: S01321 R;de Waeale, P;Feys, V; van de Voorde, A; Molemans, F;Fiers, W. Eur. J. Blochem. 176, 287-295, 1988 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A;Reference number: S01320; MUID:88329081; PMID:3138116 A;Recession: S01321 A;Molecule type: mRNA A;Residues: 1-475 < DELS A;Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781 A;Note: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Seywords: immunoglobulin F;1-19/Domain: signal sequence #status predicted <sig>F;20-475/Product: Ig gamma-2b chain #status predicted <mat> F;159-223/Domain: immunoglobulin homology <imm></imm></mat></sig>	RESULT 1 S01321 Ig gamma-2b chain precursor - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Species: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999 C; Accession: S01321 R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Eur. J. Biochem. 176, 287-295, 1988 A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe A; Reference number: S01320; MUD:88329081; PMID:3138116 A; Accession: S01321 A; Molecule type: mRNA A; Residues: 1475 ADE1 A; Molecule type: mBNA A; Residues: 1475 ADE1 A; Mote: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Reywords: immunoglobulin F; 1-19/Domain: signal sequence #status predicted <mat> F; 20-475/Product: Ig gamma-2b chain #status predicted <mat> F; 159-223/Domain: immunoglobulin homology <imm></imm></mat></mat>

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A Residues: 1-139 cMRNA
A Residues: 1-139 cMRNA
A Residues: 1-139 cMRNA
A Residues: 1-139 cMRNA
B Residues: 1-139 cMRNA
B Residues: 1-130 cMRNA
B Residues: 1-130 cMRNA
C C C COmment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomon
C S Superfamily: immunoglobulin V region; immunoglobulin homology
C Keywords: heteroterramer; immunoglobulin; pyroglutamic acid
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F:34-117/Domain: immunoglobulin homology cIMM>
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic
                                                                                                                               A Residues: 234-251 (KIM>
A; Residues: 234-251 (KIM>
C; Comment: The a allele sequence is shown.
C; Comment: The a minel sequence is shown.
C; Compens: 138/1; 258/1; 368/1
A; Introns: 138/1; 258/1; 36/1
A; Introns: 138/1; 258/1; 36/1
A; Introns: 138/1; 258/1/Region: immunoglobulin homology <IMI>
E; 236-257/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             To heavy chain precursor V region (6A4) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C; Accession: PS0024
R; Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H. Gene 74, 335-345, 1988
A; Title: Cloning and characterization of CDNAs coding for the heavy and light chains A; Reference number: PS0023; MUID:89232725; PMID:3149944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F.281-350/Domain: immunoglobulin homology <IM2>
F.387-454/Domain: immunoglobulin homology <IM3>
F.387-454/Domain: immunoglobulin homology <IM3>
F.387-454/Domain: immunoglobulin homology <IM3>
F.3152/Disulfide bonds: interchain (to light chain) #status predicted
F.364-220, 288-348,394-452/Disulfide bonds: #status predicted
F.324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARG-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYLLTSYNMHWVKQTP 60
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A;Title: 0-glycosylation in hinge region of mouse immunoglobulin G2b A;Reference number: A53598; MUID:94216359; PMID:7512967 A;Accession: A53598 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%; Score 549; DB 2;
llarity 76.3%; Pred. No. 9.5e-37;
Conservative 9; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4.7e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 -NWEGALDYWGQGTSVTVSSAKTTPPPVYPLVPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.6%;
70.8%;
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Matches 109; Conservative
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A; Residues: 138-172, 'P',174-189, 'FP',193-376, 'T',378-474 <TU1>
A; Note: Lys-474 is probably removed posttranslationally
B; Tucker, Pw.; Marcu, R.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, N303-1306, 1979
A; Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogld
A; Reference number: A26232; MUID:80081502; PMID:117549
A; Accession: A26332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 138-161, L',163-189, 'FP',193-474 <YAM>
A; Cross-references: GB:J00461
A; Note: the sequence was determined from the germline gene
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A; Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A; Reference number: A26235, MUID:80081501; PMID:117548
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A;Cross-references: GB:J00461
A;Cross-references: GB:J00461
B;Kin, H.; Yamaguchl, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash J. Bioll. Chem. 269, 12345-12350, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S25057
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mulecule type: mulp: 60120716; PMID: 6766534
A; Concents: a allete
A; Accession: A02157
A; A; Accession: A02157
A; A; Accession: A02157
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C;Date: 31.Mar.1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Date: 31.Mar.1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S25057; A02157; A26235; A26232; A26233; A53598
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific A;Reference number: S25057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
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                                                                                                                                                                                                               Gaps
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R;Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence of A;Reference number: A26233; WUD:82173203; PMID:6803173
A;Contents: b allele
                                                                                                                                                                                                           2;
                                                                                                                                             Length 469
          C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                           26;
                                                                                                                                   Ouery Match 69.0%; Score 563; DB 2;
Best Local Similarity 71.7%; Pred. No. 2.7e-37;
Matches 109; Conservative 15; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qamma-2b chain - mouse
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26; Indels

DB 1;

9

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22; Indels

Length 139;

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C;Accession: $38950
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp A;Reference number: $38950; MUID:94128242; PMID:8297501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: $40295
R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mab735 again A;Reference number: $40295
A;Accession: $40295
                                                                                                                NQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEGALDYWGQGTSVTVSSAK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
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C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Reywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
     1 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY
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A;Molecule type: protein
A;Residues: 1-246 <KLES
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;137-201/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                      121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                                        PYGMDYWGQGTSVTVSSAKTTPPSVYPLAP 150
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78.6%;
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C3 region <CH3>
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TTAPSVYPLAP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S38950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 12
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Matches
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A; Mesidues: 1-151 <CHE>
A; Residues: 1-151 <CHE>
A; Residues: 1-151 <CHE>
A; Residues: 1-151 <CHE>
A; Residues: 1-151 <CHE>
A; Reperimental source: cell line 4C11
C; Comment: This protein is an anti-1dlotypic antibody that induces an anti-phosphorylche
C; Comment: This protein is an anti-1dlotypic antibody that induces an anti-phosphorylche
C; Superfamily: immunoglobulin v region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin homology cinches
F; 20-136/Product: Ig heavy chain v region 4CII #status predicted <MAT>
F; 20-136/Product: Ig heavy chain v region 4CII #status predicted <MAT>
F; 50-54/Region: complementarity-determining 1
F; 69-85/Region: complementarity-determining 3
F; 118-125/Region: complementarity-determining 3
F; 118-125/Region: Complementarity-determining 3
F; 118-125/Region: Complementarity-determining 3
F; 1137-151/Domain: C region (fragment) #status predicted <COR>
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Gene 122, 321-328, 1992
A.Fitle: A general method for chimerization of monoclonal antibodies by inverse polymera
A.Reference number: PNO444; MUID:93138402; PMID:1339379
A.Accession: PNO444
A.Molecule type: mRNA
A.Residues: 1-150 < KAL>
A.Residues: 1-150 < KAL>
A.Residues: 1-150 < KAL>
A.Coss-references: GB:L02346
C.; Superfamily: immunoglobulin V region; immunoglobulin homology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 1922 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
MOI. Immunol. 25, 33-40, 1988
A;Fitle: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-150/Product: Ig heavy chain V region #status predicted <WAT>
F:20-117/Domain: variable region <VRG>
F:34-117/Domain: immunoglobulin homology <IMM>
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69.3%; Pred. No. 1.5e-36;
ive 16; Mismatches 30; Indels
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69.5%; Pred. No. 1.1e-36;
ive 17; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 EGALDYWGQGTSVTVSSAKTTPPPVYPLVPG 151
                            NWEGALDYWGQGTSVTVSS 137
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119
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Best Local S
Matches 104
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Matches 10
                                                                                                                                 RESULT 5
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Length 137;

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64.8%;
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99; Conser
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      Query Match
Best Local Si
Matches 999
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R;Kofler, R.; Strohal, R; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J. Clin. Invest. 82, 852-860, 1988  
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUID:88331394; PMID:3138286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 NIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEGALDYWG 128
                                                                                                                                                                                                                                                                     80 NOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEGALDYWGQGTSVTVSSAK 139
                                                                                                                                                                                                                QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma chain (WM65) - mouse (fragment)
C;Species: Wus musculus (house mouse)
C;Date: 06-Jan.1995 #sequence_revision 06-Jan.1995 #text_change 05-Nov-1999
C;Accession: S29594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 FLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIG
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A; Reference number: S29593
A; Accession: S29594
A; Status: preliminary
A; Molecule type: mRNA
A; Mesidues: 1-178 <SEX>
A; Cross references: EMBL: X57857; NID: 952590; PIDN: CAA40992.1; PID: 952591
C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M20831; NID:g196949; PIDN:AAA38848.1; PID:g196950 CS:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;34-117/Domain: immunoglobulin homology <IMA>
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted F;132/Disulfide bonds: interchain (to light chain) #status predicted F;224,227,229/Disulfide bonds: interchain #status predicted F;224,27/Rinding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                           Length 446;
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                                                                                        65.9%; Score 537.5; DB 2; 78.6%; Pred. No. 2.7e-35; Wiematches 16;
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68.1%; Pred. No. 2.3e-35;
iive 21; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain precursor V region (BXW16) - mouse C; Species: Mus musculus (house mouse)
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Best Local Similarity 68.1%
Matches 98; Conservative
                                                                                                                                                 Conservative
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A; Residues: 1-137 <KOF>
                                                                                                         Query Match
Best Local Simi
Matches 103;
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A;Title: Hypermutation is observed only in antibody H chain V region transgenes that
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A; Residues: 1-140 <SIM>
A; Residues: 1-140 <SIM>
A; Cross-references: GB:J00493; NID:g195006; PIDN:AAA38128.1; PID:g195007
A; Experimental source: strain A/J, hybridoma 93G7
R; Siekevitz, M.; Gefter, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
Eur. J. Immunol: 12, 1023-1032, 1982
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C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 22-Jun-1999
C;Accession: A94264; A91261; A02028
R;Sims, J; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, Science 216, 309-311, 1982
A;Title: Somatic mutation in genes for the variable portion of the immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Glusti, A.M.; Manser, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PH1482 Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
Score 529; DB 2;
Pred: No. 3.6e-35;
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                                                             Conservative 17; Mismatches
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63.3%;
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R, Glusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
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Best Local Similarity 71.65
Matches 101; Conservative
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                              134
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0012
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kleber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988 #142863; PMID:3125424
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0012
A;Molecule type: mRNA
A;Residues: 1-166 cCHE>
A;Residues: 1-166 cCHE>
A;Residues: 1-166 cCHE>
A;Residues: 1-166 cCHE>
C;Comment: This protein is an anti-idiotypic antibody which induces an anti-phosphorylc; C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-32/Domain: signal sequence #status predicted cSIG>
F;33-151/Forduct: Ig heavy chain V region 4C11 #status predicted cMAT>
F;47-130/Domain: immunoglobulin homology cIMM>
F;63-67/Region: complementarity-determining 1
F;82-98/Region: complementarity-determining 2
F;82-98/Region: complementarity-determining 2
F;82-98/Region: complementarity-determining 2
F;82-98/Region: complementarity-determining 2
                                                                             A; Molecule type: DNA
A; Residues: 20.76, 'TK', 79-118, 'V', 120-125, 'Y', 127-134, 'T', 136-140 <SIE>
A; Residues: 20.76, 'TK', 79-118, 'V', 120-125, 'Y', 127-134, 'T', 136-140 <SIE>
A; Cross-references: GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:g196202
A; Experimental source: strain AJJ, hybridoma 36-65
A; Note: the sequence was determined from the differentiated gene
A; Note: from analysis of the sizes of several other differentiated genes that hybridize
  dominant anti-arsonate idiotype
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                                                                                                                                                                                                                                                                                          C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; hybidoma; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted
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A;Title: The genetic basis of antibody production: the A;Reference number: A91261; MUID:83131846; PMID:6186498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 523.5; DB 1;
; Pred. No. 1e-34;
14; Mismatches 22;
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; Pred. No. 1.2e-34;
14; Mismatches 34;
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121 YGGSYDFDYWGQGTPLTVSS 140
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67.8%;
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F;152-166/Domain: C
                                                 A; Accession: A91261
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Best Local 3
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Ig heavy chain precursor V-D-J region (6-19) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 23-Jul-1999
C;Accession: A39276
R;Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990
A;Title: Cryoglobulinemia induced by a murine 1gG3 rheumatoid factor: skin vasculitis A;Reference number: A39276; MUID:91088540; PMID:2263605
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                A; Title: Hypermutation is observed only in antibody H chain V region transgenes that d for somatic mutation.
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                                                                                                                                                                    Ig heavy chain V region (clone X41-2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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A;Cross-references: GB:M55312; NID:g196002; PIDN:AAA63337.1; PID:g196003
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <INM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: hybridoma cell
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 34-117/Domain: immunoglobulin homology <IMM>
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A;Reference number: PH1482; MUID:93171820; PMID:8436910
A;Accession: PH1489
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
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8.2e-34;
ches 20;
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Pred. No. 3.6e-34;
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71.6%; Pred. No. 8.2e.
ive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Mismatches
FGNSLDYWGOGTSVNVSSAKTTPPSVYPLAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 YGGSYYFDYWGQGTTLTVSS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 EGA---LDYWGQGTSVTVSS 137
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119 NWEGA--LDYWGQGTSVTVSS 137

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120 WEGALDYWGQGTSVTVSSAKTTPPPVYPLVPG 151

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Search completed: August 30, 2003, 22:08:53 Job time : 18.4832 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 30, 2003, 19:57:10 ; Search time 10.7819 Seconds (without alignments) 667.331 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-08-836-455-4 816 1 MECSWVFLFLLSITTGVHSQ.....TVSSAKTTPPPVYPLVPGSL 153

Scoring table:

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mus musc	P01751 mus musculu	P01755 mus musculu	P06327 mus musculu	P01747 mus musculu	mus	snm 6	P01750 mus musculu		P01748 mus musculu	75	P06328 mus musculu	P01759 mus musculu	P01745 mus musculu	P01756 mus musculu	P01757 mus musculu	snu	P06330 mus musculu	a	homod	homo	homo	mus m	P01783 mus musculu	rattu	homo	P01768 homo sapien	mus m	homo	4 homo	I mus m	0 mus m	P01772 homo sapien
SUMMARIES	ID	HV02_MOUSE	HV07_MOUSE	HV11_MOUSE	HV52_MOUSE	HV03_MOUSE	HV14_MOUSE	HV05_MOUSE	HV06_MOUSE	HV48_MOUSE	HV04_MOUSE	HV09_MOUSE	HV49_MOUSE	HV15_MOUSE	HV01_MOUSE	HV12_MOUSE	HV13_MOUSE	HV10_MOUSE	HV51_MOUSE	HV50_MOUSE		HV1B_HUMAN	HV1C_HUMAN	HV00_MOUSE		HV01_RAT	HV3J_HUMAN	HV3G_HUMAN	HV43_MOUSE	HV1A_HUMAN	HV3C_HUMAN	HV41_MOUSE	HV40_MOUSE	HV3K_HUMAN
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	Score	23	493	470	4	459.5	458	451	44			4	430	429.5	426.5	425.5	421.5	418	417	416	389	388	375	342	333	321.5	308.5	308		301.5	301	300.5	299	299
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HV42_MOUSE	HV37_MOUSE	HV38_MOUSE	HV3L_HUMAN	HV05_CARAU	HV3U_HUMAN	HV3H_HUMAN	HV39_MOUSE	HV3B_HUMAN	HV3T_HUMAN	HV26_MOUSE	HV35_MOUSE
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											285 3

ALIGNMENTS

	ALIGNMENTS
RESULT HV02_M ID H	HVO2_MOUSE HVO2_MOUSE STANDARD; PRT; 140 AA.
A E E	21-JUL-1986 (Rel. 01, Created)
I D	15-SEP-2003 (Rel. 42, Last annotation update)
OS	Ig heavy chain V region 93G7 precursor. Mus musculus (Mouse).
88	Chordata; Craniata; Vertebrata; Euteleost
88	Матта!ia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
RN	[1]
7 X	
RX	12818; PubMed=6801765;
& &	STAINS J., KADDILLS I.H., ESLESS F., STAUGHLET C., TUCKET F.W., Capra J.D.;
RT	"Somatic mutation in genes for the variable portion of the
RI	immunoglobulin heavy chain.";
를 당	Science 210:309-311(1962). -!- SIMILARITY: Contains 1 immunoqlobulin-like domain.
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88	use by non-profit institutions as long as its content is in no way
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ပ္ပင္ပ	entities requires a license agreement (See http://www.lsb-sib.ch/announce/
3 5	Of Send an ellant to itcenseersb-sib.cn).
2 g	128
DR	PIR; A94264; HVMSG7.
DR	
DR.	IPR007110;
ž :	IPR003006;
אַ ב <u>ַ</u>	INCEPTIO; IFKNOW3590; IG_V.
Z Z	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
3 5	Immunoglobulin V region; Hybridoma; Signal.
- E	CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT	N 20 139 IG-LIKE.
F. S	NON_TER 140 140 SEOUENCE 140 AA: 15514 MW: 25A4CBBE31DASCE8 CRC64:
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ž ř	Query Marcn Best Local Similarity 72 1%: Pred No 1 9e-40:
×	1; Conservative 1
Qy	1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
QQ	1 MGWSFIFLELLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60
Qy	61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120

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                                                                                                                                                                                                                                                                                            "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                HYBRIDOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                        Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                       L 44:62-53/(1981),
MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDON
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAVY CHAIN V REGION B1-8/186-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.4%; Score 493; DB 1; Length 139; 69.1%; Pred. No. 1e-37; ive 15; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY - DETERMINING-1.
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15419 MW; 1B57DD4FD0C9F465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1A6U; 27-MAY-98.
PDB; 1A6W; 15-UUL-98.
InterPro: IPR00110; 1g-like.
InterPro: IPR00306; 1g_MHC.
InterPro: IPR00306; 1g_W.
SMART; 2000407; 1g; 1.
SMART; PS500406; 1Gv; 1.
PR0STTE; PS50835; 1G_LIKE; 1.
Immunoglobulin V region; Signal; 3D-structure.
                                                                                                                       101751; P01752;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region B1-8/186-2 precursor.
                                                                                                               139 AA
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JH2 SEGMENT.
BY SIMILARITY.
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                                                                                                                PRT;
                                              121 YGGSYDFDYWGQGTPLTVSS 140
                                                                                                                                                                                                                                                 STRAIN=C57BL/6;
MEDLINE=81234548; Pubmed=6788376;
                                 121 EGA---LDYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00529; AAA38170.1; -. PIR; A90809; MHMS18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96; Conservative
                                                                                                               STANDARD;
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139 AA;
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                                                                                                                                                                                                                                                                                    Baltimore D.;
                                                                                                               HV07_MOUSE
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SEQUENCE
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Matches 9
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                        GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMOISSLTSEDSAVYFCARGNW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCLL 24:025-03/(1981).
-!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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pred. No. 1.2e-35;
3; Mismatches 33; Indels
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                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                137 AA
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JH2 SEGMEN
                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region S43 precursor.
                                                                                                                                                                                                                                                                  PRT;
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PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                              121 EGA -- LDYWGQGTSVTVSS 137
                                                                                                                       PIR; A02038; GMK843.
HSSP, P01810; 2FBJ.
INDERPO; DFR007110; Ig-like.
InterPro; IPR007105; Ig-MHC.
InterPro; IPR003596; Ig_WHC.
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137
137 AA;
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SMART; SM00406: TC...
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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21-JUL-1986
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P01755;
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HV11_MOUSE
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64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 WVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 EWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IG HEAVY CHAIN V REGION VH558 A1/A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-85099340; Pubmed-2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12971 MW; 8B0BC138856DFC9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 461; DB 1;
Pred. No. 6.5e-35;
                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
119 heavy chain V region VH558 Al/A4 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Æ.
                                                                                                   117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                   PRT;
                                                                                                                                                                                                                                                     unrearranged VH gene segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V region; Signal.
                                                121 GRYFDYWGOGTTLTVSS 137
                              121 EGALDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 1. SMART; SM00406; 1Gv; 1. PROSITE; PS50835; 1G_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                              EMBL; M13787; AAA38499.1; -. PIR; A02029; HVMSA1. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87; Conservative
                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                              Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 II7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                  HV52_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV03_MOUSE
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ID HV03_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGGLEWIGNIFPGNGDTYYNQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYNEK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 FKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEGA---LDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
Marshak-Rothstein A.;
"The genetic basis of antibody production: the dominant anti-arsonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              idiotype response of the strain A mouse.";

Eur. J. Immunol. 12:1023-1032(1982).

-!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER

DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS

CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME SEGMENT, JH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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-- SIMILARITY: Contains 1 .immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13307 MW; FF04E4A167B654AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
HSSP; P01789; 1MCP.
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75.4%; Pred. No. 9.1e-35;
11ve 10; Mismatches 16;
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21-JUL-1986 (Rel. 01, Last sequence update)
22-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region 108A precursor.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pram; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=83131846; PubMed=6186498;
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MEDLINE-81245215; Pubmed-6789211;
                                                                                                          Ig heavy chain V region 36-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity 75.4%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Query Match
Best Local Similarity
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SEQUENCE
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entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGMSWIFLFLLSGTAGVHSEVQLQQSGPELVKPGASVKISCKASGYTFTDYNMHWVKQSH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Heavy chain variable region contribution to the NPD family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).

-i- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG HEAVY CHAIN V REGION 108A. IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.1%; Score 458; DB 1; 74.4%; Pred. No. 1.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
pheavy chain V region 3 precursor.
IGH-VU558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 74.4%; Pred. No. 1.2e-
Matches 87; Conservative 11; Mismatches
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MEDLINE-81234548; Pubmed=6788376;
                                                                                                                                  HSSP, PO1810; 2FBJ.
HSSP, PO1810; 2FBJ.
MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 1g; 1.
SMART: SM0406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                           EMBL; J00488; AAA38519.1;
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                                                                                                                           PIR; A02041; HVMS8A.
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                                                                                                                                                                                                                                                                                 InterPro; IPR(
Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HV05_MOUSE
P01749;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGGLEWIGNIYPSDSETHYNQKEKDKATLTVDKSSSTAYMQLSSLTSEDSAVXYCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baltimore D.;
"Heavy chain variable region contribution to the NPb family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
cell 24:625-637(1981).
-1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID*10090;
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                                                                                                                                                                                                                                                                                                                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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                                                                                                                                                         COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG HEAVY CHAIN V REGION 102.
                                                                                                                                                                                                                                                                                                                                                                                    19; Indels
                                                                                                         IG HEAVY CHAIN V REGION 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12867 MW; 740A65DD851FCA8C CRC64;
                                                                                                                                                                                                                                                                                            13016 MW; 427C861C53975EDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 446; DB 1;
Pred. No. 1.5e-33;
                                                                                                                                                                                                                                                                                                                                       Score 451; DB 1;
Pred. No. 5.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last Sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V region 102 precursor.
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BY SIMILARITY.
                                                                                                                                                                                                                                                  BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK-2
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                                                                                                                                                                                                                             FRAMEWORK-3
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HSSP: P01810; 2FbJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig_WHC.
Ffam; PR00047; ig; 1.
SMART; SM00406; IGv.1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=81234548; PubMed-6788376;
Pfam; PF00047; ig; 1.
SMART; SM00406; 1GV; 1.
PROSTTE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                         55.3%;
73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.78;
74.18;
                                                                                                                                                                                                                                                                                                                                                            Local Similarity 73.5
les 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
117 AA;
                                                                                                                                                                                                                                                                                            117 AA;
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20
20
50
55
69
86
41
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HSSP, P01810; ZFBJ.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                      PIR; A02030; HVMS23.
                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV09_MOUSE
P01753; P11271;
                                                                                                                     STRAIN-C57BL/6
                                                                                                                                                    Baltimore D.;
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NON_TER
SEQUENCE
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                   1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCA 116
                                                                          1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
 Gaps
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-84248078; PubMed-6429663;
Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                     "Illegitimate recombination generates a class switch from C mu to C delta in an IgD-secreting plasmacytoma.";
PIR. A02033, HWRST,
HSSP; P01801, 2FBJ,
InterPro; IPR0031010; Ig-like.
InterPro; IPR003596; Ig_MC.
                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG HEAVY CHAIN V REGION TEPC 1017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 445.5; DB 1; Length 138;
; Pred. No. 1.9e-33;
19; Mismatches 28; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING - 1.
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9; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15576 MW; 748157E4C6907B8E CRC64;
                                                                                                                                                           23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AA.
                                                                                                                                          138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-1
                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1.
SWART; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.6%;
62.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88; Conservative
                                                                                                                                          STANDARD;
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138
138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                              Fucker P.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
HV04_MOUSE
ID HV04_MOUSE
                                                                                                                                       HV48_MOUSE
P03980;
86;
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DOMAIN
DISULFID
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region.";
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                                                                                                                                                Mús musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 186-1 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6;
MEDLINE-81234548; PubMed=6788376;
Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 54.3%; Score 443; DB 1; Length 117; 1 Similarity 72.6%; Pred. No. 2.7e-33; 85; Conservative 9; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12772 MW; C530F829C906F69B CRC64;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region 23 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; · 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 1g; 1. SMART; SM0406; 1Gv; 1. SMO81E; PS00305; 1G_LKE; 1. Immunoglobulin V region; Signal.
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Immunoqlobulin V region; Signal.
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NON_TER
SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ell 24:625-637(1981).
1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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MEDLINE=85699340; PubMed=2578321;
Yancopoulos G.D., Alt F.W.;
"Developmentally controlled and tissue-specific expression of unrearranged VH gene segments.";
Cell 40:271-281(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 440; DB 1; Length 117;
Pred. No. 5e-33;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                HEAVY CHAIN V REGION 186-1.
                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                12890 MW; 16191A088CB17F5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN.1988 (Rel. 06, Created)
01-JAN.1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
pleavy chain V region VH558 B4 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.9%; Scor. 72.6%; Pred. No. oc. 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
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                                                                                                                                                                                                                            Immunoglobulin V region; Signal.
                                                                                              InterPro; IPR007110; 19-11ke.
InterPro; IPR003006; 1g_MHC.
InterPro; IPR003596; 1g_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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HSSP; P01810; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M13788; AAA38506.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                               HVMS61.
                                                                                                                                                                                                                                                                                                                                                                                                                              117 AA;
                                                          PIR; D90809; HVMS6
HSSP; P01810; 2FBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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DISULFID
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                                                                                                                                                                                                                                                                        1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                  1 MGWSCIMLFLAATATGVHSPVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-8222222; Pubmed-6806821;
Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
Blattner F.R.;
                                                                                                                                                                                                                                                                                         0; · Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Simultaneous expression of immunoglobulin mu and delta heavy chains by a cloned B-cell lymphoma: a single copy of the VH gene is shared by two adjacent CH genes."; Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mús musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
B4
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                                                                                                                                                                                                                                         ; Score 430; DB 1; Length 117;
; Pred. No. 4e-32;
10; Mismatches 24; Indels
                                               COMPLEMENTARITY-DETERMINING-1.
IG HEAVY CHAIN V REGION VH558
                                                                                               COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IG HEAVY CHAIN V REGION BCL1 IG-LIKE.
                                                                                                                                                                                            12834 MW; B8862FAC67ABD345 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6827CFBC6DB3F35E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
25-SEP-2003 (Rel. 42, Last annotation update)
1g heavy chain V region BCL1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AA
                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 429.5;
                                                                                                                        FRAMEWORK - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 1g; 1. 5-7. SMART; SM00406; IGV; 1. 7. FROSITE; PS50835; IG_LIKE; 1. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15078 MW;
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HSSP, P01772; 2FB4.
InterPro; IPR007110;
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
                                                                                                                                                                                                                                            52.7%;
70.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J00494; AAA38130.1; -.
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                                                                                                                                                                                                                                                                                         83; Conservative
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136
1117
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68
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1117
1117
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117
117 AA;
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136 AA;
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P01759;
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Matches
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Job time
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                                                                                                          61 GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR--G 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCARGIYINSSPYFDSWGQGTTLTVS 120
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                                                                                                                         Zakut R., Cohen J., Givol D.;
Nucleic Acids Res. 8:4839-4840(1980).
-!- MISCELLANBOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
FROM A MYELOMA THAT SECRETES IGG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-81053741; Pubmed-6253904;
Zakut R., Cohen J., Givol D.;
"Cloning acquence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11.";
Nucleic Acids Res. 8:3591-3601(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.3%; Score 426.5; DB 1; Length 121; 68.6%; Pred. No. 8.6e-32; ive 14; Mismatches 21; Indels 3
    5.3e-32;
~hes 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A93708; GVMS11.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MPC 11.
                                                                                                                                                                                                                                                                  121 AA
          Pred. No. 5.3e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IG-LIKE.
                                                                                                                                                                                61.2%; Fit
                                                                                                                                                                 NWEGALDYWGQGTSVTVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SNART; SN00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; 19-11ke.
InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_v.
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                        Conservative
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
        Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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P01745;
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                                                                                                                                                                119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain constant region domains.";
Biochemistry 21:5415-5424 (1982).
-!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                          21-JUL-1986 (Rel. 01, Created)
15-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region MOPC 104E.
Ig heavy chains (Mouse).
Eukaryocalus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                  Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
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BY SIMILARITY.
N-LINKED (GLCNAC. . .) (COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                'Complete amino acid sequence of a mouse mu chain: homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
PIR; A02039; MHMS4E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE=83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.1%; Score 425.5; DB 70.3%; Pred. No. 1e-31; ive 13; Mismatches
117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART: SMO406; IGY: 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
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  STANDARD;
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SEQUENCE
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earch completed: August 30, 2003, 22:04:35 ob time : 11.7819 secs

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August 30, 2003, 21:05:00 ; Search time 36.453 Seconds (without alignments) 1083.094 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-08-836-455-4 816 1 MECSWVFLFLLSITTGVHSQ......TVSSAKTTPPPVYPLVPGSL 153

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:* sp_mhc:*
sp_organelle:*
sp_bhage:*
sp_plant:*
sp_rodent:*
sp_virus:* sp_mammal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_vertebrate:*
sp_unclassified:*
sp_urvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

			musculu	musculu	musculu	musculu	musculu	musculu	musculu	mnscnlu	musculu	musculu	musculu	musculu	musculu	mnsculu	
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Descript	094814	0991c4	099125	08vdc9	08vcx7	091wt1	Q8r3h6	0921k1	08k172	08vcx4	099131	0924q1	Q8k0z4	Q8vcv5	091wr1	Q8k0f2	
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£	Q9D8L4	099LC4	099L25	08VDC9	Q8VCX7	091WT1	Q8R3H6	Q921K1	Q8K172	Q8VCX4	Q99L31	092401	Q8K0Z4	Q8VCV5	Q91WR1	Q8K0F2	
90	11	Ξ	11	11	11	11	11	11	11	11	11	11	. 11	11	11	11	
Length	473	463	473	168	613	481	474	278	482	489	468	142	480	481	488	488	
Query	72.2	71.2	69.7	67.3	66.7	64.5	64.3	63.8	63.8	63.3	63.2	62.1	61.2	9.09	60.4	59.9	
Score	589.5	581	269	549.5	544	526.5	524.5	521	521	516.5	515.5	506.5	499	494.5	493	489	
Result No.	-	7	m	4	S	9	7	60	6	10	11	12	13	14	15	16	
		Score Match Length DB ID Description 589.5 72.2 473 11 09DBL4 mus	Query Score Match Length DB ID Description 589.5 72.2 473 11 Q9DEL4 Q9d814 mus 581 71.2 463 11 Q99LC4 Q99LC4 mus	Query Score Match Length DB ID Description 589.5 72.2 473 11 Q9DBL4 Q9dB14 Mus 581 71.2 463 11 Q99LC4 Q991C4 Mus 569 69.7 473 11 Q99L25 Q99125 Mus	Query Query Description Score Match Length DB ID Description 589.5 72.2 473 11 Q9DBL4 Q9dB14 mus 581 71.2 463 11 Q99LC4 Q99LC4 Mus 569 69.7 473 11 Q9DLC5 Q99LC4 mus 569 69.7 473 11 Q9DLC5 Q9QLC5 mus 549.5 67.7 488 11 Q8VDC9 mus Q8VdC9 mus	Score Match Length DB ID Description 589.5 72.2 473 11 Q9DBL4 Q991C4 Q991C4 mus 581 71.2 463 11 Q99LC4 Q991C4 mus 569 69.7 473 11 Q99L25 Q99LC4 mus 569 69.7 473 11 Q99L25 Q99LC4 mus 549.5 67.3 168 11 Q89CC9 Q8VCZ7 mus	Query Score Match Length DB ID Description 589.5 72.2 473 11 090BL4 094BL4 094BL4 099BL4 099BL4 099BL4 089BL4 089BL4 089BL4 089BL4 089BL4 089BL4 089BL4 08BL4 08BL4 08BL4 0BBL4 1BBL4 1BBL4<	Score Match Length DB ID 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092L1K1 092L1K1	Score Match Length DB ID Description 589.5 72.2 473 11 09DBL4 0991L4 0991L4 mus 581 71.2 463 11 09DL24 0991L4 0991L4 0991L4 mus 589.5 67.3 11 099L25 0991L5 0991L5 mus 549.5 67.3 168 11 089LC9 0991L5 mus 526.5 64.5 481 11 091LWT1 091LWT1 091LWT1 mus 524.5 64.3 474 11 081R3H6 091LWT1 mus 521 63.8 482 11 081LX1 0921K1 0931K1 mus 521 63.8 482 11 081LX1 088K172 mus 516.5 63.3 489 11 084CX4 088CX4 mus	Query Query Description 589.5 72.2 473 11 Q9DBL4 Q9dB14 mus 581 71.2 473 11 Q9DLC4 Q9D1C4 Q991L5 mus 569.5 69.7 473 11 Q99LC4 Q991L5 mus 569.5 67.3 168 11 Q9VC5 Q89LC5 Mus 544 66.7 613 11 Q8VC7 Q8VCX7 Q8VCX7 Mus 526.5 64.5 481 11 Q8VCX7 Q8VCX7 Mus 521 63.8 278 11 Q921K1 Q921K1 Mus 521 63.8 482 11 Q8K172 Q8K172 Q8K172 516.5 63.2 469 11 Q94CX4 Q8VCX4 Q8VCX4 515.5 63.2 468 11 Q94CX4 Q8VCX4 Q8VCX4 615.5 63.3 468 11 Q94CX4 Q8VCX4 Q8VCX4 </td <td>Query Query B ID Description 589.5 72.2 473 11 Q9DBL4 Q9dB14 Q9dB14 Q9dB14 Q9dB14 Q9dB14 Q9B1C4 QBCC7 QBCC7<td>Score Match Length DB ID Description 589.5 72.2 473 11 09DBL4 099124 099124 mus 581 71.2 463 11 09DL24 099124 099124 mus 586 69.7 473 11 09BL25 099125 099125 mus 544 66.7 613 11 08VDC9 08VCX 08VCX mus 526.5 64.3 474 11 08VCX 091WT1 091WT1 mus 521 64.3 474 11 08R3H6 0991XI mus 521 63.8 482 11 08VCX 08172 mus 515.5 63.2 468 11 08VCX 08VCX 08VCX mus 515.5 63.2 468 11 099L31 08VCX 089CX4 mus 506.5 62.1 142 11 09241 mus 506.5 62.1 142 11 09241 mus 506.5 62.1 142 11 09244 mus</td><td>Score Query Description 589.5 72.2 473 11 Q9DBL4 Q9dB14 Wuss 581 71.2 473 11 Q9DLC4 Q9dB14 Mus 549.5 67.3 16 11 Q9DLC4 Q99125 Wuss 549.5 67.3 16 11 Q9VC25 Q99125 Wuss 526.5 64.5 481 11 Q9VC27 Q8VCx7 Wuss 521.6 481 11 Q9VCX7 Q91ArL Wuss 521.6 482 11 Q91X71 Q8VX4 Wuss 521.6 482 11 Q91X71 Q8VX4 Wuss 515.5 63.2 468 11 Q99LX1 Q8VX4 Wuss 515.5 63.2 468 11 Q99L31 Wuss 506.5 62.1 142 11 Q8CA4 Wuss 494.5 60.6 480 11 Q8CA4 Wuss <td>Query Query 589.5 72.2 473 11 Q9DBL4 Q9dB14 mus 581 71.2 463 11 Q9DL25 Q94124 mus 569.7 473 11 Q9DL25 Q99125 mus 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099125 mus 544 66.7 613 11 08VDC9 08VCX 08VCX mus 526.5 64.3 474 11 08VCX 091WT1 091WT1 mus 521 64.3 474 11 08R3H6 0991XI mus 521 63.8 482 11 08VCX 08172 mus 515.5 63.2 468 11 08VCX 08VCX 08VCX mus 515.5 63.2 468 11 099L31 08VCX 089CX4 mus 506.5 62.1 142 11 09241 mus 506.5 62.1 142 11 09241 mus 506.5 62.1 142 11 09244 mus</td> <td>Score Query Description 589.5 72.2 473 11 Q9DBL4 Q9dB14 Wuss 581 71.2 473 11 Q9DLC4 Q9dB14 Mus 549.5 67.3 16 11 Q9DLC4 Q99125 Wuss 549.5 67.3 16 11 Q9VC25 Q99125 Wuss 526.5 64.5 481 11 Q9VC27 Q8VCx7 Wuss 521.6 481 11 Q9VCX7 Q91ArL Wuss 521.6 482 11 Q91X71 Q8VX4 Wuss 521.6 482 11 Q91X71 Q8VX4 Wuss 515.5 63.2 468 11 Q99LX1 Q8VX4 Wuss 515.5 63.2 468 11 Q99L31 Wuss 506.5 62.1 142 11 Q8CA4 Wuss 494.5 60.6 480 11 Q8CA4 Wuss <td>Query Query 589.5 72.2 473 11 Q9DBL4 Q9dB14 mus 581 71.2 463 11 Q9DL25 Q94124 mus 569.7 473 11 Q9DL25 Q99125 mus 549.5 67.3 168 11 Q9DL25 Q99125 mus 526.5 64.5 481 11 Q8VCZ9 Q8VCX7 mus 526.5 64.3 474 11 Q8VCX7 Q91X41 mus 521 63.8 278 11 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481 11 09WTT 091Wt1 08VCX7 08VCX7 08VCX7 08VCX7 08VCX7 08VCX7 08VCX7 08VCX4 08T3h6 08VCX7 08VCX4 08VCX4 08VCX4 08VCX4 091Wt1 08VCX4 091Xt1 08VCX4 08VCX4 091Xt1 08VCX4 08VCX4

0924r0 mus musculu 0914r4 mus musculu 0924r4 mus musculu 0924r1 mus musculu 0924r1 mus musculu 0924r1 mus musculu 0924g mus musculu 0924g mus musculu 0924q mus musculu 0924q mus musculu 0924r6 mus musculu 091va2 mus musculu 094qf mus musculu 094qf mus musculu 094qf mus musculu 094qf mus musculu	
0924R0 091WT3 0924R4 0924R4 0924R1 0924Q3 0924Q3 0924Q9 0924Q9 0924R8 0924R8 0924R8 0924R8 0924R8 0924R8 0924R8 0924R8	Q96GA6 Q9QXE9 Q924P5
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11112222222222222222222222222222222222	444

ALIGNMENTS

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Sembi P.;
                       Q99L25
Q99L25;
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 RESULT 3
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            099125
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                                                                                                                                                                                                                 61 GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMOISSLTSEDSAVYFCARGNW 120
                                                                                                                                                                                                                              61 GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID=10090;
                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                      DB 11; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 463;
                                                                                                                                             24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.2%; Score 581; DB 11; Length 4 70.8%; Pred. No. 1.1e-46; ive 16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Straubberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC00342, AAM03435.1;
HSSP; P01842; 7FAB.
MGD; MGI:96446; 1gh-4.
InterPro; IPR007110; 1g-1ike.
InterPro; IPR003006; 1g_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intertro, ..., 19; 4.

Pfam; PF000406; Ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
      InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003966; Ig_V.
Ffam; PF0047; Ig; 4.
SWART; SW00406; IGV; 1.
PROSITE; PS008296; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 18100660009 gene.
                                                                                                                   ; Score 589.5; DB 1
; Pred. No. 1.8e-47;
13; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EG--ALDYWGQGTSVTVSSAKTTPPPVYPLVPGS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YSYDLFAYWGQGTLVTVSAAKTTPPSVYPLAPGS 154
                                                                                                                                                                                                                                                              E-GALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                                                                                         463 AA
                                                                                                                    72.28;
74.88;
                                                                                                                                           Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 70.8
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
MGI:96443; Igh-1.
                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             121
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                                                                                                                      Query Match
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SOR DE RESERVA
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61 GOGLEWIGNIFPGNGDTYYNOKFKGKASLTADTSSSTAYMOISSLTSEDSAVYFCARGNW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 13, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to Rikes cDNA 1810060009 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 473;
                                                                                                                                                                                                                  Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; --
HSSP; P01842; FTAB.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003596; Ig_wv.
Ffam; PF00047; Ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS050835; IG_LIKE; 4.
PROSITE; PS050835; IG_LIKE; 4.
SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c; Chernajovsky Y.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Targeting r cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJ416332; CAC94867.1; -.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
2a (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.7%; Score 569; DB 11;
69.2%; Pred. No. 1.6e-45;
ive 16; Mismatches 21;
473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 69.2%
Matches 110; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                         Similarity
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                Strausberg R.;
                                                                                                                   rissue=colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R
                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8R3H6
Q8R3H6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
Q8R3H6
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                                                                                                     1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                            Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 66.7%; Score 544; DB 11; Length 6 al Similarity 69.5%; Pred. No. 5.1e-43; 105; Conservative 17; Mismatches 25; Indels
                                                         67.3%; Score 549.5; DB 11; Length
69.5%; Pred. No. 3e-44;
iive 16; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC048315, AAH18315.1;
MGD; MGI:96448; Igh-6.
InterPro; IRR007110; Ig-11ke.
InterPro; IRR003006; Ig_MHC.
InterPro; IRR003506; Ig_MHC.
                                    SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41A9384DD4C22862 CRC64;
                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 67.9 kDa protein.
                                                                                                                                                                                               120 WEGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                             119 NWEGALDYWGQGTSVTVSSAKTTPPPVYPLV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RW--YFDVWGAGTTVTVSSESQSFPNVFPLV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 AA.
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           il protein.
613 AA; 67855 MW;
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG_LIKE; 1.
NON TER 168 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
                                                         Query Match 67.37
Best Local Similarity 69.55
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 1g; 5.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches 10
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Q91WT1;
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Q8VCX7
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AC 09
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65 EWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCAR-GNWEGA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 WVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length 481;
                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC013490; ARH13490.1; -
INTERPROPTIO: IPR007110; Ig-11ke.
INTERPROPTIO: IPR003006; Ig_MHC.
INTERPROPTIO: IPR003596; Ig_MC.
Pfam: PF00047; ig; 4.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC025447; AAH25447.1; ...
InterPro; IPR001345; CytC_heme_bind.
InterPro; IPR007110; I9_like.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 1.
HYPOTHE: LOAD POTE-ID.
SEQUENCE: 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DMAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothei.cal 52.1 kpa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 51.7 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 526.5; DB 1 Pred. No. 1.7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 LDYWGQGTSVTVSSAKTTPPPVYPL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 FDYWGQGTTLTVSSEPAREPTIYPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 2.
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Matches 101; Conservative
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
SMART; SM00407; Ig; 4.
SMART; SM00407; IGc1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Cre
01-MAR-2002 (TrEMBLrel. 20, Las
001-MAR-2003 (TrEMBLrel. 23, Las
Hypothetical 53.2 kDa protein.
IGH-VJ558 OR AI893585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 4
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 64.54
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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BC028249;
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                                                                                                                                                      66 WIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW--EGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLE 65
                                MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_FaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Unknown (Frotein for MGC:18977).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012207; AAH12207.1; -.
InterPro: IPR007110; Ig-11ke.
InterPro: IPR007110; Ig-20.4.
InterPro: IPR007596; Ig_w.
InterPro: IPR0047; 19; 2.
SMART; SMO046; IGv. 1.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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QBK172;
QBC07-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to expressed sequence AI893585.
                                                                                                                                                                                                                                                                                                             WEGALDYWGQGTSVTVSSAKTTPPPVYPLVPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 LDYWGQGTSVTVSSAKTTPPPVYPLVP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.8%
Best Local Similarity 69.4%
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q921K1
Q921K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                           1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.3%; Score 516.5; DB 11; Length 489; 64.5%; Pred. No. 1.5e-40; ive 18; Mismatches 30; Indels 7;
                                                                                           Length 482;
                                                                                                                                            35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018322; AAH18322.1; -. MGD; MGI:96486; Igh-VJ558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 protein.
489 Aa; 53208 MW; CC85B1194DAFEF2C CRC64;
PROSITE; PS50855; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 RGNWEGALD---YWGOGTSVTVSSAKTTPPPVYPL 148
                                                                                             63.8%; Score 521; DB 11;
68.2%; Pred. No. 5.7e-41;
iive 12; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                            121 EGALDYWGQGTSVTVSSAKTTPPPVYPL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    489
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EMBL; BC029188; AAH29188.1; -
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
 SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 142
NON_TER 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003597; 19_c1.
InterPro; IPR003006; 1g_MHC.
InterPro; IPR003596; 1g_V.
Pfam; PP00047; ic: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 65.3%;
                                                                                                                98; Conservative
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                          140 TTPPPVYPLV 149
                                                                                                                                                                                                                                                                                     120 OSFPNVFPLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00409; IG; 3.
SMART; SM00407; IGc1; 3
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
TISSUE-Breast tumor;
                                                                                                  Similarity
                                                                                   Query Match'
Best Local S:
Matches 98,
                                                          SEQUENCE
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Q8VCV5
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  S FF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MECSWVFLFLLSITTGVHSQAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kozono Y., Kozono H., Azuma T.;
"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
"Direct Estimation of Relative Affinity Reveals
Affinity Maturation of B Cell Antigen Receptors in Response to (4-
Hydroxy-3-Nitrophenyl)Acetyl (NP).";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB069913; BAB63929.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_W.
PF00047; ig; 1.
                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%; Score 515.5; DB 11; Length
64.2%; Pred. No. 1.8e-40;
ive 23; Mismatches 30; Indels
                                                                                                                                                                                                                                         Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003878; AAH03878.1; -.
INTER-PROPERTY: IPRO7110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                       SWARY; SMO0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02401;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Similar to RIKEN cDNA 1810060009 gene.
. 121 RGNYDGSLAWFVYWGQGTLVTVSAEPAREPTIYPL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 WEGALDYWGQGTSVTVSSAKTTPPPVYPLVP 150
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01-JUN-2001 (TrEMBLrel. 17, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Last
V23-D-J-C mu protein (Fragment).
V23-D-J-C MU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             97; Conservative
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                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 19; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Best Local S
                                                                   Q99L31
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Q924Q1
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                                         RESULT 11
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80 NOKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNWEGALDYWGQGTSVTVSSAK 139
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                                                                                                                                          20 QAYLQQSGAELVRSGASVKMSCKASGYTLTSYNMHWVKQTPGQGLEWIGNIFPGNGDTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TTEMBLrel. 22, Created)
01-OCT-2002 (TTEMBLrel. 22, Last sequence update)
01-MAR-2003 (TTEMBLrel. 23, Last sequence update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                        DB 11; Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32; Indels
                                                                              22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS5025; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
SROUTENCE 480 AA; 51645 MW; 8690A63C669CDBED CRC64;
142 AA; 15622 MW; 24A265CE4EA4318B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 499; DB 11;
; Pred. No. 6.8e-39;
18; Mismatches 32;
                                      62.1%; Score 506.5; DB 1
75.4%; Pred. No. 2.8e-40;
iive 9; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYWGQGTSVTVSSAKTTPPPVYPL-VPGSL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AYWGQGTLVTVSAESARNPTIYPLTLPPAL 153
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GQGLEWIGNIFPGNGDTYYNQKFKGKASLTADTSSSTAYMQISSLTSEDSAVYFCARGNW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 60.6%; Score 494.5; DB 11; Length 481; Similarity 63.2%; Pred. No. 1.8e-38; 98; Conservative 21; Mismatches 33; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strougherg R.;
Strougherg R.;
Strougherg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC01359; AAH13539.1;
MGJ:96486; Igh-V1558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al protein.
481 AA; 52326 MW; 52B44C5826807143 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 AA; 52964 MW; F12068460B400B9D CRC64;
                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EGA-LDYWGQGTSVTVSSAKTTPPPVYPL-VPGSL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 YGAWFAFWGQGTLVTVSAESARNPTIYPLTLPPAL 154
481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 AA
                                                       01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last seq
01-WAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical 53.0 kba protein.
IGH-VJ558 OR AI893585.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; 19; 4.
SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                          Hypothetical 52.3 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, BC018455, AAH18455.1; -
Interpro; IPR007110; 19-11ke,
Interpro; IPR003006; 19_MHC.
Interpro; IPR003596; 19_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
SEQUENCE 48
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SEQUENCE 41
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                         Gaps
                         8;
 Length 488;
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60.4%; Score 493; DB 11;
61.3%; Pred. No. 2.6e-38;
live 24; Mismatches 28;
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